

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	71	22	18	76
# contigs (>= 5000 bp)	18	6	0	20
# contigs (>= 10000 bp)	5	2	0	9
# contigs (>= 25000 bp)	2	1	0	3
# contigs (>= 50000 bp)	2	0	0	3
Total length (>= 1000 bp)	387690	113267	28053	526663
Total length (>= 5000 bp)	274803	79499	0	402790
Total length (>= 10000 bp)	184195	56912	0	337077
Total length (>= 25000 bp)	145481	34367	0	253765
Total length (>= 50000 bp)	145481	0	0	253765
# contigs	116	30	59	166
Largest contig	94894	34367	4208	135693
Total length	415798	118717	58165	585901
Reference length	3290996	3290996	3290996	3290996
GC (%)	40.91	40.58	39.27	42.68
Reference GC (%)	38.19	38.19	38.19	38.19
N50	8596	6042	986	14985
N75	3487	3544	753	3839
L50	8	3	20	6
L75	28	9	36	29
# misassemblies	5	1	1	7
# misassembled contigs	4	1	1	4
Misassembled contigs length	10918	1756	2021	7315
# local misassemblies	3	7	22	5
# structural variations	0	0	0	0
# unaligned contigs	0 + 72 part	0 + 13 part	0 + 25 part	0 + 113 part
Unaligned length	293703	79800	13175	445246
Genome fraction (%)	3.430	1.033	1.301	4.013
Duplication ratio	1.082	1.145	1.051	1.065
# N's per 100 kbp	75.76	1280.36	4396.11	777.78
# mismatches per 100 kbp	1665.51	1715.46	1489.96	1533.92
# indels per 100 kbp	42.52	26.48	21.02	48.46
Largest alignment	8486	3348	4205	10276
NA50	-	-	672	-
NGA50	-	-	-	-
LA50	-	-	26	-

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	5	1	1	7
# relocations	1	0	0	0
# translocations	3	1	1	6
# inversions	1	0	0	1
# possibly misassembled contigs	17	5	5	22
# misassembled contigs	4	1	1	4
Misassembled contigs length	10918	1756	2021	7315
# local misassemblies	3	7	22	5
# structural variations	0	0	0	0
# mismatches	1880	583	638	2026
# indels	48	9	9	64
# short indels	43	8	8	51
# long indels	5	1	1	13
Indels length	108	26	21	228

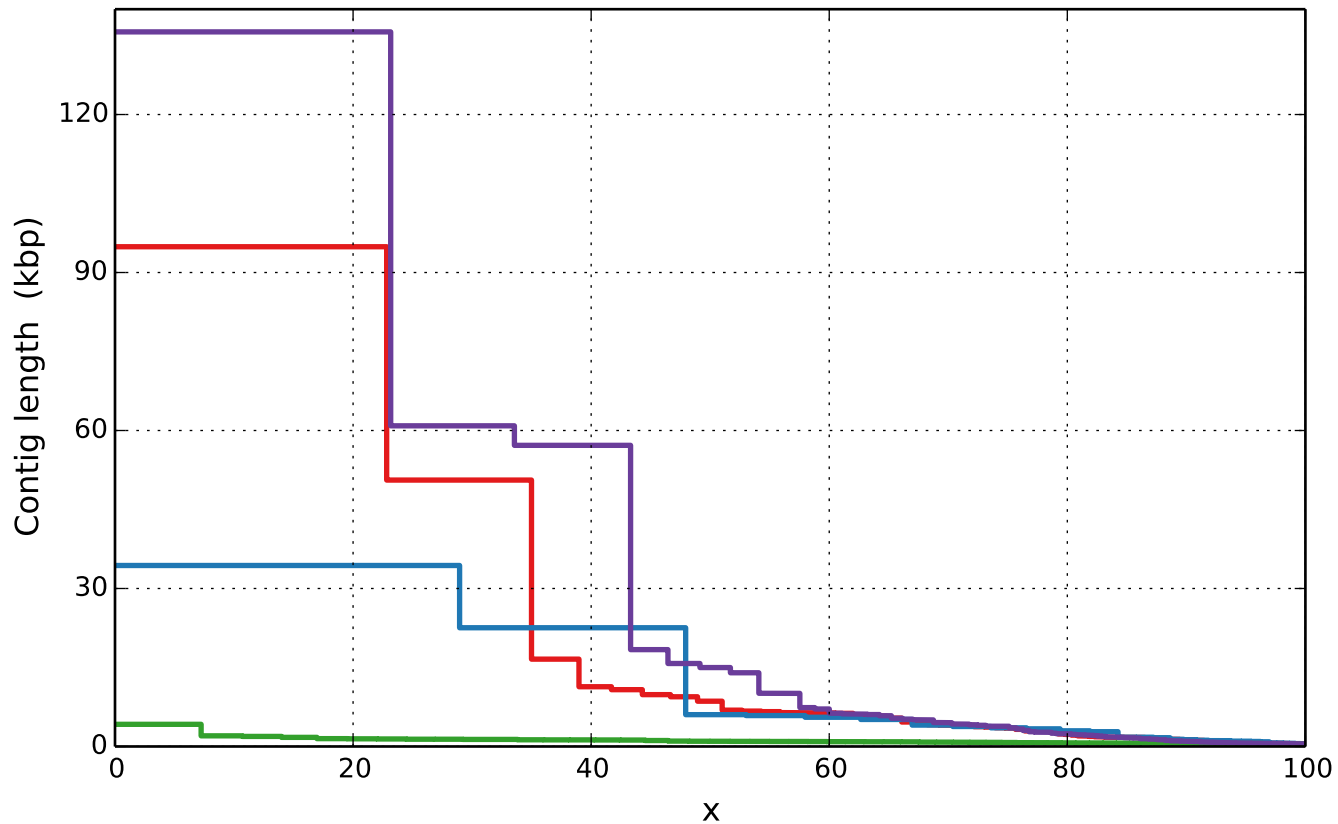
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	72	13	25	113
# with misassembly	2	2	3	5
# both parts are significant	14	3	4	20
Partially unaligned length	293703	79800	13175	445246
# N's	315	1520	2557	4557

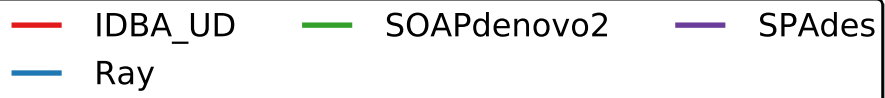
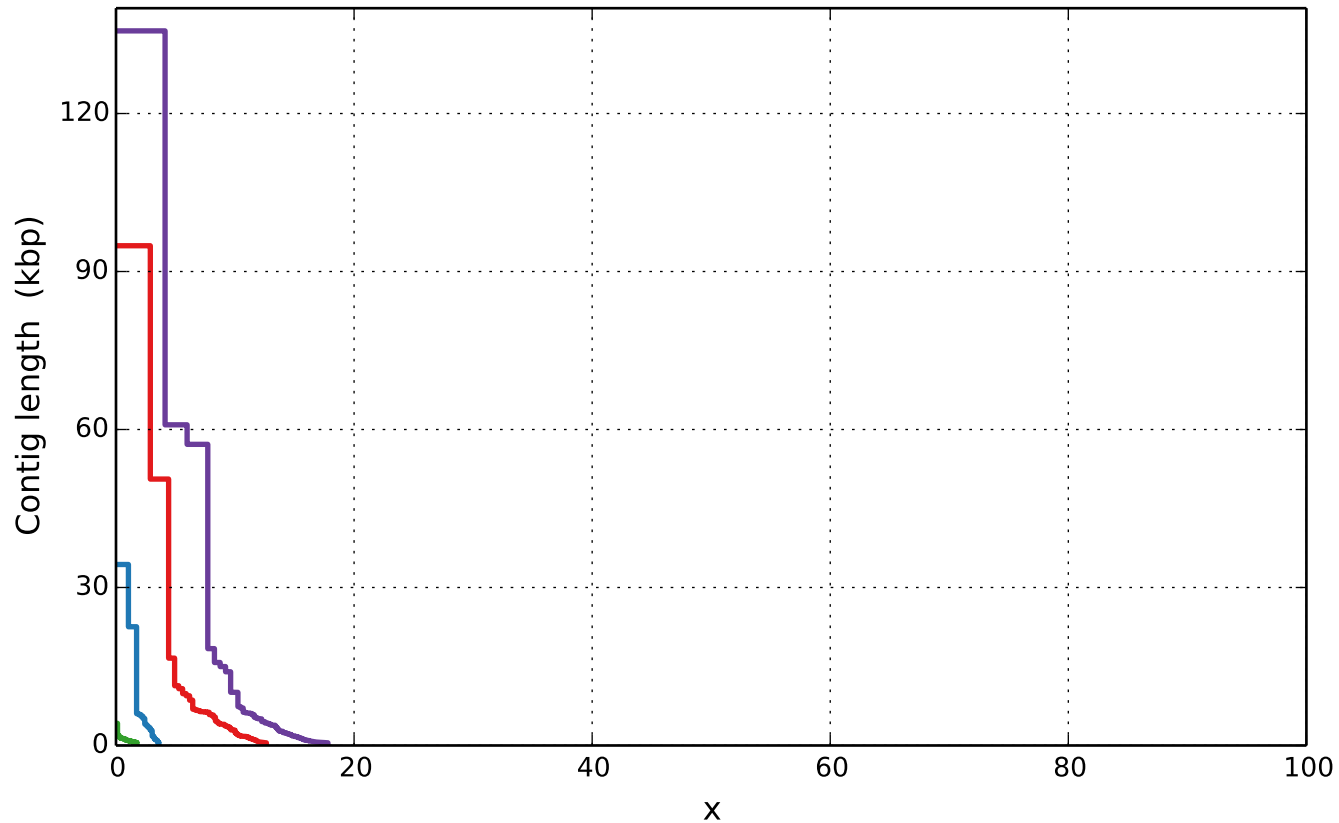
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

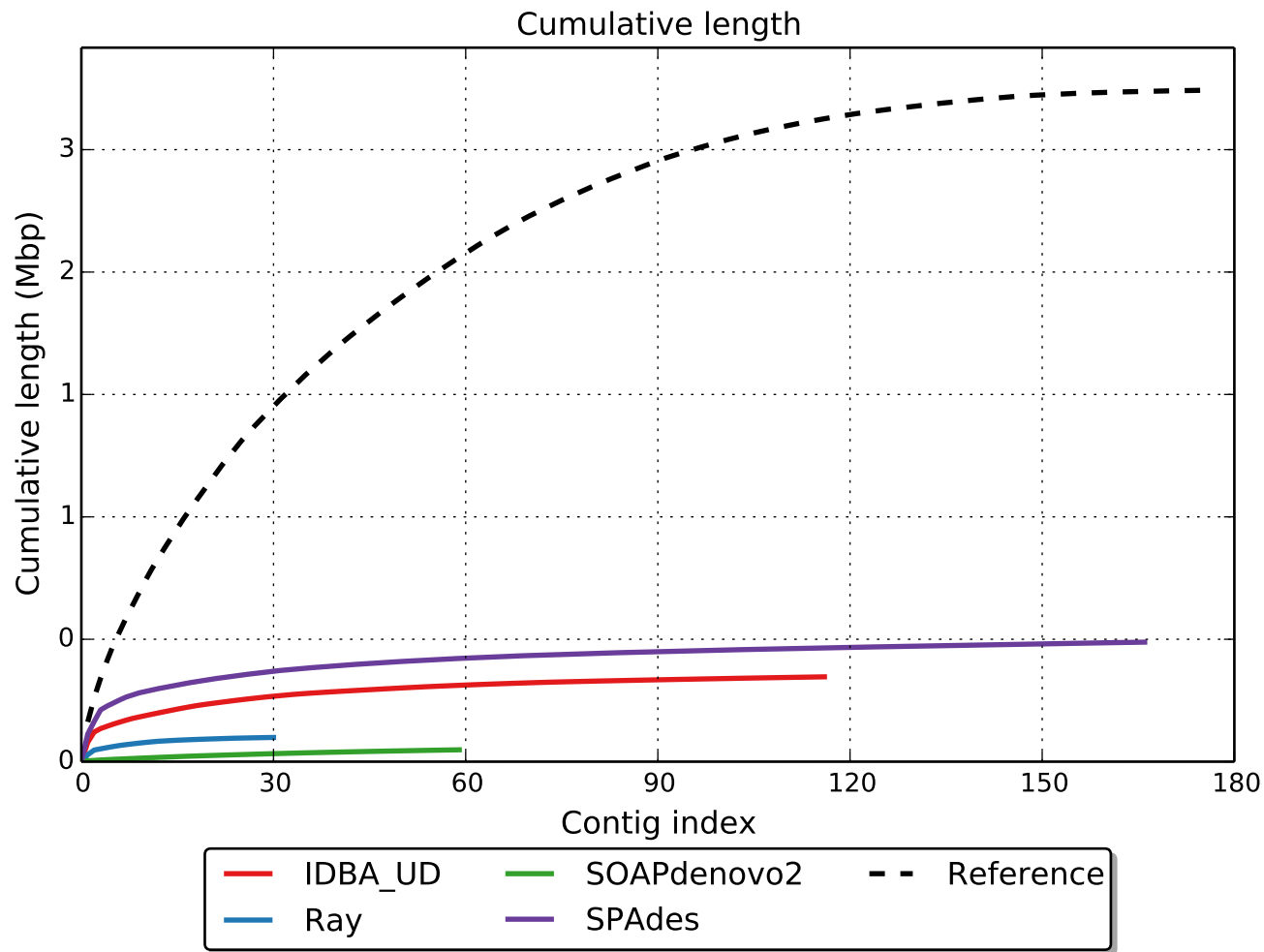
Nx



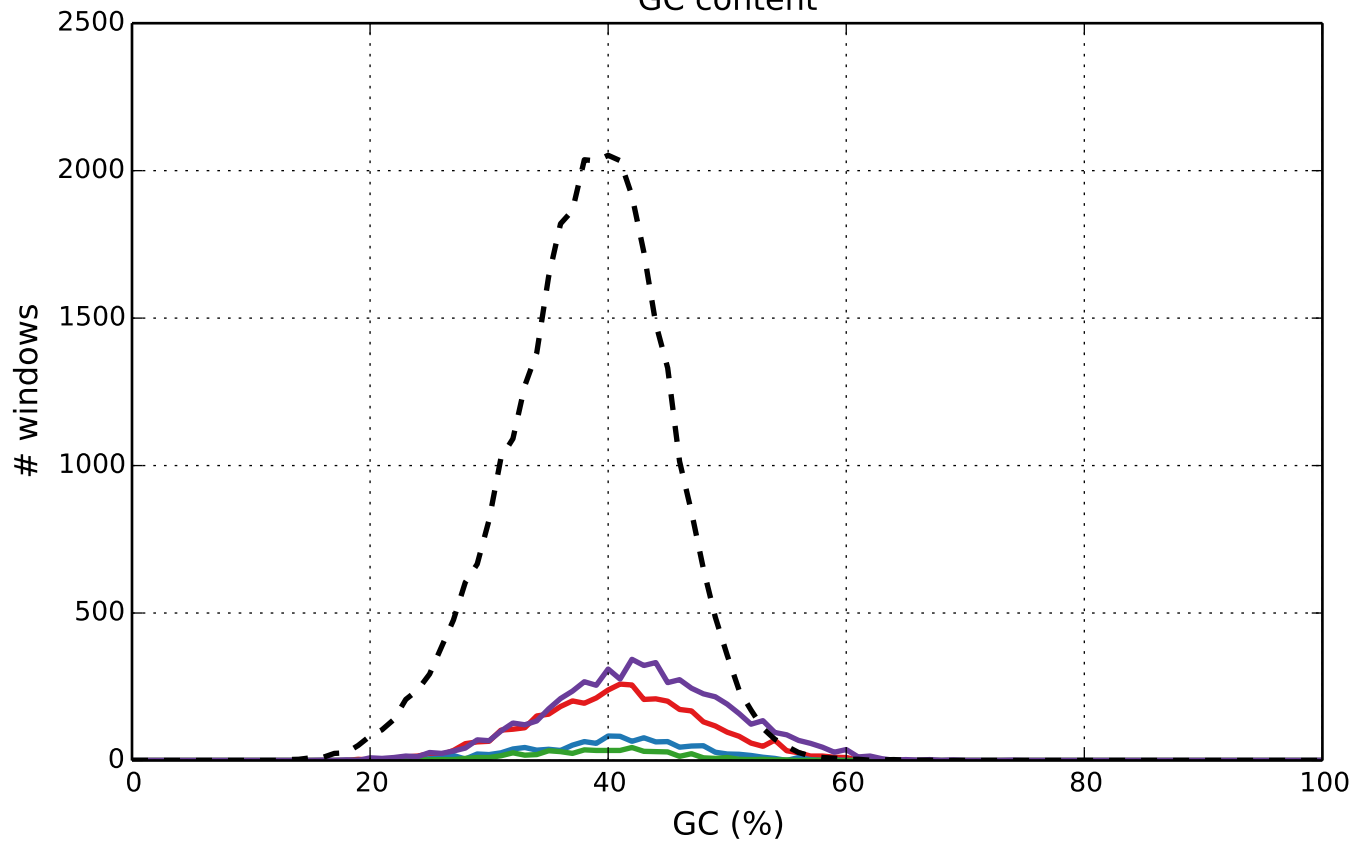
— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray

NGx





GC content



— IDBA\_UD    — SOAPdenovo2    - - Reference  
— Ray    — SPAdes

# Misassemblies

