

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	59	42	33	39
# contigs (>= 5000 bp)	17	17	2	14
# contigs (>= 10000 bp)	11	8	0	10
# contigs (>= 25000 bp)	6	1	0	3
# contigs (>= 50000 bp)	2	0	0	1
Total length (>= 1000 bp)	519060	262244	68288	331549
Total length (>= 5000 bp)	427503	200591	12527	269785
Total length (>= 10000 bp)	375250	132970	0	242154
Total length (>= 25000 bp)	294583	35631	0	124555
Total length (>= 50000 bp)	164253	0	0	55339
# contigs	83	60	70	57
Largest contig	94894	35631	7126	55339
Total length	536473	274761	94044	344558
Reference length	3842594	3842594	3842594	3842594
GC (%)	45.70	45.59	45.59	46.46
Reference GC (%)	50.11	50.11	50.11	50.11
N50	32853	9721	1546	16575
N75	9172	4559	894	5771
L50	5	9	16	6
L75	14	19	36	13
# misassemblies	1	0	1	3
# misassembled contigs	1	0	1	2
Misassembled contigs length	36911	0	2108	51060
# local misassemblies	1	12	10	2
# structural variations	0	0	0	0
# unaligned contigs	0 + 40 part	0 + 15 part	0 + 13 part	0 + 32 part
Unaligned length	384708	112342	8099	169512
Genome fraction (%)	3.443	3.644	2.193	4.148
Duplication ratio	1.147	1.160	1.020	1.098
# N's per 100 kbp	101.59	1071.11	1688.57	209.25
# mismatches per 100 kbp	1801.14	1759.87	1298.38	2004.28
# indels per 100 kbp	58.95	33.57	14.24	65.24
Largest alignment	21306	9719	7126	21306
NA50	-	625	1384	-
NGA50	-	-	-	-
NA75	-	-	708	-
LA50	-	47	18	-
LA75	-	-	42	-

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	1	3
# relocations	1	0	1	3
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	13	12	2	20
# misassembled contigs	1	0	1	2
Misassembled contigs length	36911	0	2108	51060
# local misassemblies	1	12	10	2
# structural variations	0	0	0	0
# mismatches	2383	2464	1094	3195
# indels	78	47	12	104
# short indels	75	43	12	102
# long indels	3	4	0	2
Indels length	127	120	12	148

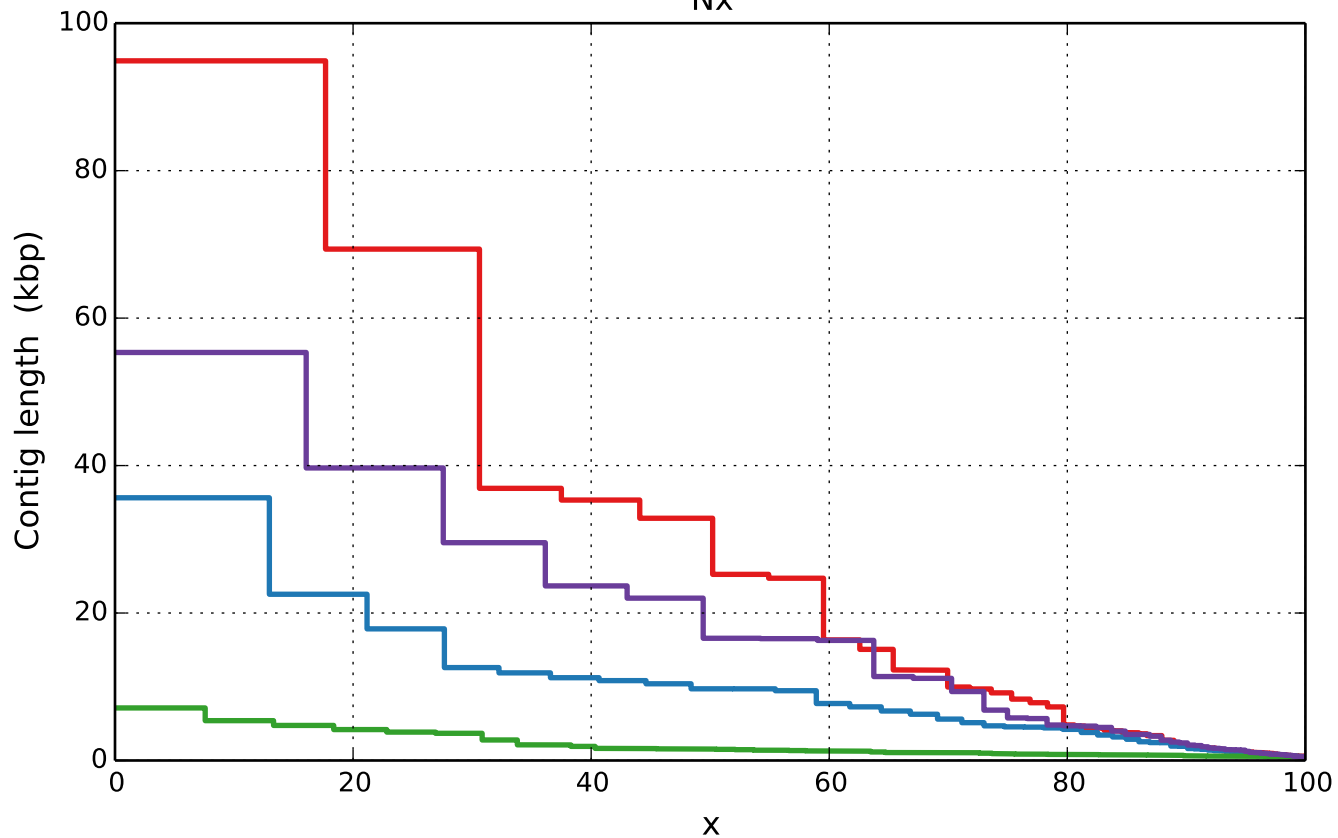
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	40	15	13	32
# with misassembly	3	0	1	3
# both parts are significant	12	6	1	16
Partially unaligned length	384708	112342	8099	169512
# N's	545	2943	1588	721

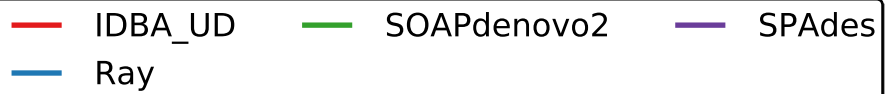
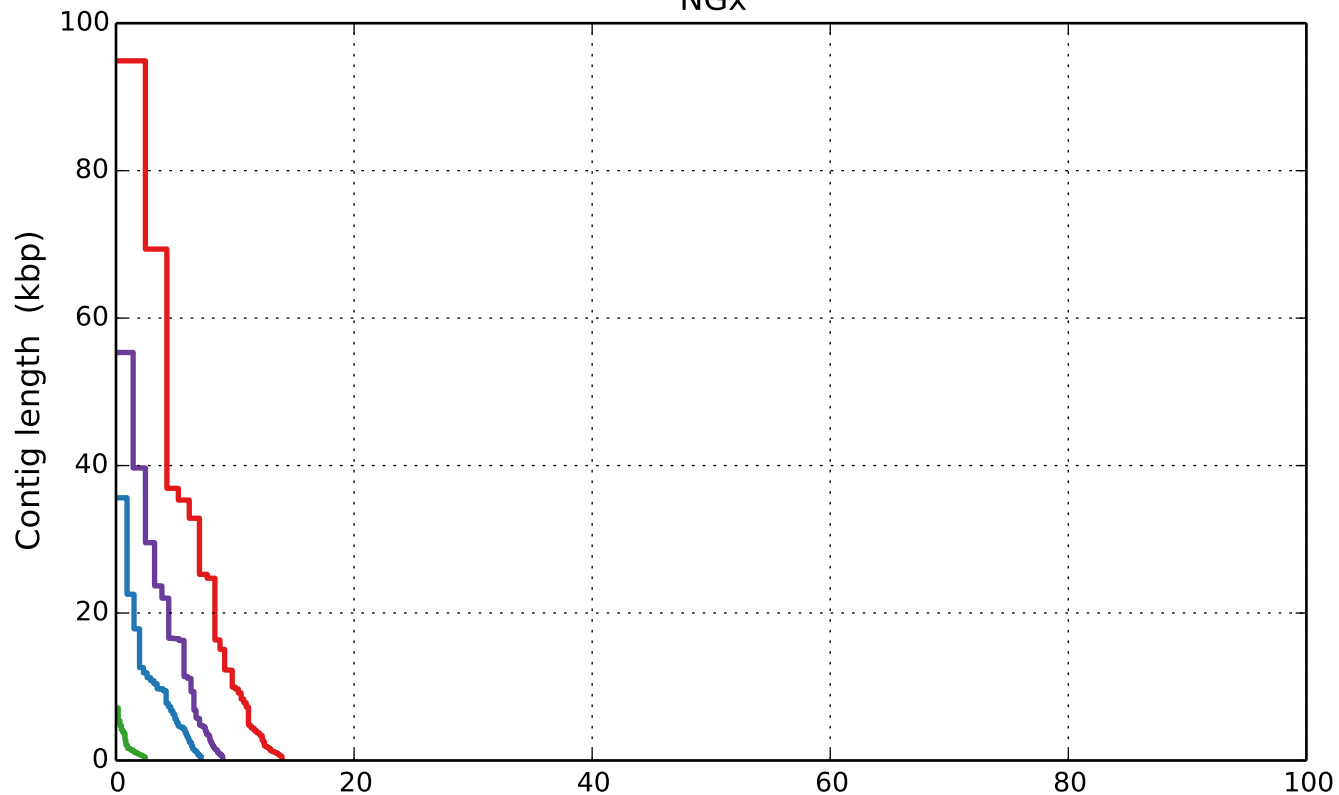
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

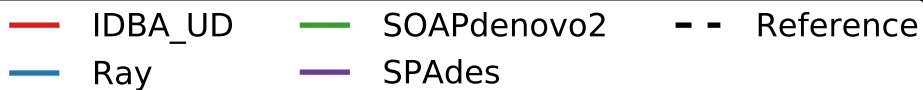
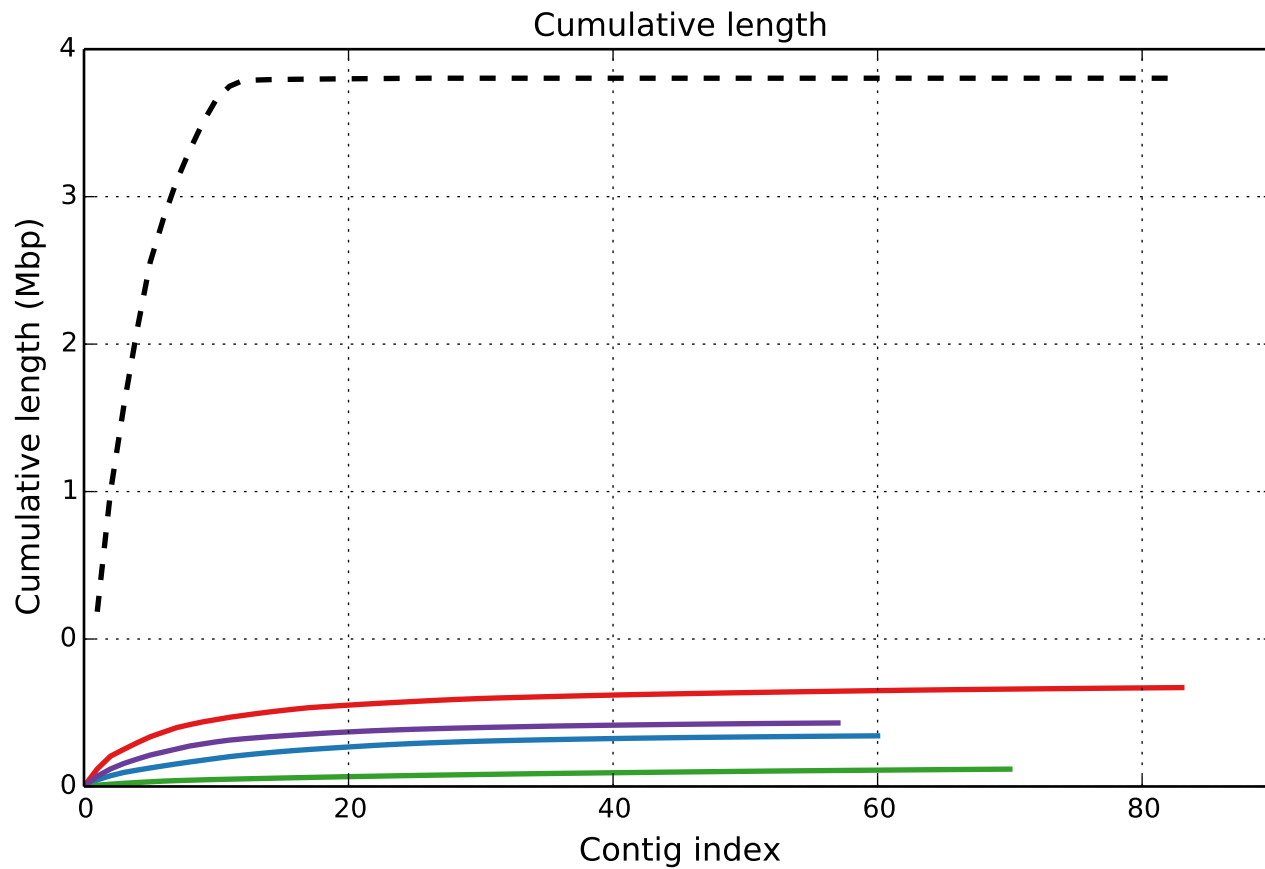
Nx



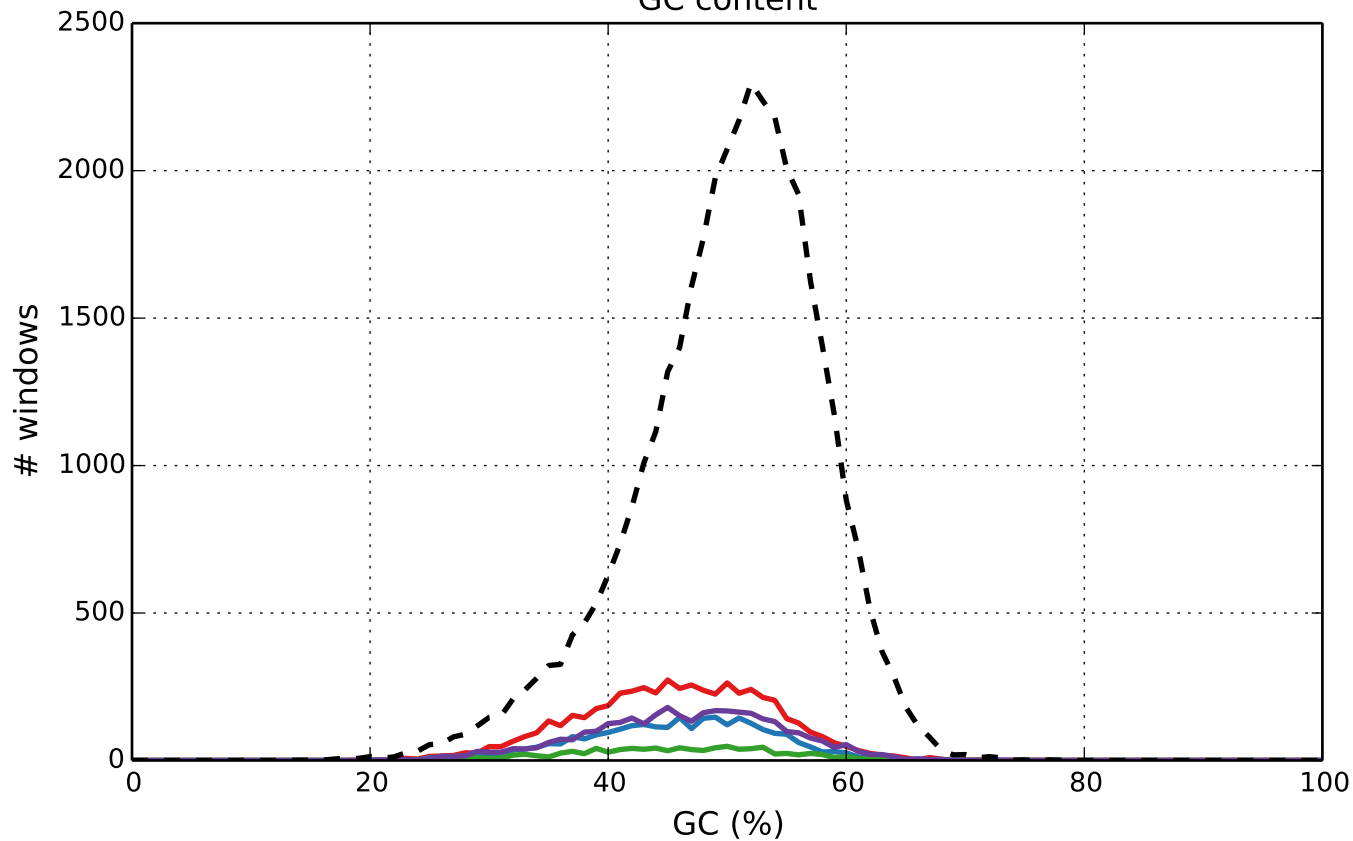
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— Ray

NGx

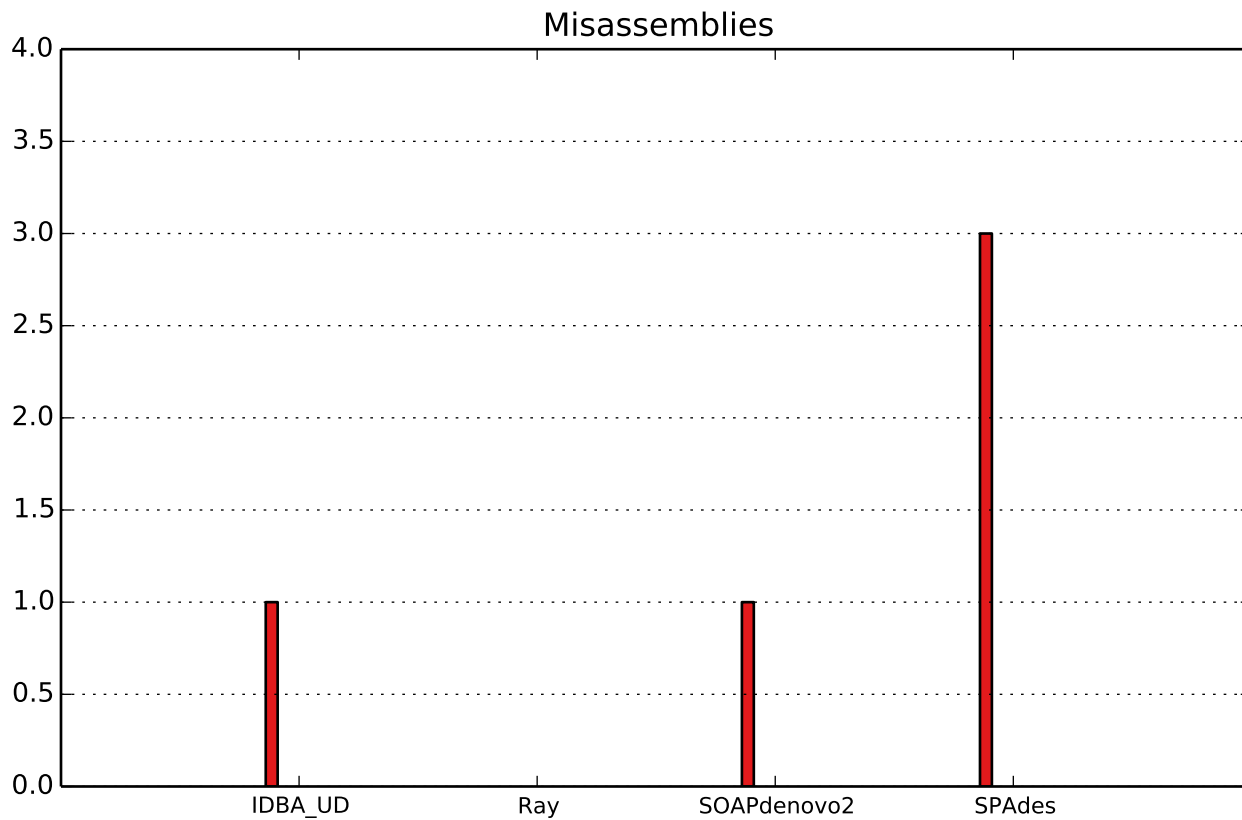




GC content



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 # relocations

