

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	446	18	67	549
# contigs (>= 5000 bp)	15	3	0	34
# contigs (>= 10000 bp)	2	2	0	11
# contigs (>= 25000 bp)	2	0	0	3
# contigs (>= 50000 bp)	1	0	0	2
Total length (>= 1000 bp)	984584	64138	89383	1485591
Total length (>= 5000 bp)	200273	35653	0	468064
Total length (>= 10000 bp)	115267	30105	0	321660
Total length (>= 25000 bp)	115267	0	0	209248
Total length (>= 50000 bp)	88224	0	0	171496
# contigs	976	29	592	947
Largest contig	88224	19602	4208	120419
Total length	1373657	71185	431911	1773396
Reference length	3142181	3142181	3142181	3142181
GC (%)	39.17	41.70	38.25	39.10
Reference GC (%)	37.20	37.20	37.20	37.20
N50	1611	5548	704	2434
NG50	-	-	-	848
N75	935	1651	587	1275
L50	212	3	223	161
LG50	-	-	-	642
L75	494	10	392	413
# misassemblies	39	1	11	33
# misassembled contigs	35	1	11	30
Misassembled contigs length	74323	2338	10403	72814
# local misassemblies	9	2	796	12
# structural variations	0	0	0	0
# unaligned contigs	0 + 247 part	0 + 7 part	0 + 100 part	0 + 345 part
Unaligned length	262943	38909	38924	566359
Genome fraction (%)	34.982	0.971	10.756	37.100
Duplication ratio	1.010	1.058	1.163	1.035
# N's per 100 kbp	284.13	1359.84	10944.38	1669.28
# mismatches per 100 kbp	1042.41	1608.73	1137.39	1173.41
# indels per 100 kbp	46.31	42.59	13.02	75.40
Largest alignment	7833	3348	4205	10275
NA50	1016	-	532	911
NGA50	-	-	-	-
NA75	581	-	240	-
LA50	381	-	287	488
LA75	827	-	538	-

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	39	1	11	33
# relocations	13	0	4	14
# translocations	25	1	7	18
# inversions	1	0	0	1
# possibly misassembled contigs	36	1	5	100
# misassembled contigs	35	1	11	30
Misassembled contigs length	74323	2338	10403	72814
# local misassemblies	9	2	796	12
# structural variations	0	0	0	0
# mismatches	11458	491	3844	13679
# indels	509	13	44	879
# short indels	433	13	42	627
# long indels	76	0	2	252
Indels length	1621	14	74	4274

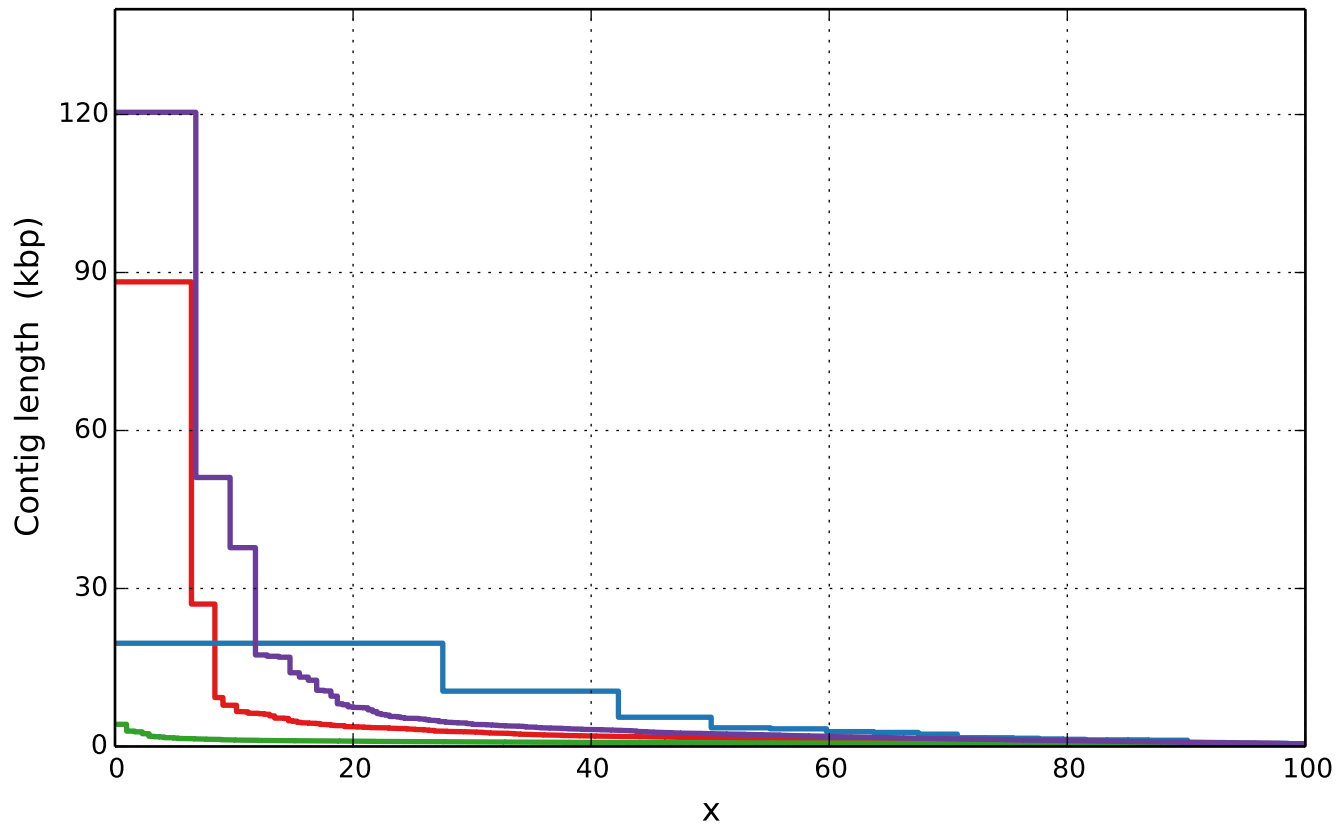
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

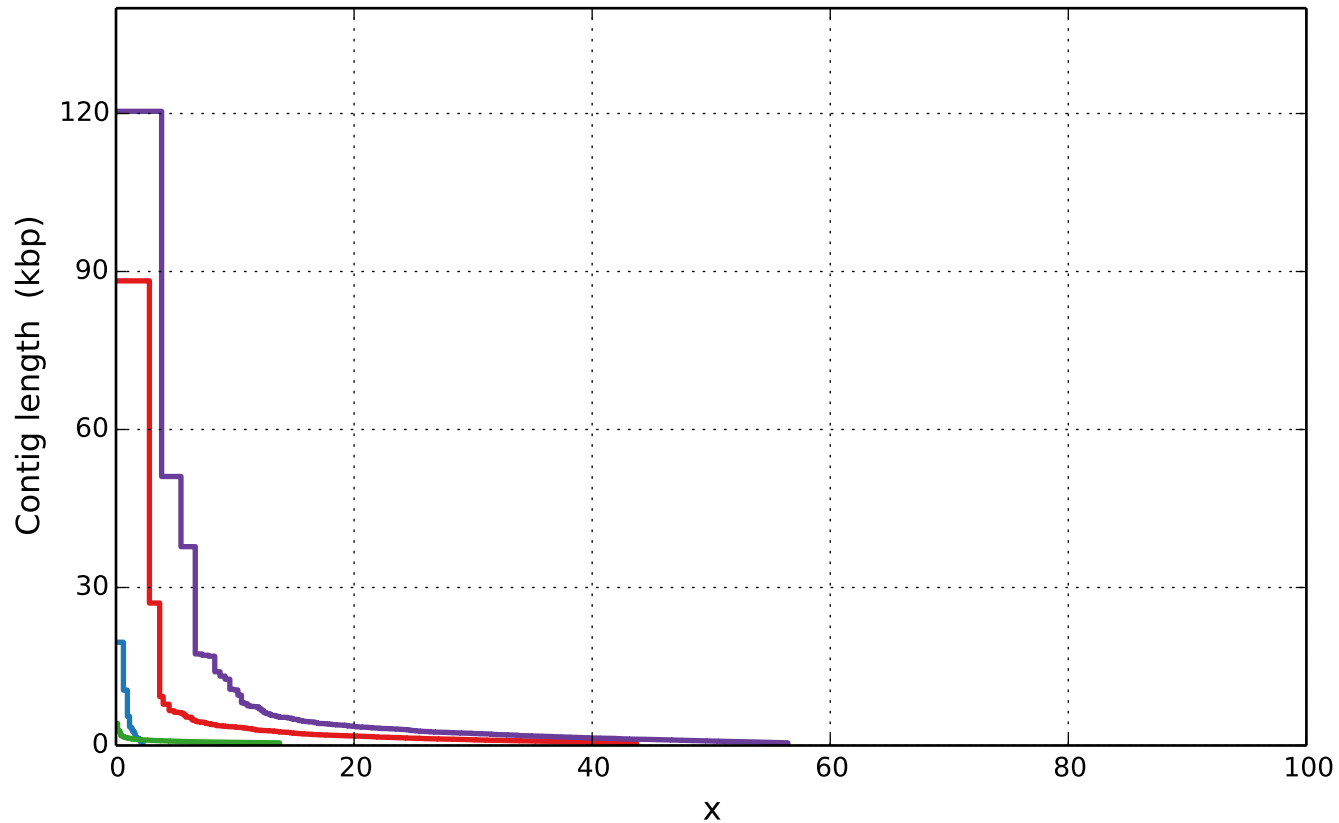
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	247	7	100	345
# with misassembly	3	0	32	4
# both parts are significant	33	1	2	82
Partially unaligned length	262943	38909	38924	566359
# N's	3903	968	47270	29603

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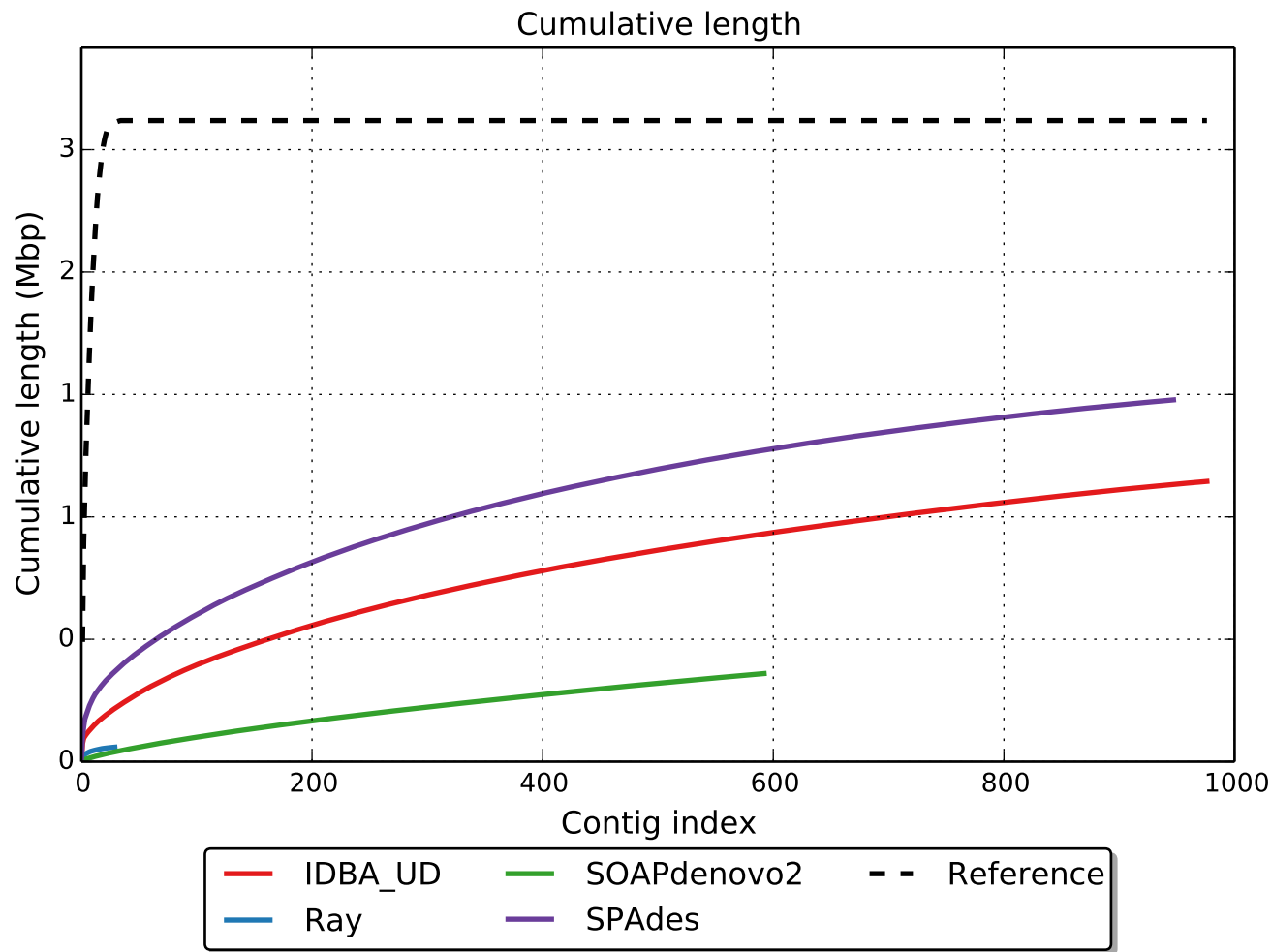
Nx



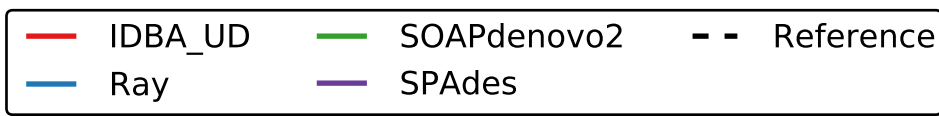
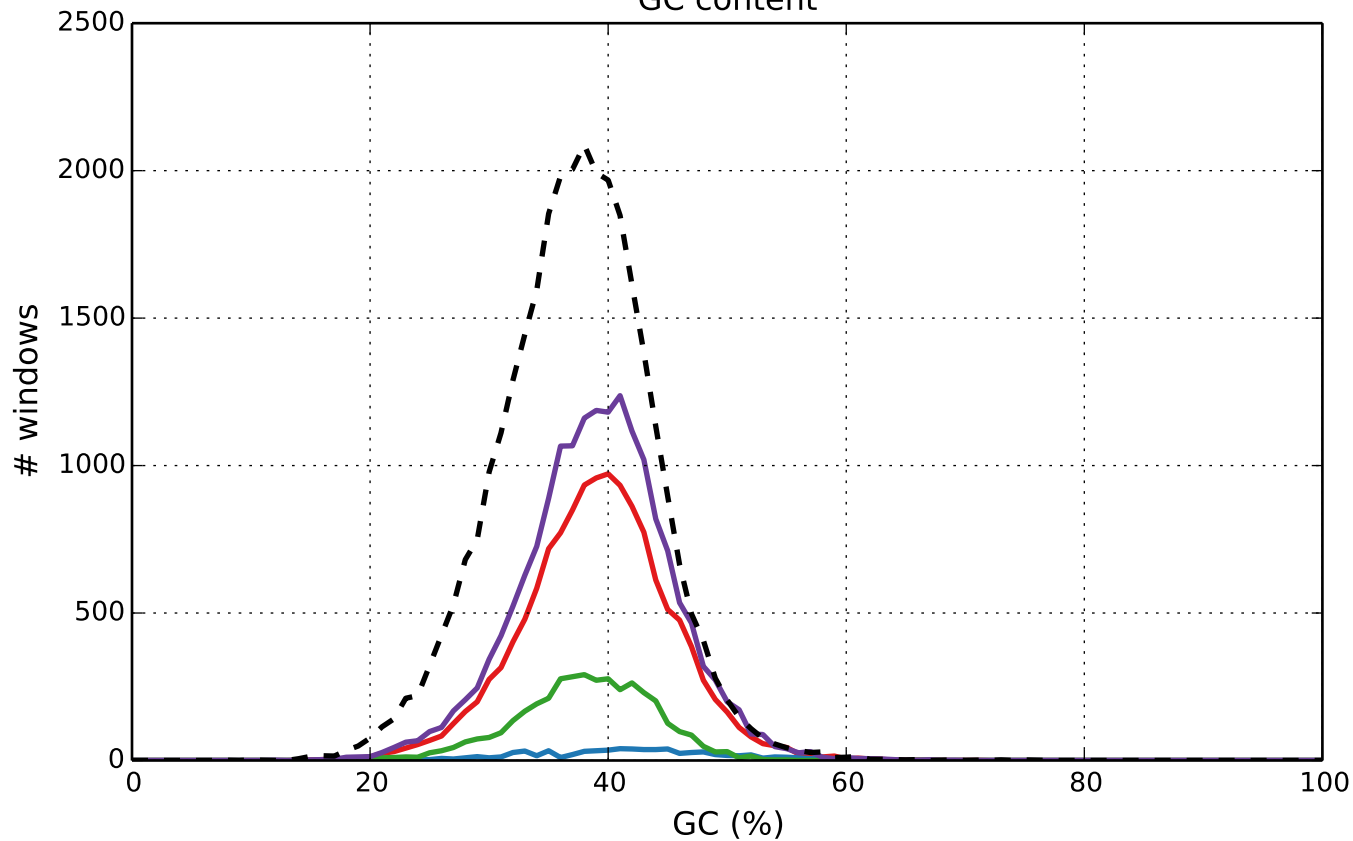
NGx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



GC content



Misassemblies

