

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	167	194	1005	100
# contigs (>= 5000 bp)	96	75	39	79
# contigs (>= 10000 bp)	77	33	3	54
# contigs (>= 25000 bp)	33	4	0	29
# contigs (>= 50000 bp)	9	3	0	15
Total length (>= 1000 bp)	2748778	1248170	2052446	2554722
Total length (>= 5000 bp)	2591549	962321	264184	2502690
Total length (>= 10000 bp)	2452218	642060	40723	2321693
Total length (>= 25000 bp)	1770744	225714	0	1899742
Total length (>= 50000 bp)	902174	191765	0	1381985
# contigs	201	252	2072	121
Largest contig	210768	74833	17296	179778
Total length	2773123	1287977	2799762	2570231
Reference length	5442925	5442925	5442925	5442925
GC (%)	43.00	43.15	42.60	43.13
Reference GC (%)	42.70	42.70	42.70	42.70
N50	37957	9929	1638	52102
NG50	1561	-	539	-
N75	16413	4997	965	23429
L50	21	34	491	14
LG50	145	-	1922	-
L75	49	76	1054	31
# misassemblies	65	41	15	71
# misassembled contigs	25	20	5	21
Misassembled contigs length	739106	224359	44802	1102777
# local misassemblies	16	50	8	26
# structural variations	4	2	1	2
# unaligned contigs	0 + 18 part	0 + 9 part	0 + 4 part	0 + 14 part
Unaligned length	645702	159148	3323	489696
Genome fraction (%)	37.455	19.551	51.044	34.816
Duplication ratio	1.044	1.061	1.007	1.098
# N's per 100 kbp	14.60	590.31	29.97	30.39
# mismatches per 100 kbp	578.67	583.37	473.14	568.97
# indels per 100 kbp	28.60	22.18	10.83	22.80
Largest alignment	117419	59123	12799	70161
NA50	13020	6909	1622	15854
NGA50	-	-	535	-
NA75	-	1833	956	-
LA50	51	55	501	43
LGA50	-	-	1947	-
LA75	-	141	1069	-

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	65	41	15	71
# relocations	62	40	15	70
# translocations	0	0	0	0
# inversions	3	1	0	1
# possibly misassembled contigs	20	10	4	31
# misassembled contigs	25	20	5	21
Misassembled contigs length	739106	224359	44802	1102777
# local misassemblies	16	50	8	26
# structural variations	4	2	1	2
# mismatches	11797	6208	13145	10782
# indels	583	236	301	432
# short indels	520	219	282	390
# long indels	63	17	19	42
Indels length	1698	682	564	1513

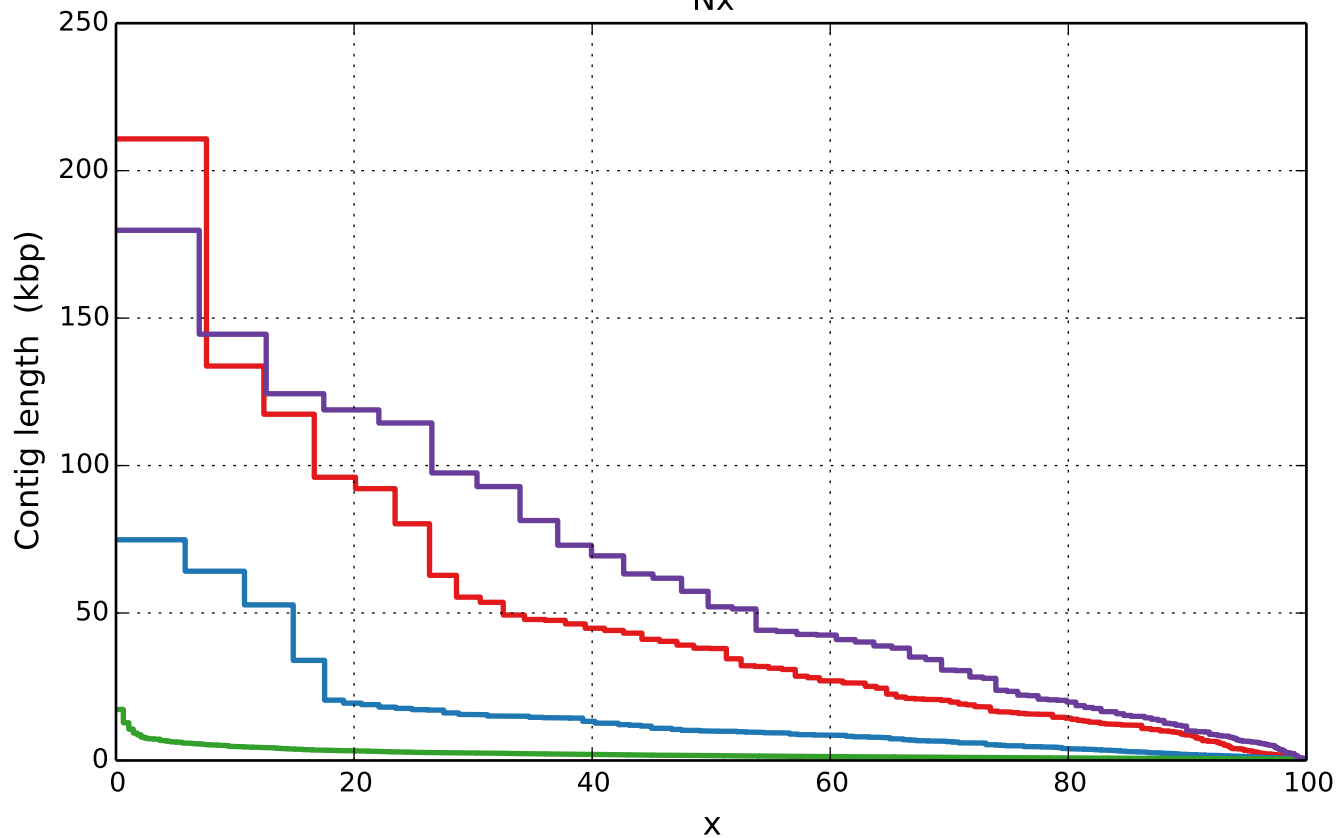
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	18	9	4	14
# with misassembly	4	1	3	5
# both parts are significant	5	2	2	13
Partially unaligned length	645702	159148	3323	489696
# N's	405	7603	839	781

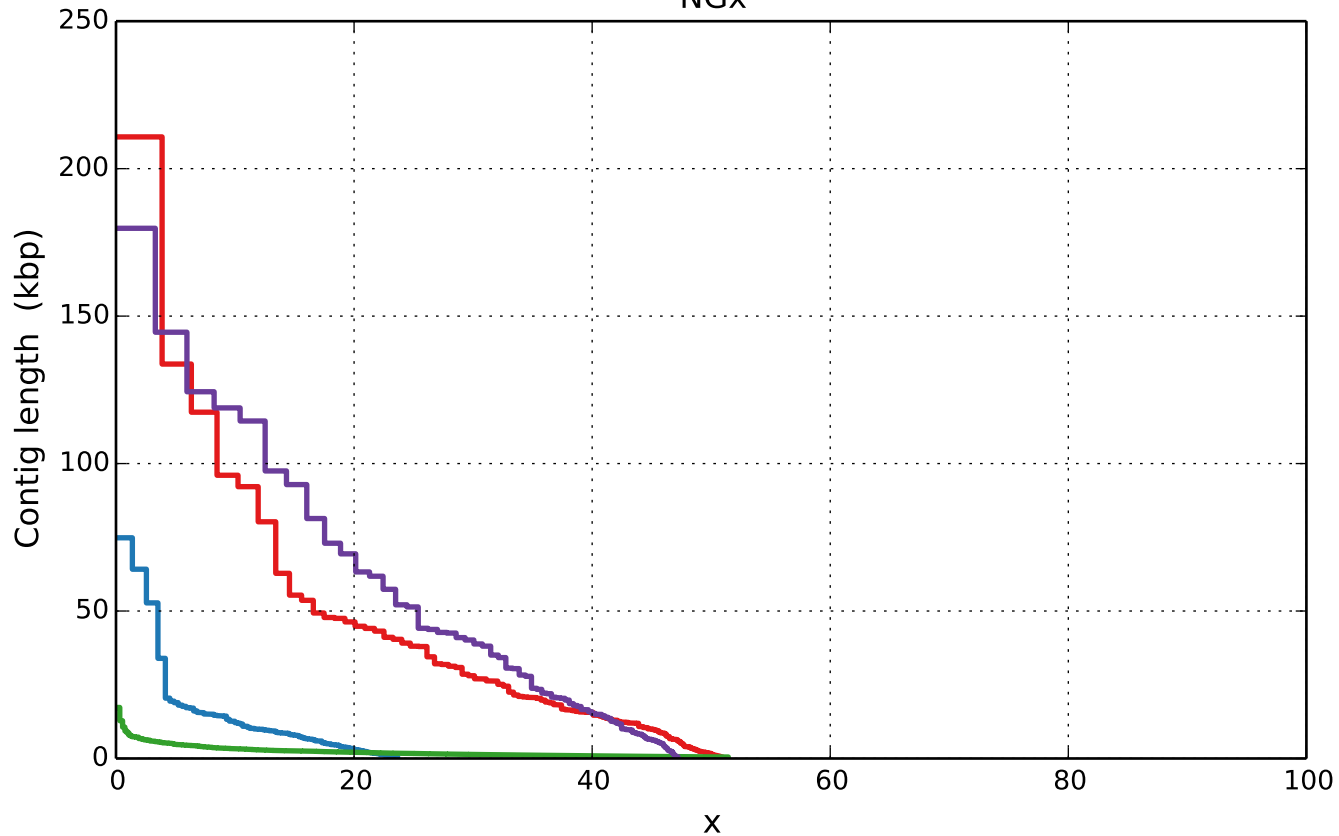
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray

NGx

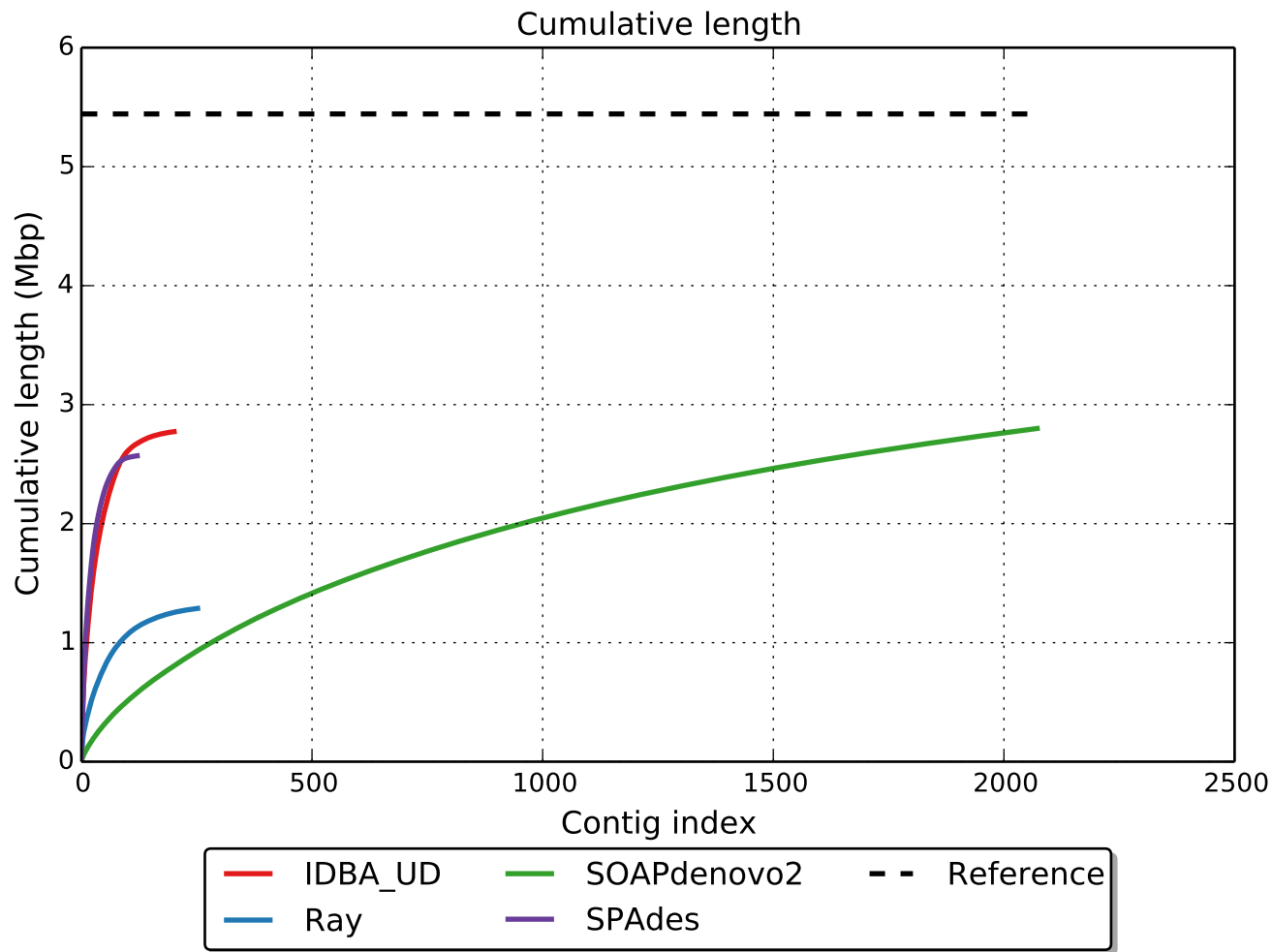


IDBA\_UD

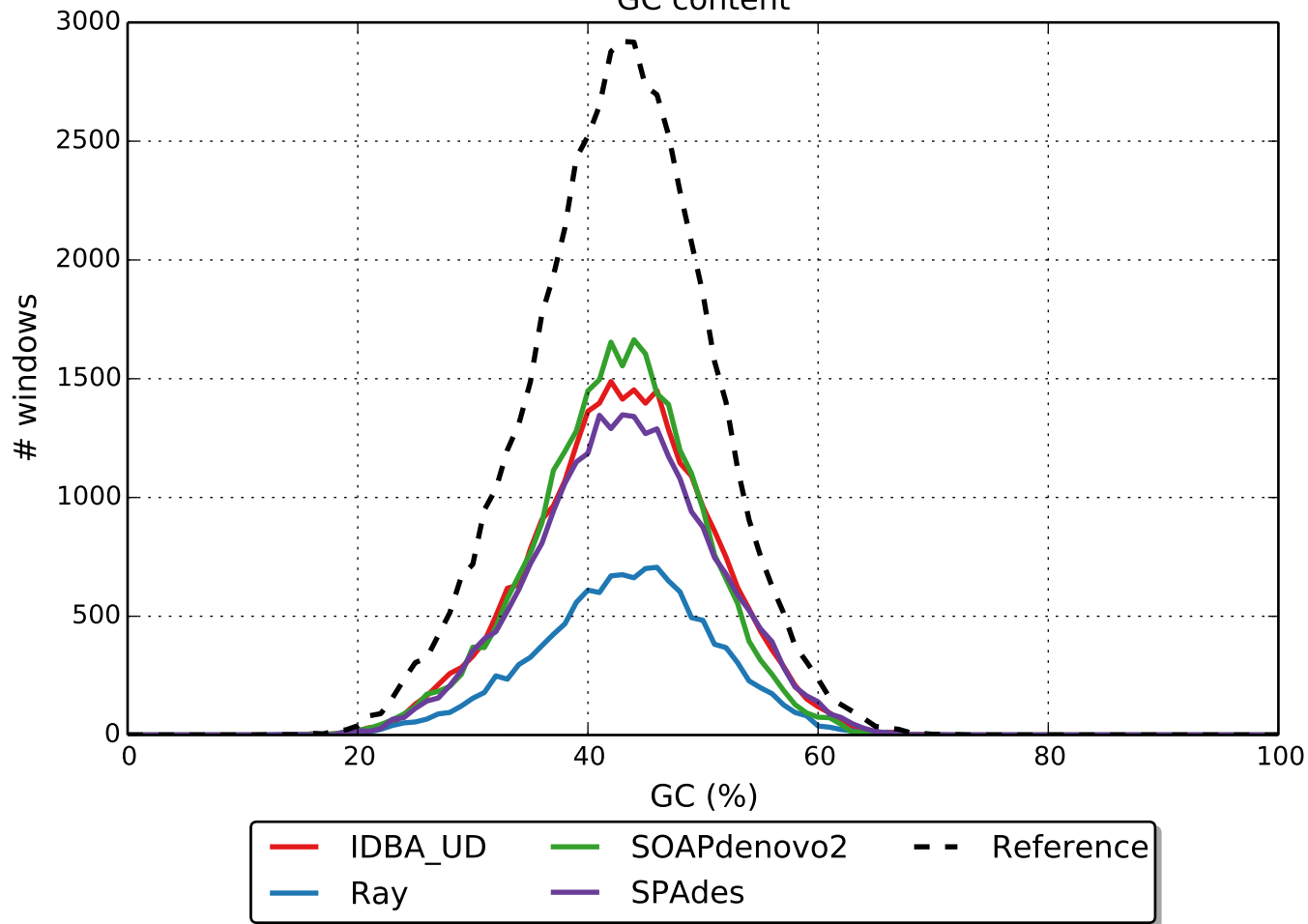
SOAPdenovo2

SPAdes

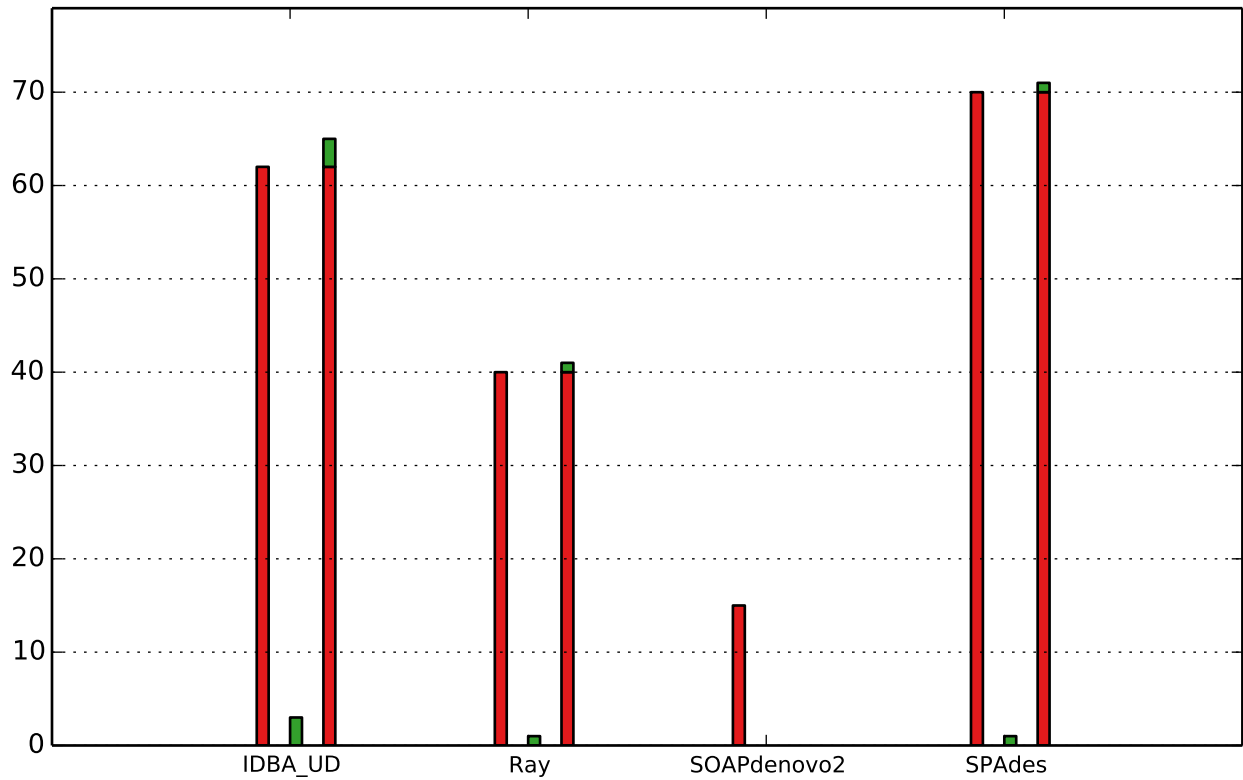
Ray



GC content



# Misassemblies

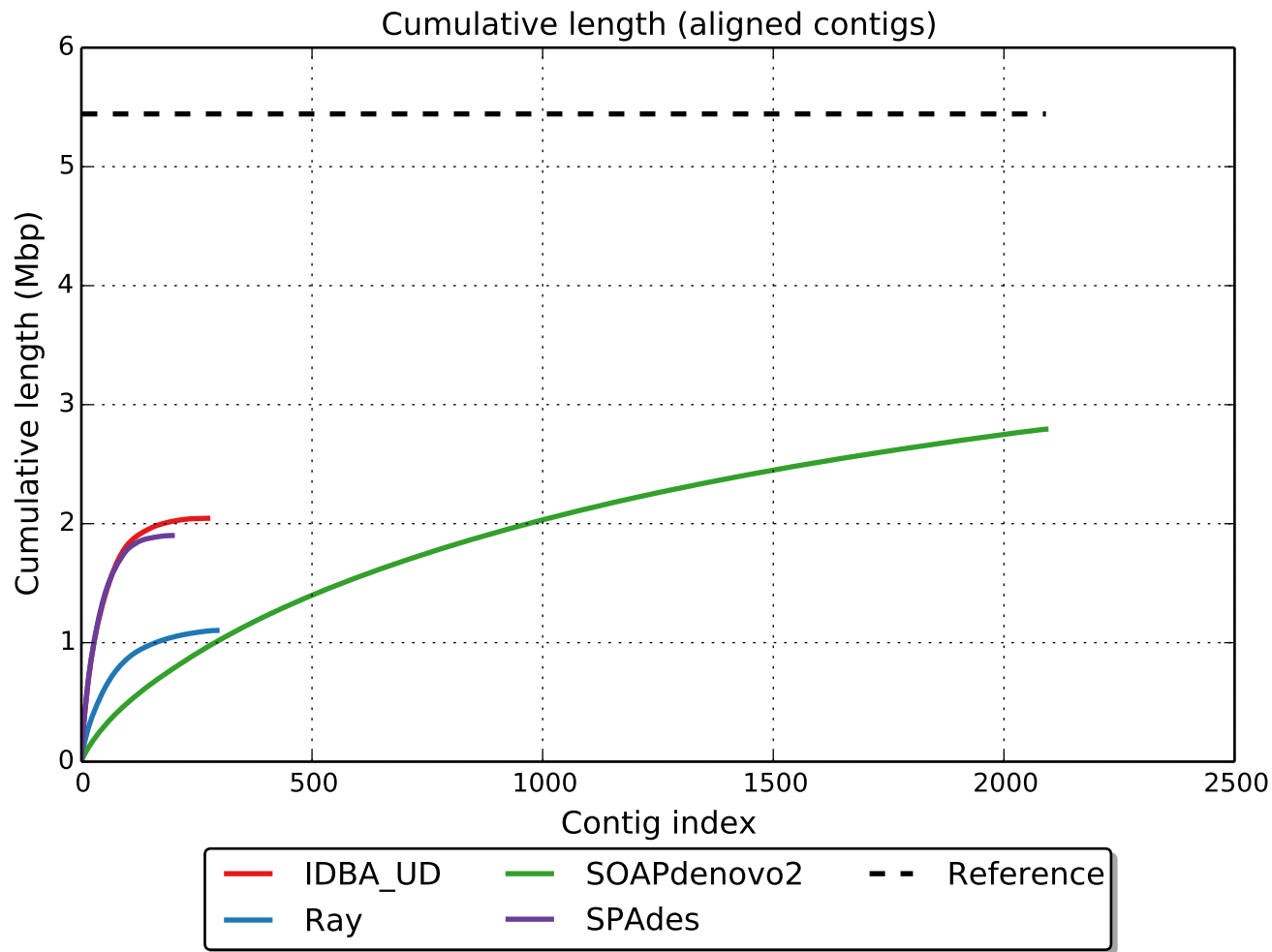


# relocations

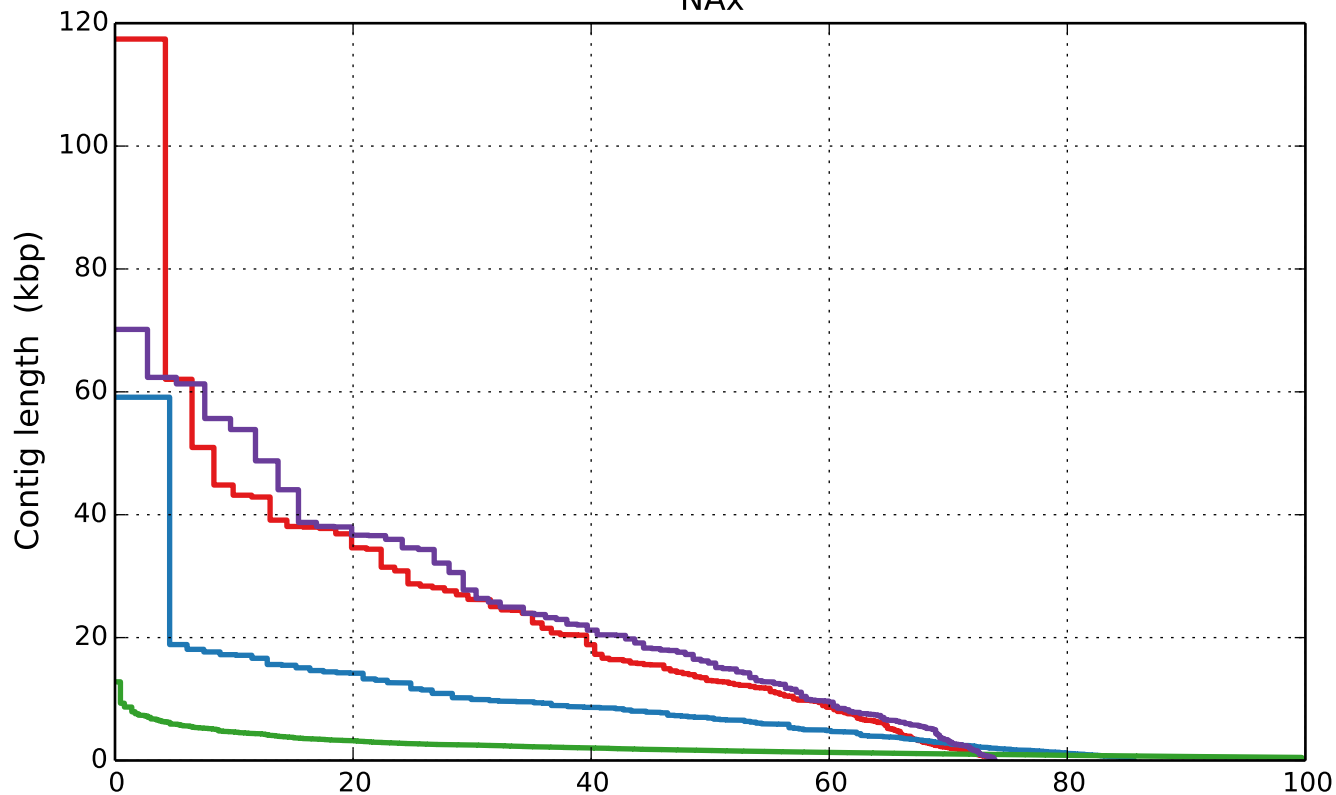


# inversions





NAx



# NGAx

