

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	716	16	128	591
# contigs (>= 5000 bp)	60	3	2	63
# contigs (>= 10000 bp)	13	2	1	22
# contigs (>= 25000 bp)	3	0	0	2
# contigs (>= 50000 bp)	1	0	0	1
Total length (>= 1000 bp)	1929982	58028	195014	1754299
Total length (>= 5000 bp)	664223	36845	15968	623904
Total length (>= 10000 bp)	364202	31398	10501	347299
Total length (>= 25000 bp)	213058	0	0	79916
Total length (>= 50000 bp)	146986	0	0	50348
# contigs	1181	36	774	938
Largest contig	146986	17196	10501	50348
Total length	2275745	71519	631472	2001690
Reference length	5974559	5974559	5974559	5974559
GC (%)	42.42	43.75	41.68	42.20
Reference GC (%)	41.88	41.88	41.88	41.88
N50	2525	5447	789	3151
N75	1320	1121	618	1525
L50	199	3	266	160
L75	521	12	492	389
# misassemblies	23	1	5	20
# misassembled contigs	23	1	5	18
Misassembled contigs length	64886	1560	4830	74662
# local misassemblies	9	0	756	8
# structural variations	1	0	0	0
# unaligned contigs	0 + 191 part	0 + 2 part	0 + 211 part	0 + 258 part
Unaligned length	457297	17602	112610	505198
Genome fraction (%)	30.119	0.886	7.678	24.432
Duplication ratio	1.011	1.019	1.131	1.025
# N's per 100 kbp	301.75	279.65	9128.20	991.71
# mismatches per 100 kbp	1769.16	578.24	1413.05	2020.99
# indels per 100 kbp	47.90	22.68	22.67	54.94
Largest alignment	17083	14202	5467	17583
NA50	1424	1098	547	1367
NGA50	-	-	-	-
NA75	652	507	-	-
LA50	402	12	372	352
LA75	986	36	-	-

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	23	1	5	20
# relocations	9	0	2	4
# translocations	13	1	3	16
# inversions	1	0	0	0
# possibly misassembled contigs	52	2	17	116
# misassembled contigs	23	1	5	18
Misassembled contigs length	64886	1560	4830	74662
# local misassemblies	9	0	756	8
# structural variations	1	0	0	0
# mismatches	31836	306	6482	29501
# indels	862	12	104	802
# short indels	761	12	99	631
# long indels	101	0	5	171
Indels length	2543	17	264	3170

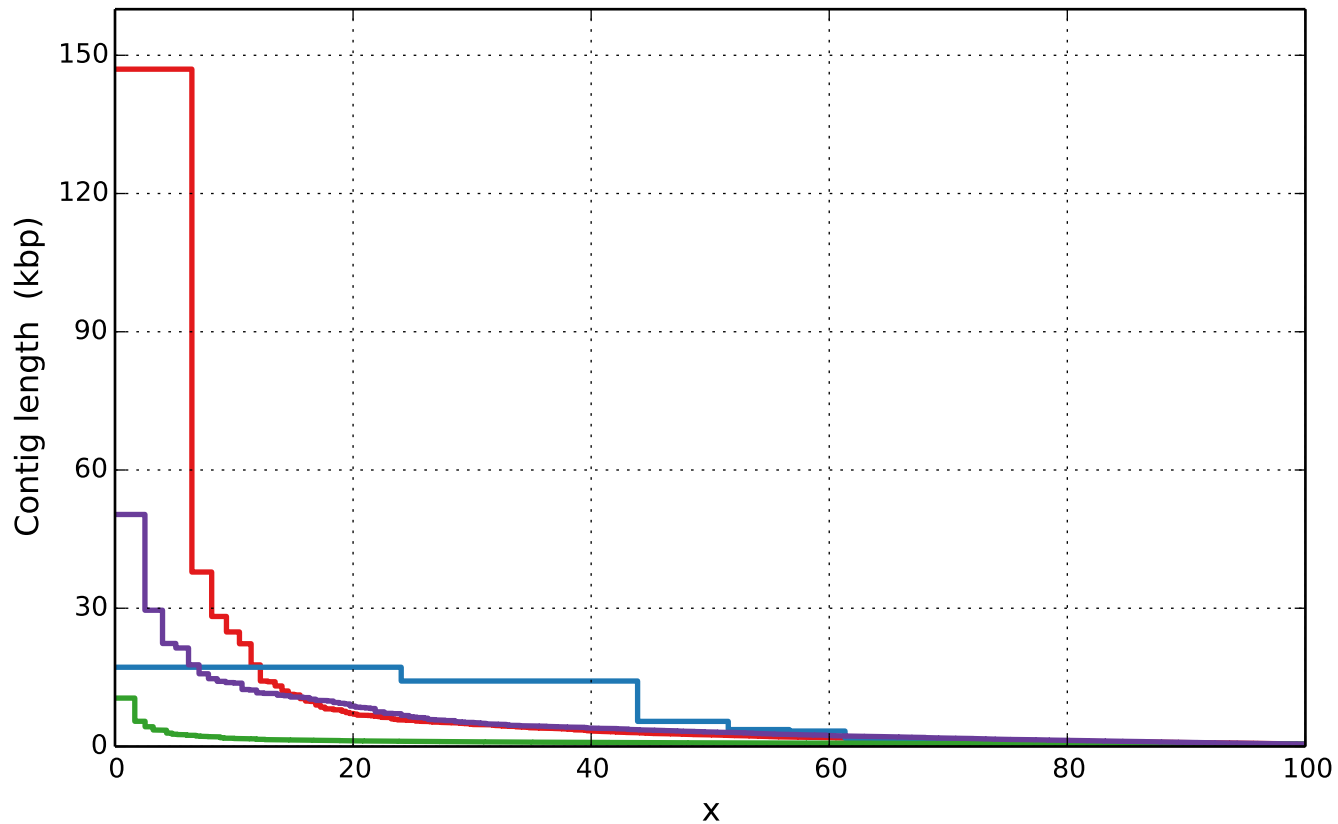
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

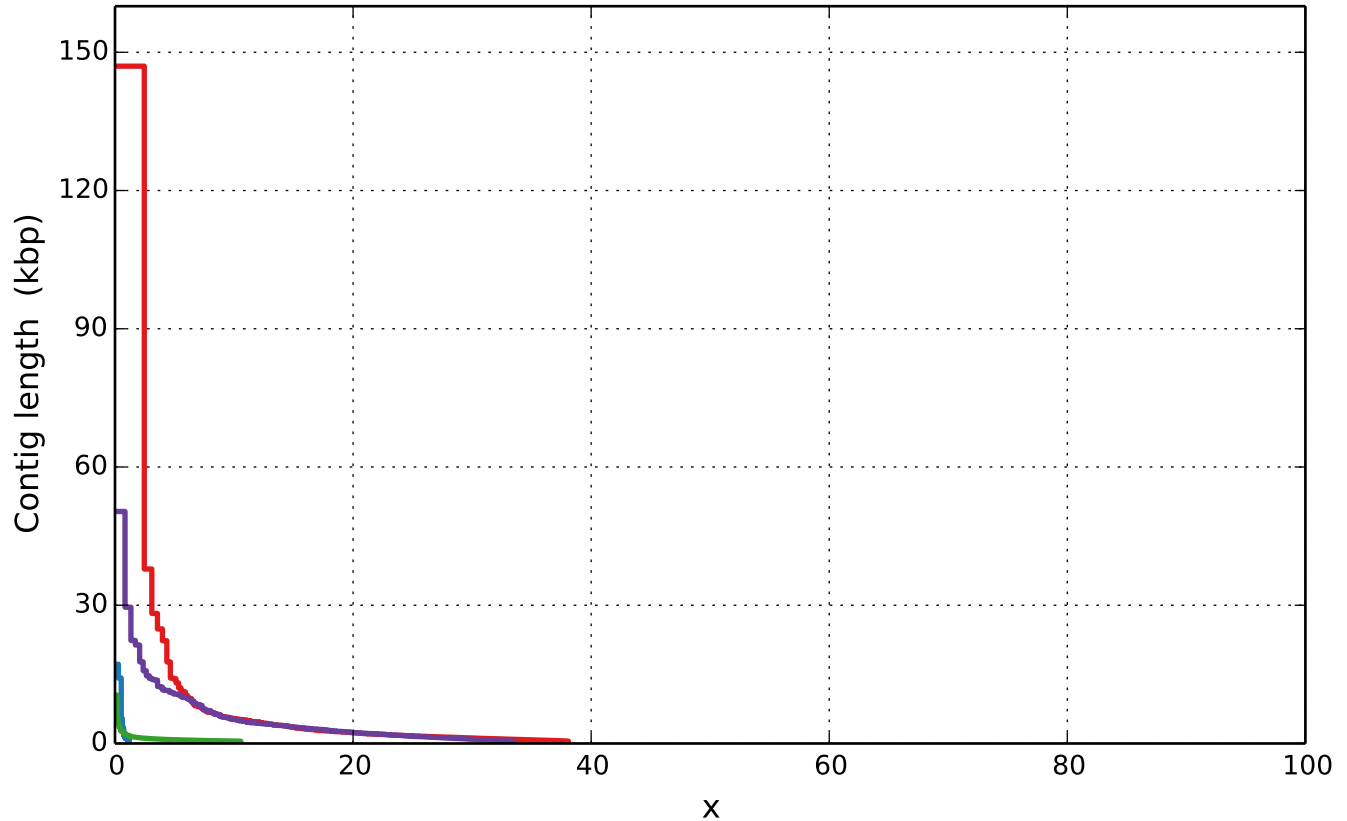
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	191	2	211	258
# with misassembly	7	0	67	9
# both parts are significant	49	2	9	104
Partially unaligned length	457297	17602	112610	505198
# N's	6867	200	57642	19851

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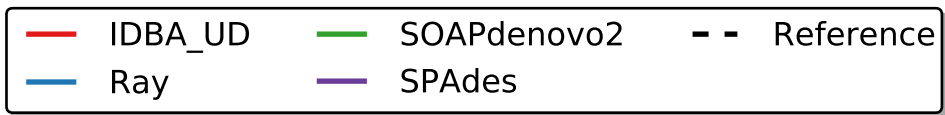
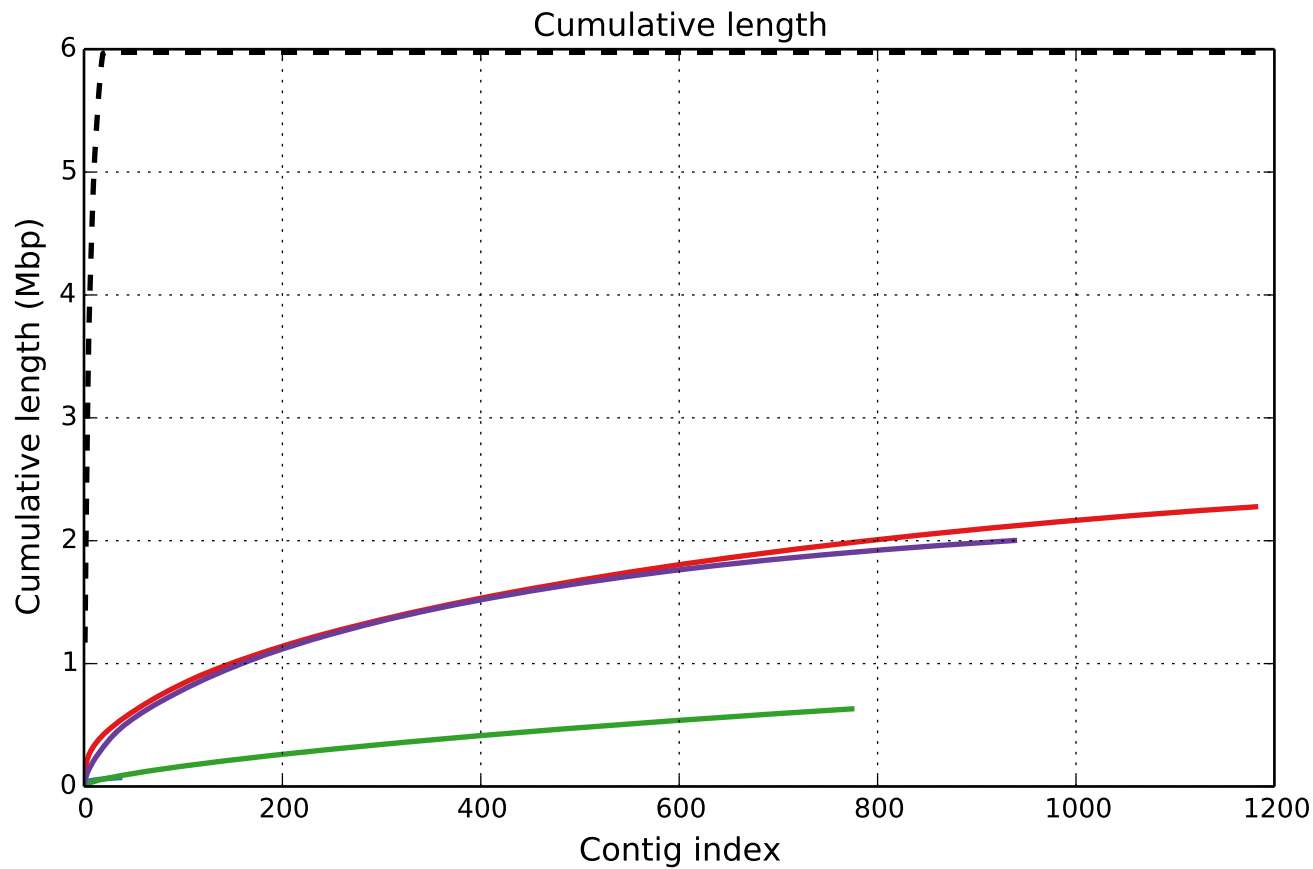
Nx

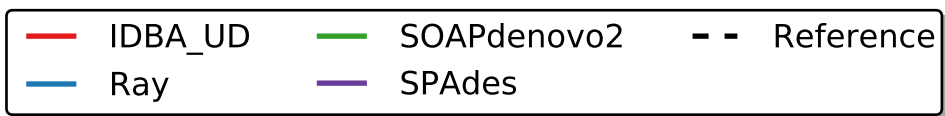
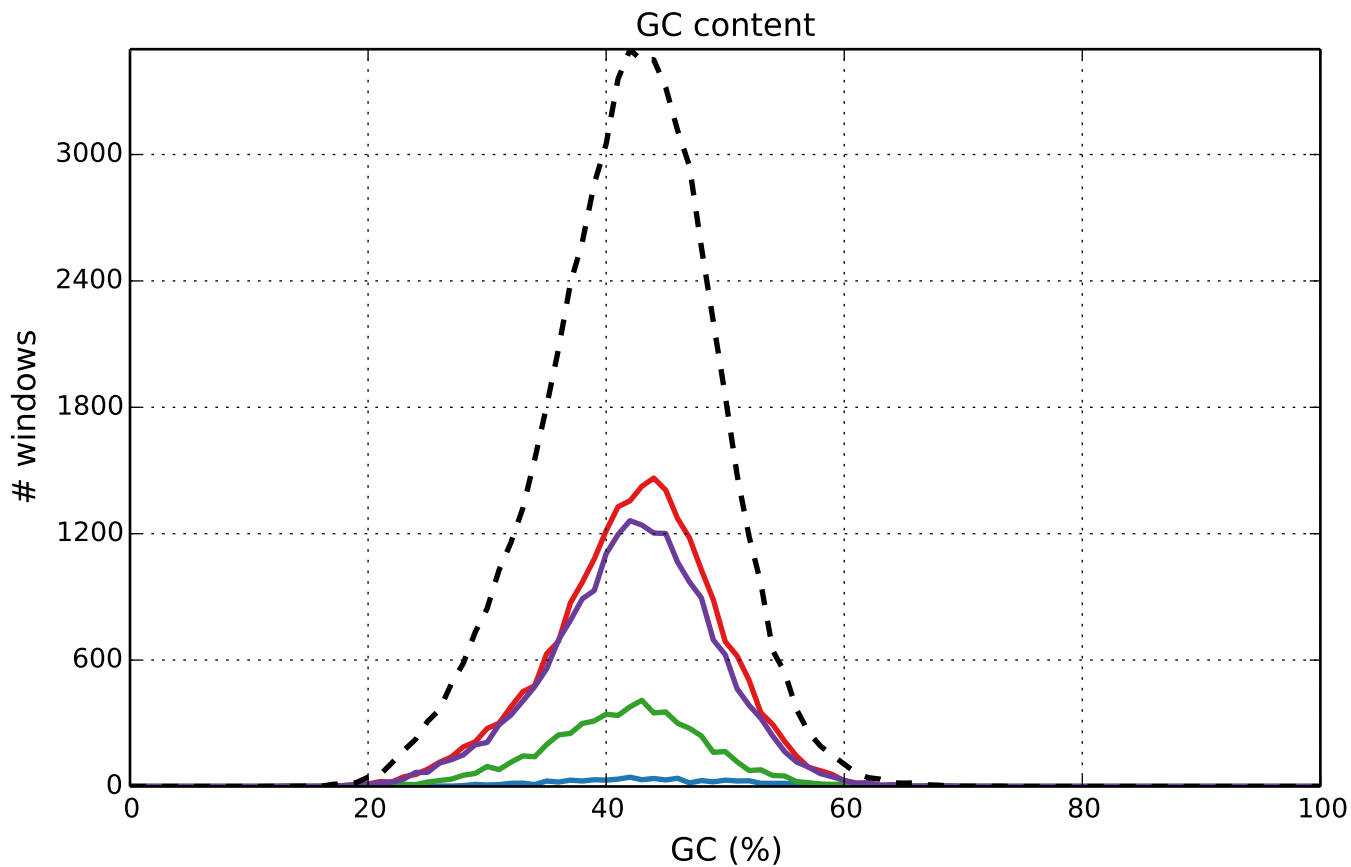


NGx



— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray





Misassemblies

