

## Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	952	77	139	1020
# contigs (>= 5000 bp)	91	25	1	127
# contigs (>= 10000 bp)	45	9	0	40
# contigs (>= 25000 bp)	30	4	0	18
# contigs (>= 50000 bp)	16	0	0	9
Total length (>= 1000 bp)	3971789	449017	216937	3732206
Total length (>= 5000 bp)	2319385	328948	6242	1817127
Total length (>= 10000 bp)	2014531	218743	0	1243893
Total length (>= 25000 bp)	1789085	150912	0	894182
Total length (>= 50000 bp)	1339152	0	0	613452
# contigs	1650	104	1005	1508
Largest contig	146287	44072	6242	106702
Total length	4484330	467299	799108	4085904
Reference length	4143550	4143550	4143550	4143550
GC (%)	42.73	43.00	41.39	42.65
Reference GC (%)	42.41	42.41	42.41	42.41
N50	5422	9519	764	4162
NG50	9188	-	-	4073
N75	1722	4317	608	1930
NG75	2135	-	-	1863
L50	77	11	351	178
LG50	51	-	-	185
L75	484	30	644	545
LG75	351	-	-	568
# misassemblies	36	3	12	35
# misassembled contigs	33	3	10	28
Misassembled contigs length	72686	14824	8916	86278
# local misassemblies	48	21	1289	48
# structural variations	18	1	3	17
# unaligned contigs	0 + 542 part	0 + 48 part	0 + 199 part	0 + 752 part
Unaligned length	2502471	295744	106847	2032518
Genome fraction (%)	46.739	3.522	14.425	47.498
Duplication ratio	1.023	1.176	1.158	1.043
# N's per 100 kbp	253.91	2064.20	10247.80	1152.74
# mismatches per 100 kbp	1110.84	1319.79	1128.78	1294.54
# indels per 100 kbp	56.23	52.76	22.08	80.53
Largest alignment	9933	9721	4753	15733
NA50	-	-	541	-
NGA50	-	-	-	-
LA50	-	-	492	-

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	36	3	12	35
# relocations	32	3	12	35
# translocations	0	0	0	0
# inversions	4	0	0	0
# possibly misassembled contigs	144	20	15	285
# misassembled contigs	33	3	10	28
Misassembled contigs length	72686	14824	8916	86278
# local misassemblies	48	21	1289	48
# structural variations	18	1	3	17
# mismatches	21513	1926	6747	25478
# indels	1089	77	132	1585
# short indels	934	70	124	1236
# long indels	155	7	8	349
Indels length	3667	218	335	6815

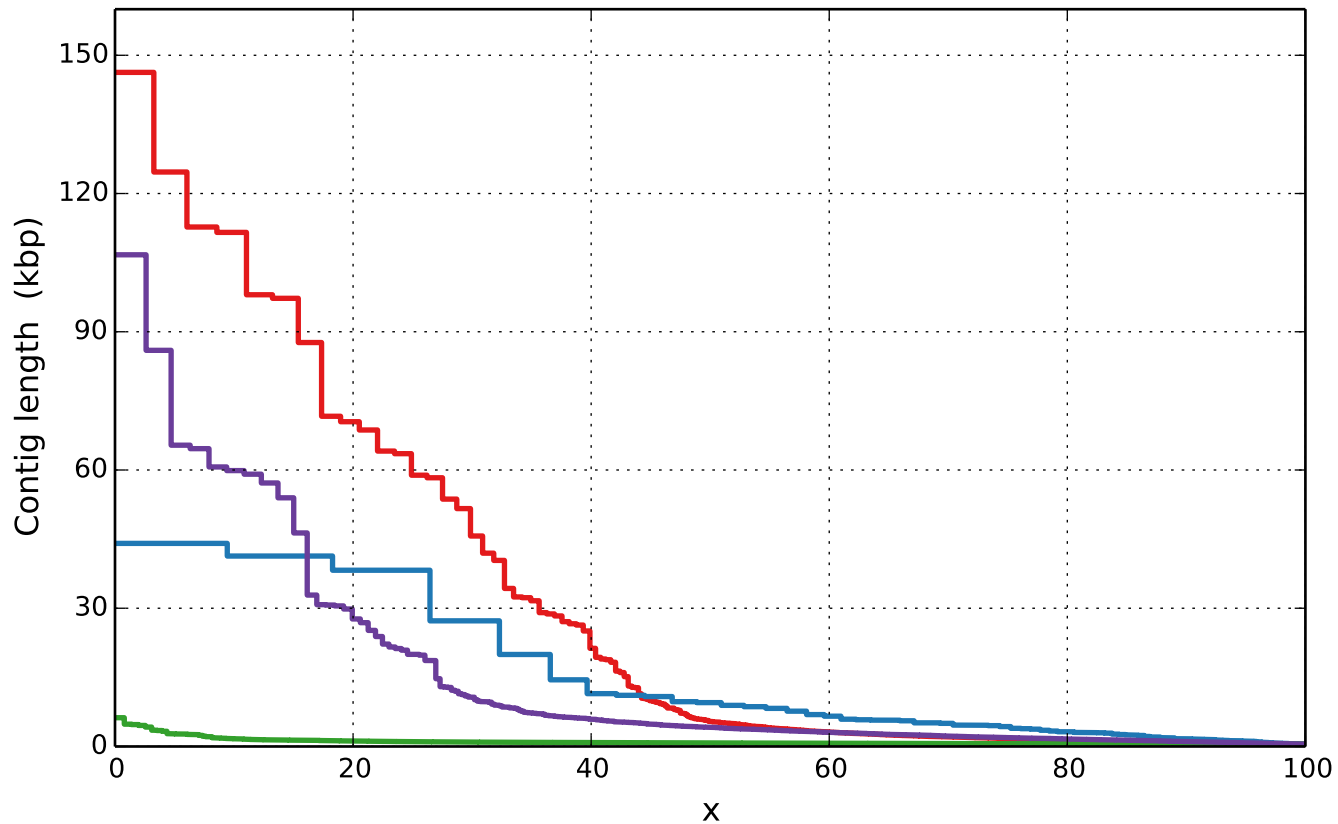
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	542	48	199	752
# with misassembly	32	6	67	37
# both parts are significant	133	13	8	252
Partially unaligned length	2502471	295744	106847	2032518
# N's	11386	9646	81891	47100

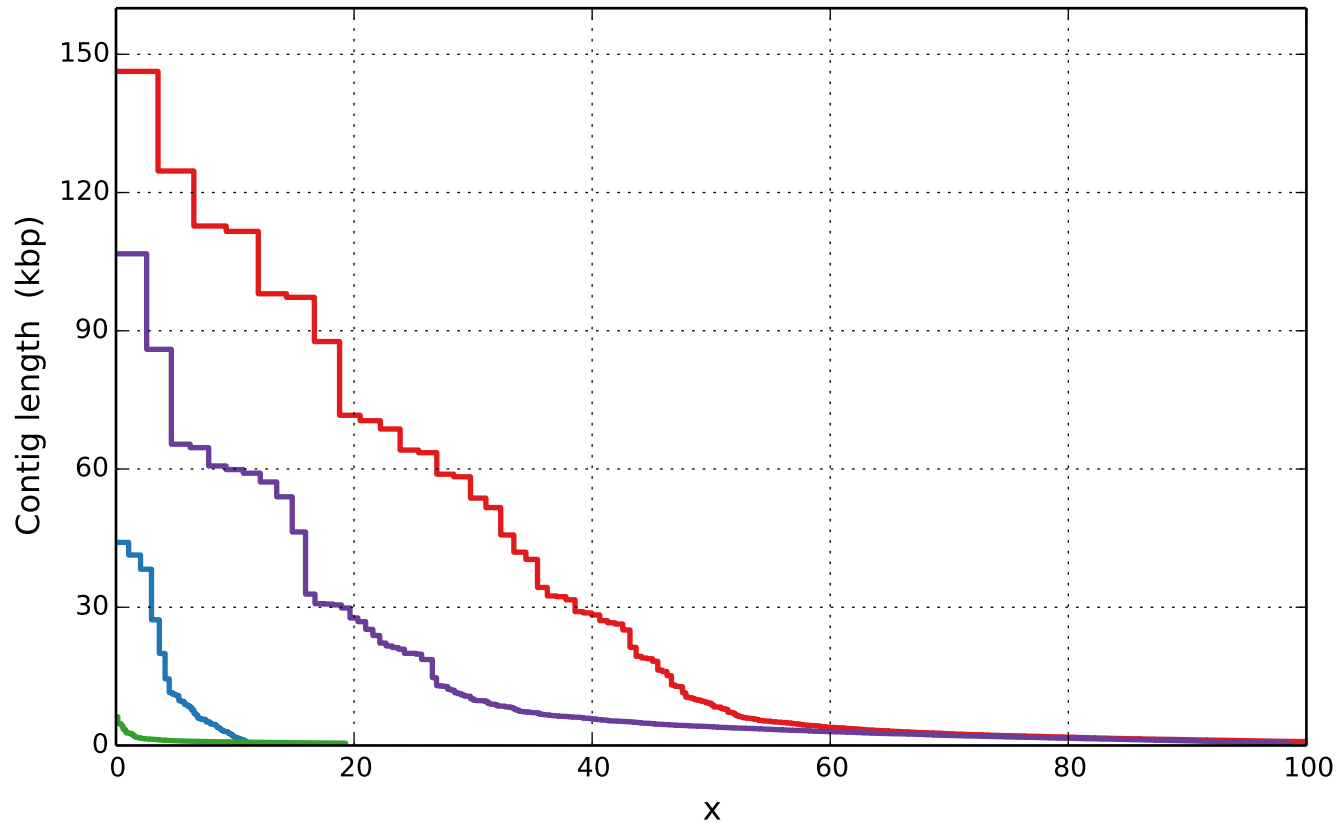
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

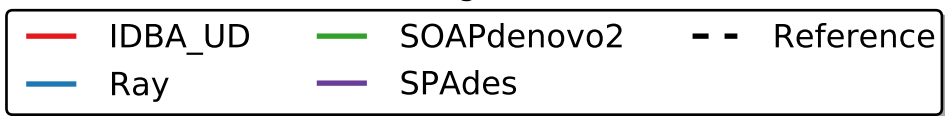
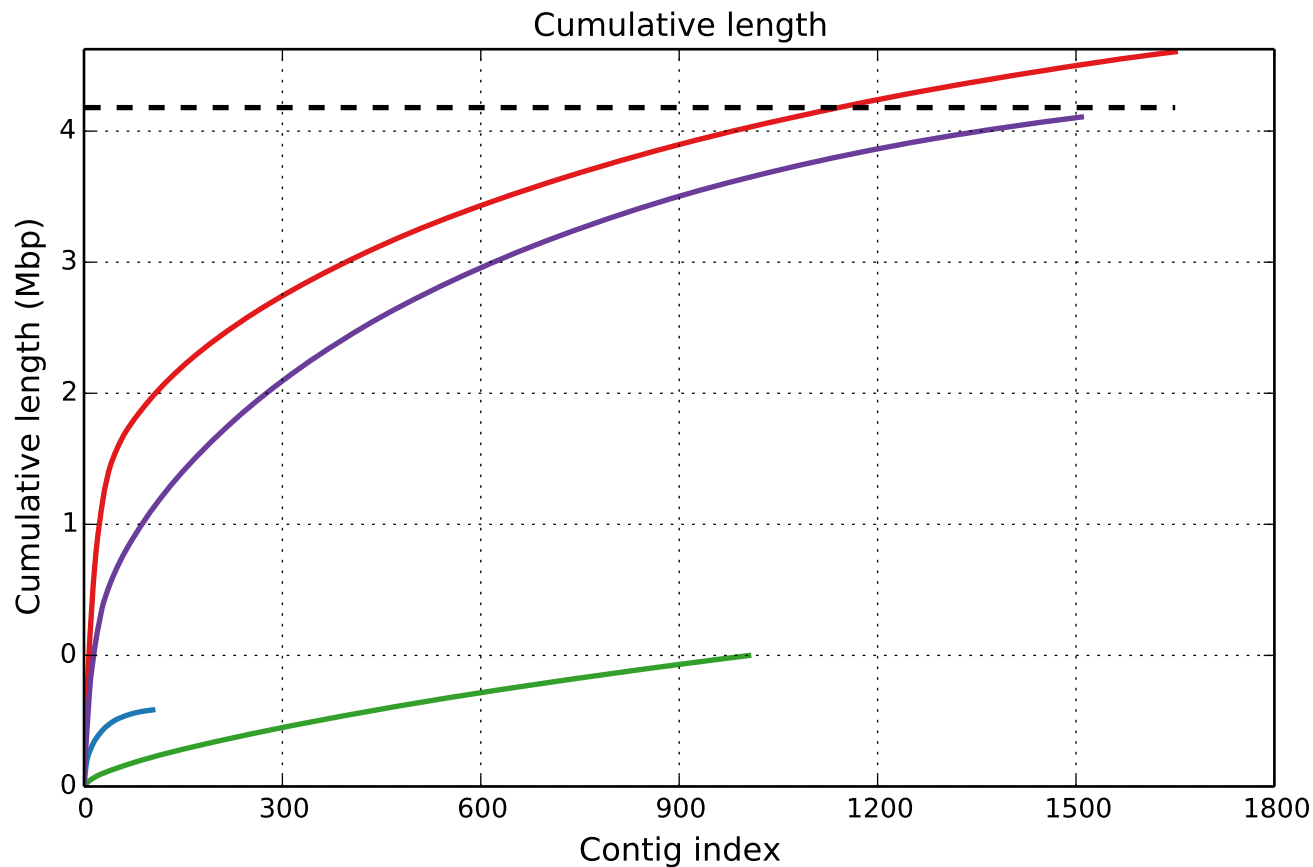


— IDBA\_UD — SOAPdenovo2 — SPAdes  
— Ray

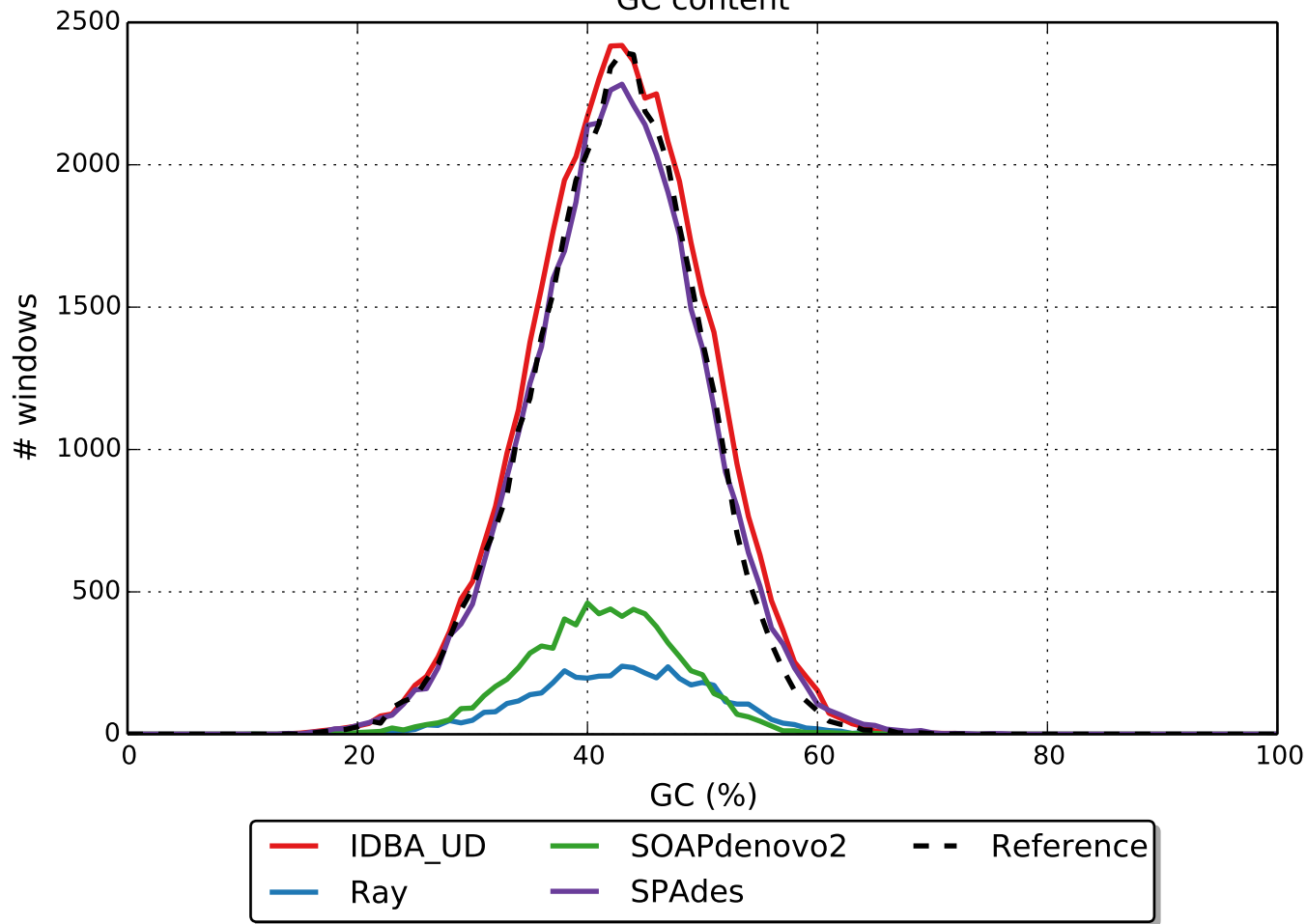
NGx



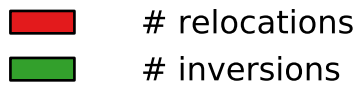
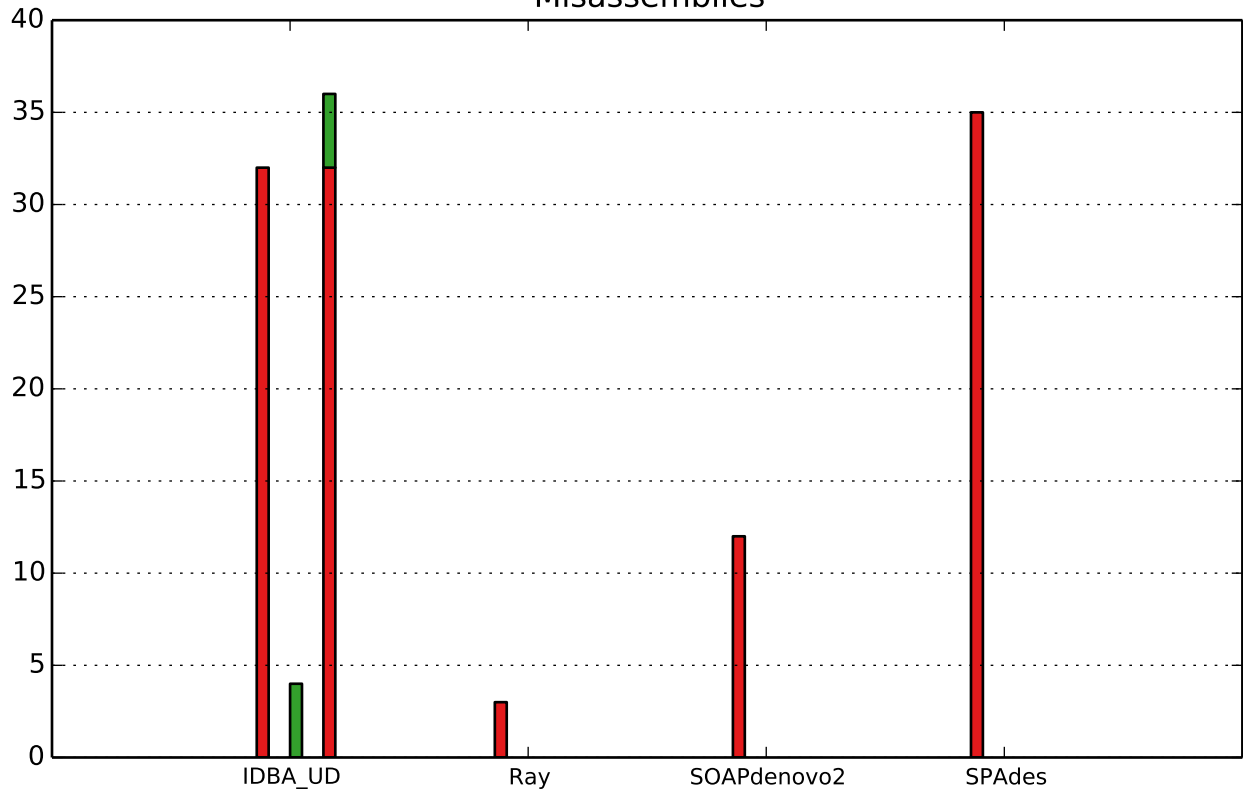
— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray



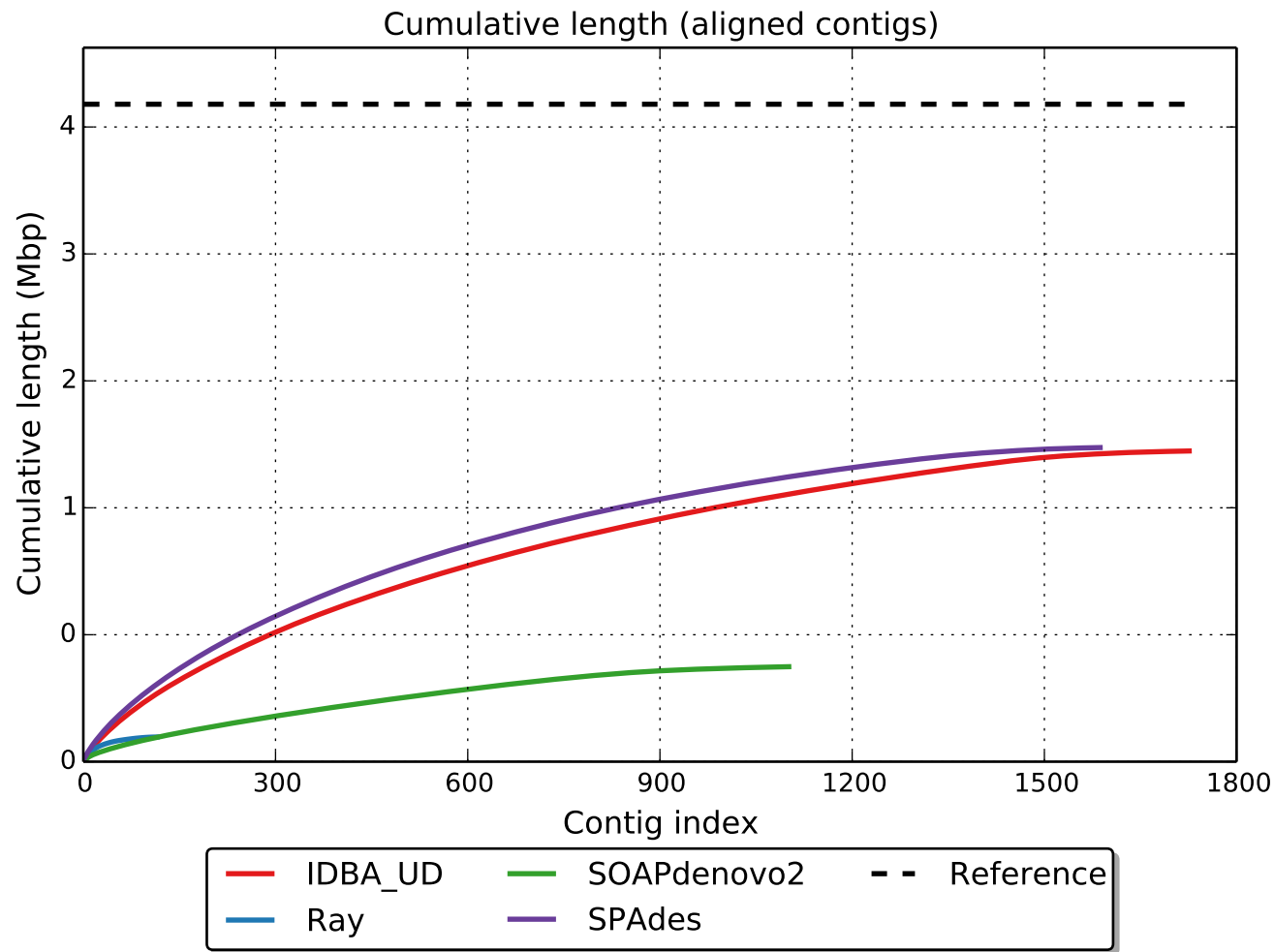
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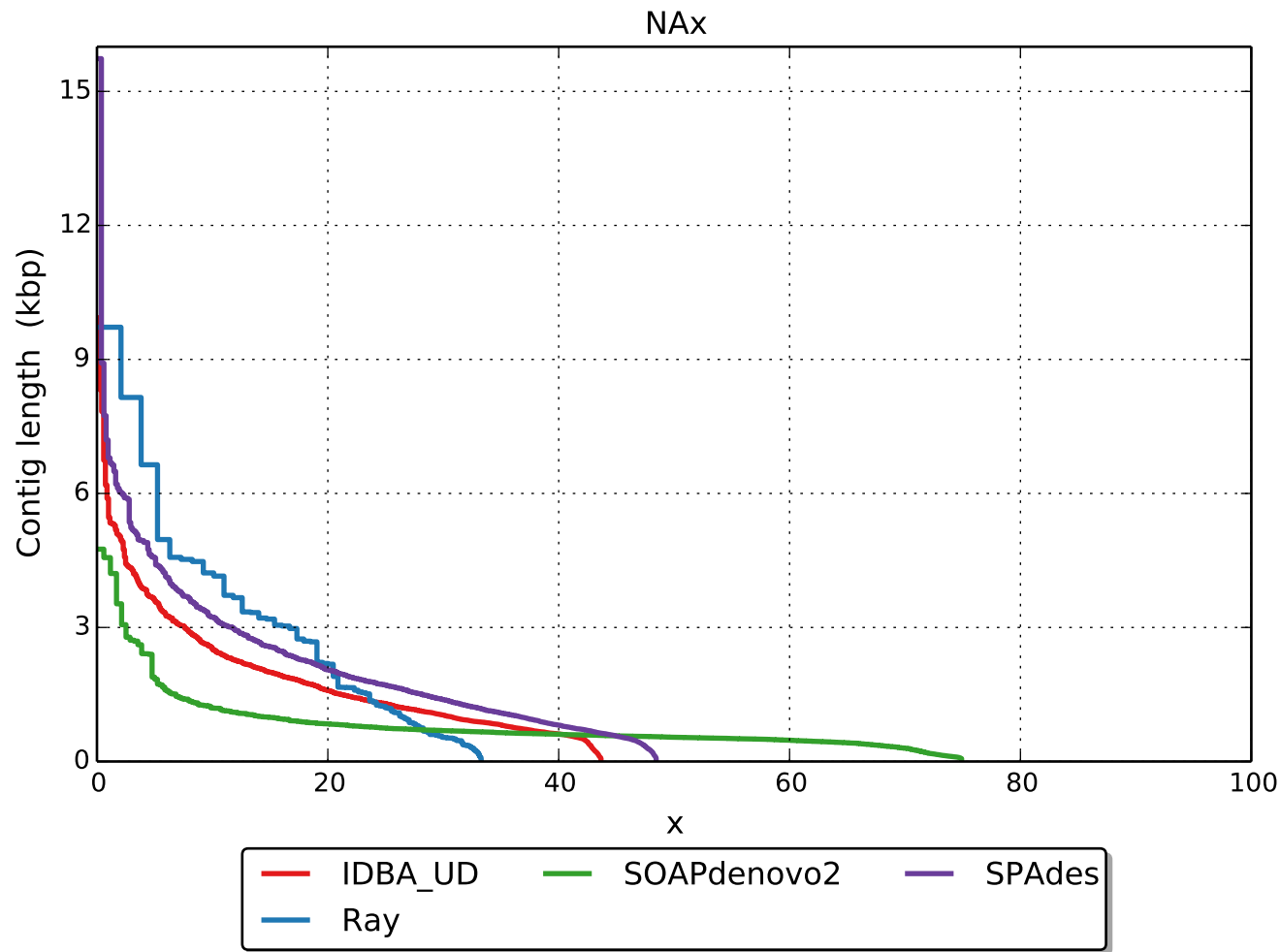


# Misassemblies









# NGAx

