Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	30	12	9	25
# contigs (>= 5000 bp)	12	3	0	10
# contigs (>= 10000 bp)	9	2	0	5
# contigs (>= 25000 bp)	9	0	0	4
# contigs (>= 50000 bp)	8	0	0	1
Total length (>= 1000 bp)	571976	64362	11144	261040
Total length (>= 5000 bp)	541171	44965	0	226369
Total length (>= 10000 bp)	519982	35026	0	189922
Total length (>= 25000 bp)	519982	0	0	165222
Total length (>= 50000 bp)	491219	0	0	53795
# contigs	51	21	21	33
Largest contig	76323	21063	1416	53795
Total length	586707	70722	19983	267127
Reference length	3102987	3102987	3102987	3102987
GC (%)	41.05	41.70	40.90	40.53
Reference GC (%)	43.09	43.09	43.09	43.09
N50	54427	9939	1080	32408
N75	53501	2493	852	8358
L50	5	3	8	3
L75	7	6	14	7
# misassemblies	1	0	0	0
# misassembled contigs	1	0	0	0
Misassembled contigs length	664	0	0	0
# local misassemblies	0	1	6	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 30 part	0 + 10 part	0 + 9 part	0 + 22 part
Unaligned length	546512	52092	4155	230923
Genome fraction (%)	1.241	0.525	0.484	1.167
Duplication ratio	1.044	1.144	1.053	1.000
# N's per 100 kbp	22.84	1907.47	4138.52	166.59
# mismatches per 100 kbp	1722.26	1381.22	1570.51	1748.72
# indels per 100 kbp	57.15	85.94	6.65	66.30
Largest alignment	4008	2427	1329	4763
NA50	-	-	758	-
NGA50	-	-	-	-
NA75	-	-	101	-
LA50	-	-	10	-
LA75	-	-	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).
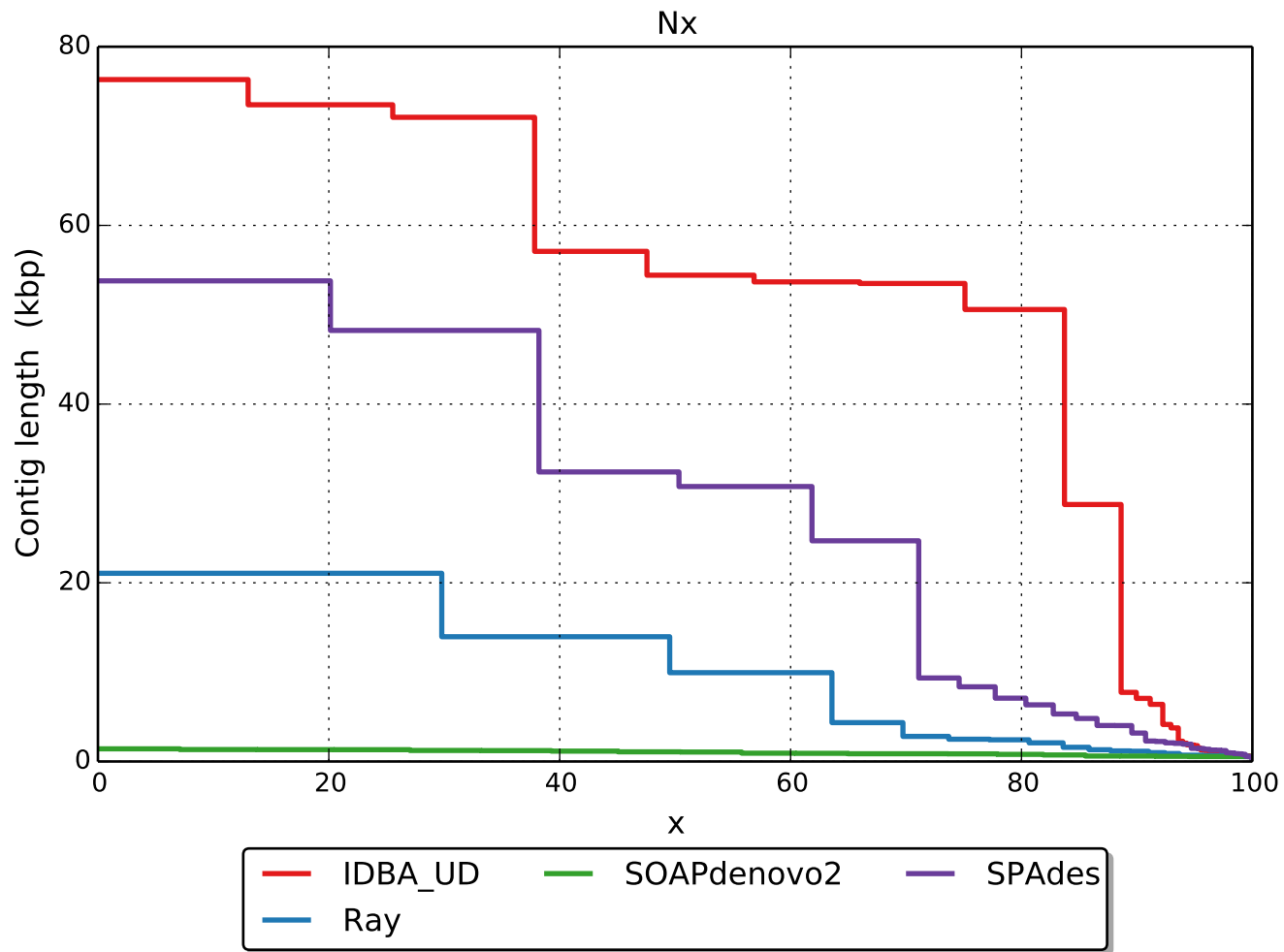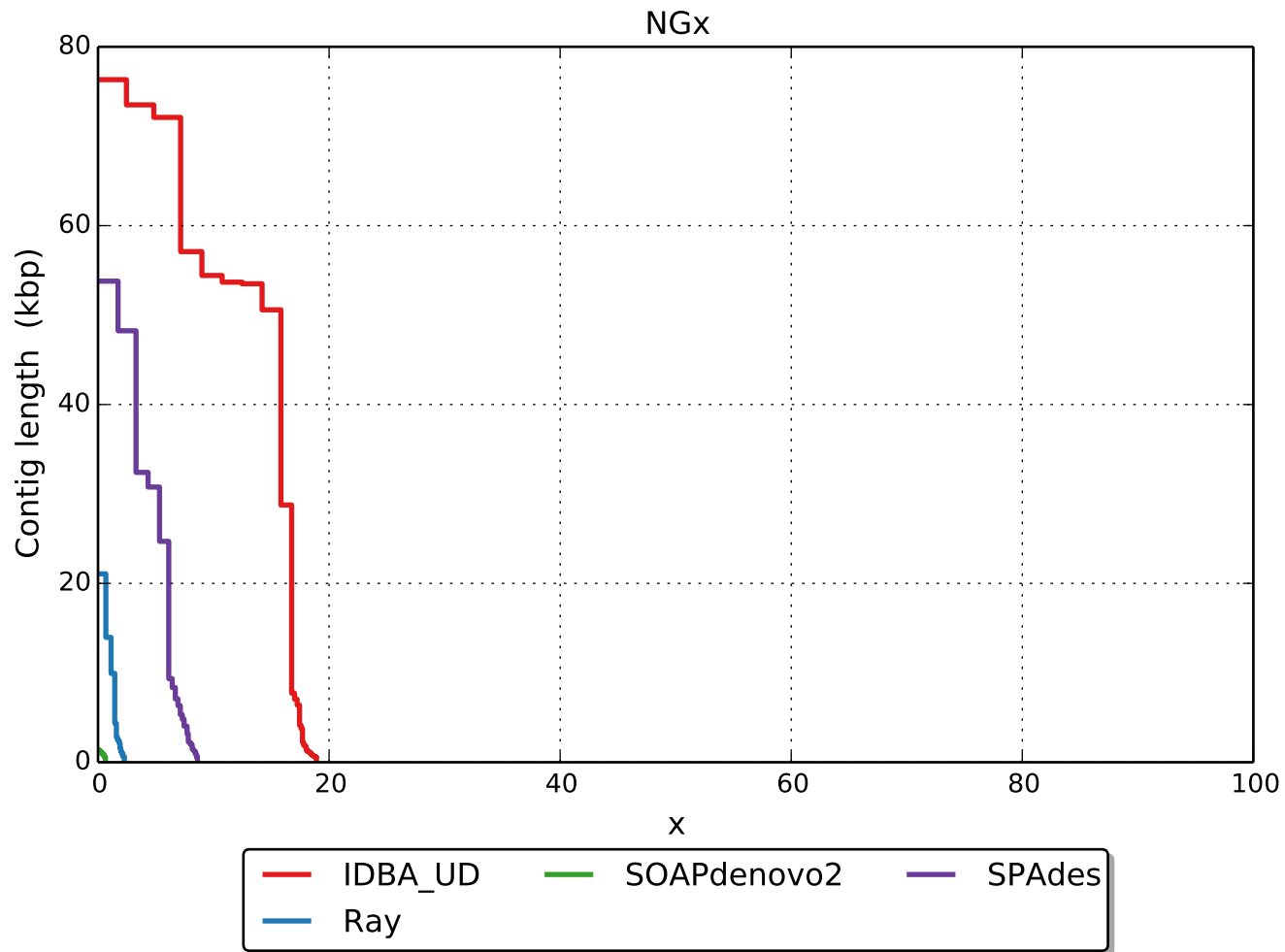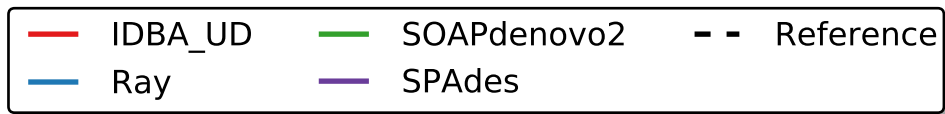
Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	1	0	0	0
# relocations	0	0	0	0
# translocations	1	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	6	2	1	10
# misassembled contigs	1	0	0	0
Misassembled contigs length	664	0	0	0
# local misassemblies	0	1	6	0
# structural variations	0	0	0	0
# mismatches	663	225	236	633
# indels	22	14	1	24
# short indels	20	14	1	20
# long indels	2	0	0	4
Indels length	53	23	1	64

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).
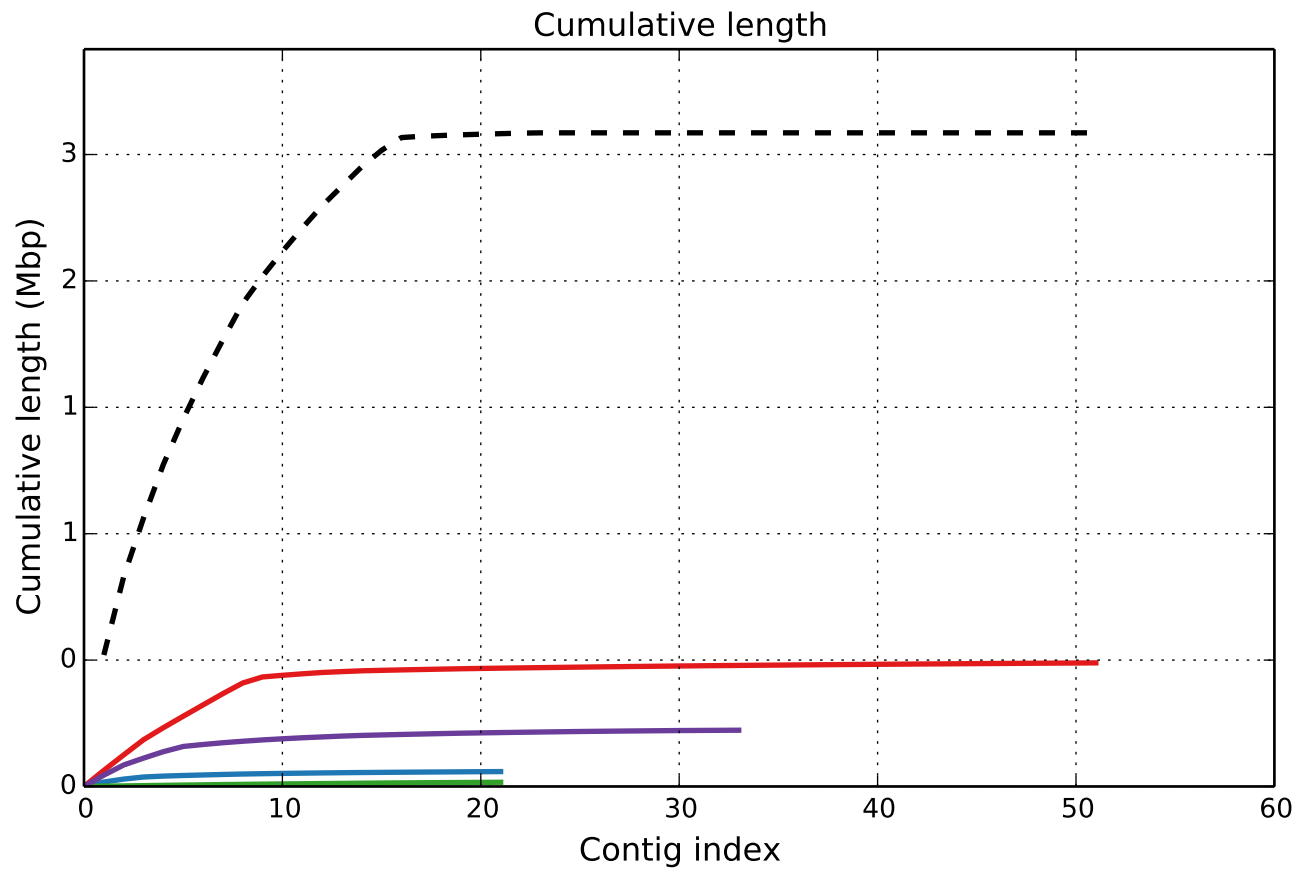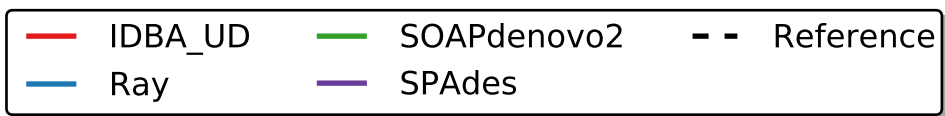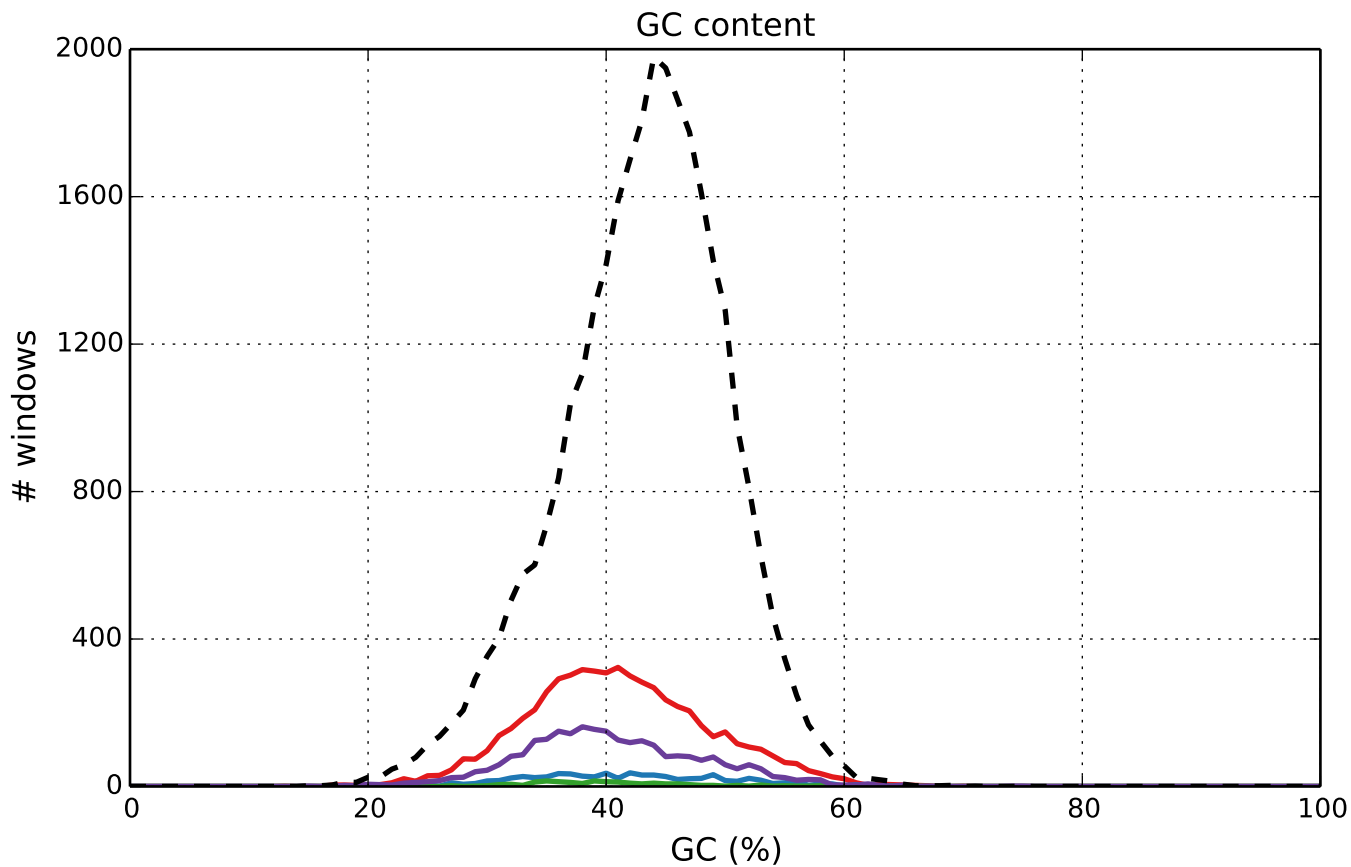
Unaligned report

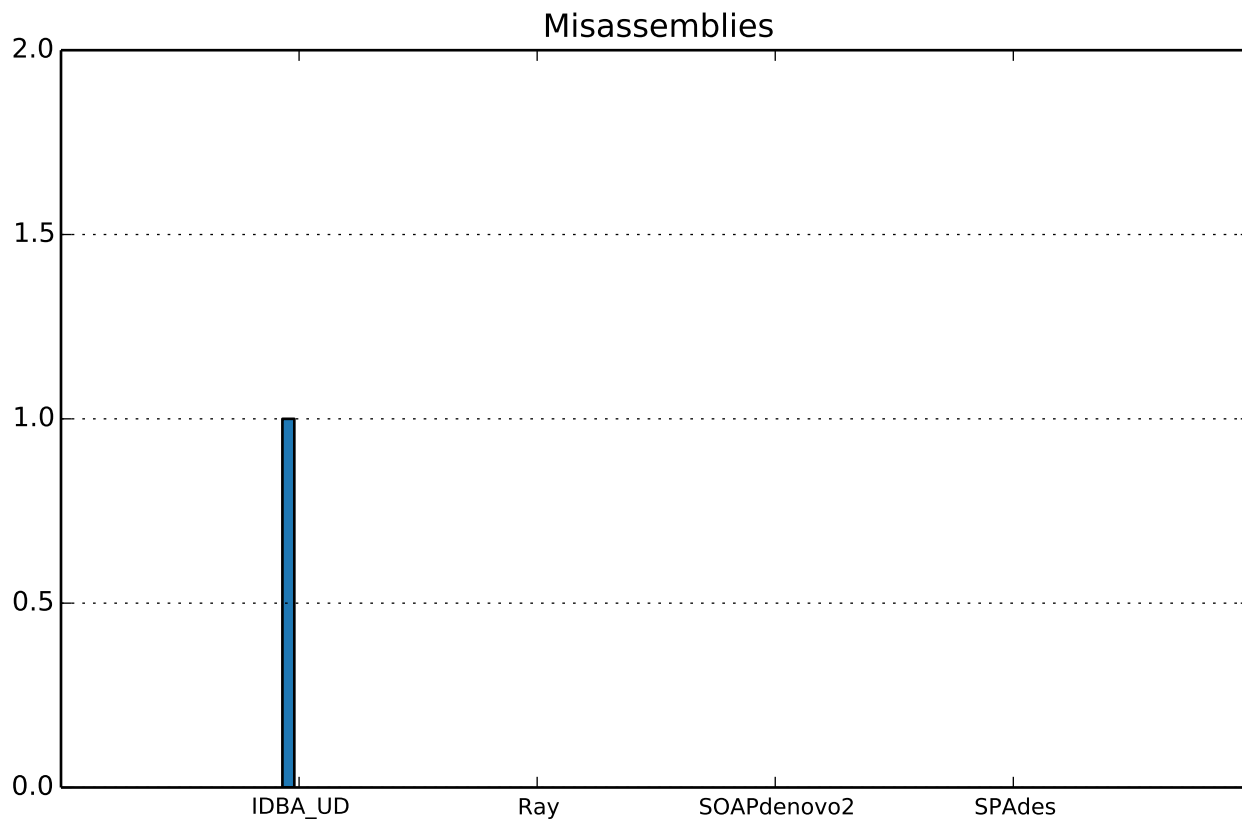|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	30	10	9	22
# with misassembly	1	0	0	0
# both parts are significant	6	1	1	10
Partially unaligned length	546512	52092	4155	230923
# N's	134	1349	827	445

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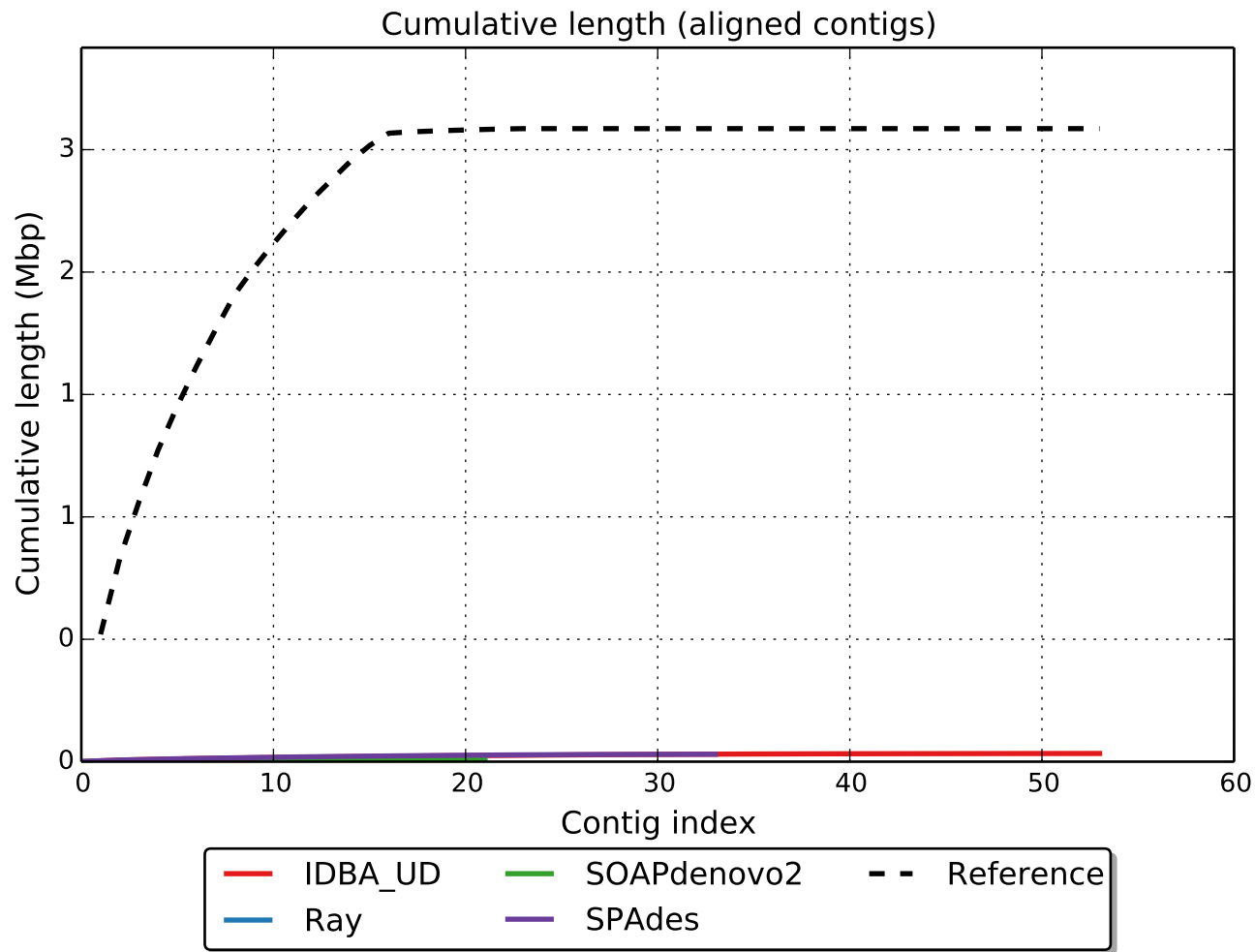(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

Cumulative length (aligned contigs)

NAx

NGAx

Genome fraction, %

Legend: IDBA_UD, Ray, SOAPdenovo2, SPAdes