

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	63	20	11	60
# contigs (>= 5000 bp)	23	15	0	20
# contigs (>= 10000 bp)	21	10	0	16
# contigs (>= 25000 bp)	18	3	0	12
# contigs (>= 50000 bp)	13	0	0	8
Total length (>= 1000 bp)	1540852	247774	20357	978785
Total length (>= 5000 bp)	1467880	238999	0	897853
Total length (>= 10000 bp)	1455927	204319	0	875029
Total length (>= 25000 bp)	1423630	84692	0	806941
Total length (>= 50000 bp)	1265222	0	0	669184
# contigs	102	22	37	133
Largest contig	182993	29730	2987	156462
Total length	1567469	249157	37782	1027882
Reference length	2731235	2731235	2731235	2731235
GC (%)	46.52	47.10	39.95	46.29
Reference GC (%)	42.70	42.70	42.70	42.70
N50	81029	21542	1159	59871
NG50	29169	-	-	-
N75	69354	12255	729	32855
L50	7	5	10	6
LG50	16	-	-	-
L75	12	9	21	11
# misassemblies	1	0	4	3
# misassembled contigs	1	0	3	3
Misassembled contigs length	1050	0	2120	5863
# local misassemblies	4	1	12	3
# structural variations	0	0	0	1
# unaligned contigs	0 + 69 part	0 + 17 part	0 + 14 part	0 + 88 part
Unaligned length	1489887	234620	10695	947634
Genome fraction (%)	2.763	0.492	0.924	2.820
Duplication ratio	1.028	1.081	1.074	1.042
# N's per 100 kbp	65.46	2377.62	6971.57	434.97
# mismatches per 100 kbp	2093.41	1509.52	1664.68	1956.38
# indels per 100 kbp	99.37	89.23	27.74	89.58
Largest alignment	11333	6373	2426	4969
NA50	-	-	535	-
NGA50	-	-	-	-
LA50	-	-	20	-

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

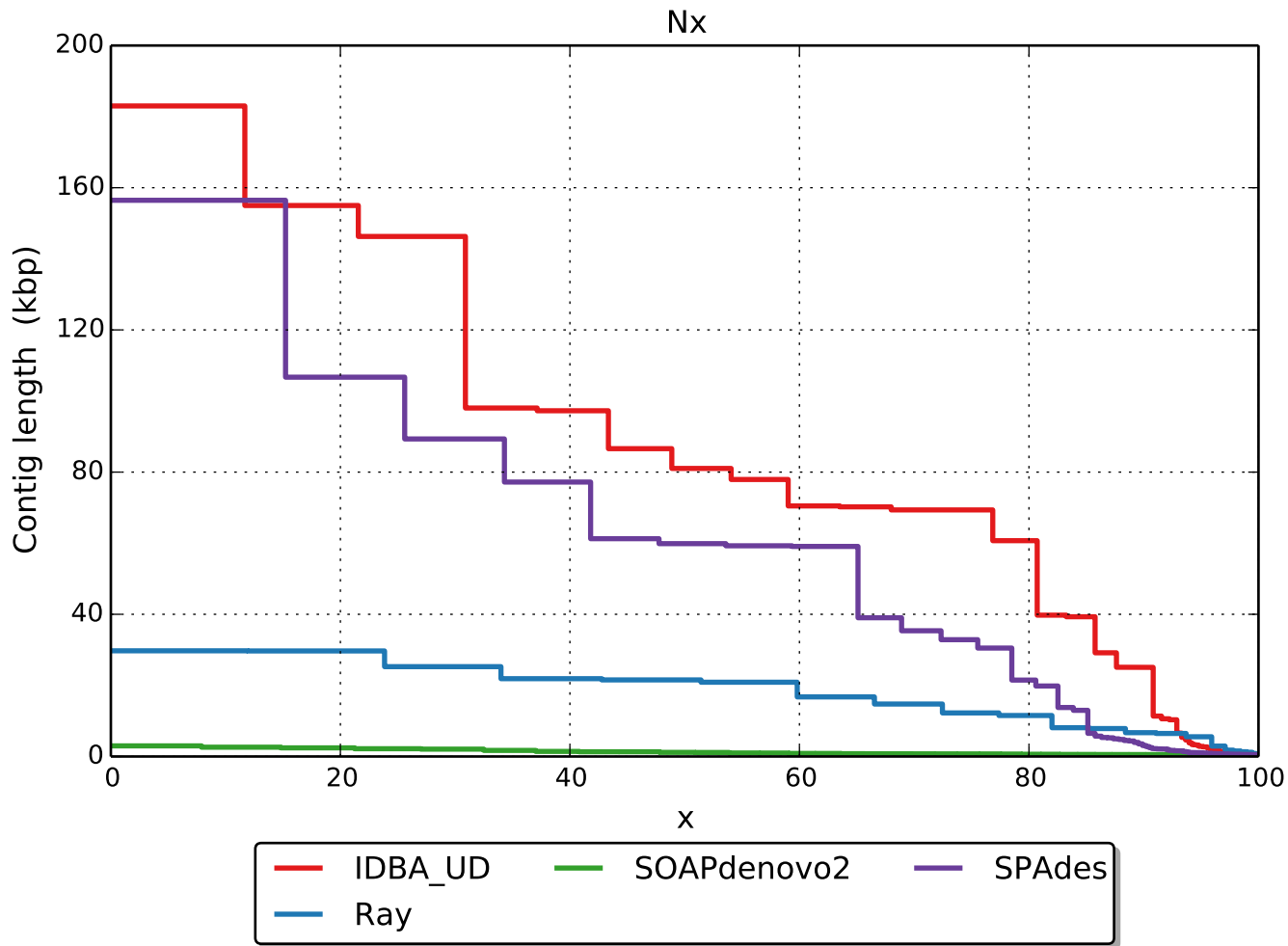
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	1	0	4	3
# relocations	1	0	4	3
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	9	2	3	8
# misassembled contigs	1	0	3	3
Misassembled contigs length	1050	0	2120	5863
# local misassemblies	4	1	12	3
# structural variations	0	0	0	1
# mismatches	1580	203	420	1507
# indels	75	12	7	69
# short indels	74	12	7	57
# long indels	1	0	0	12
Indels length	112	13	7	210

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).

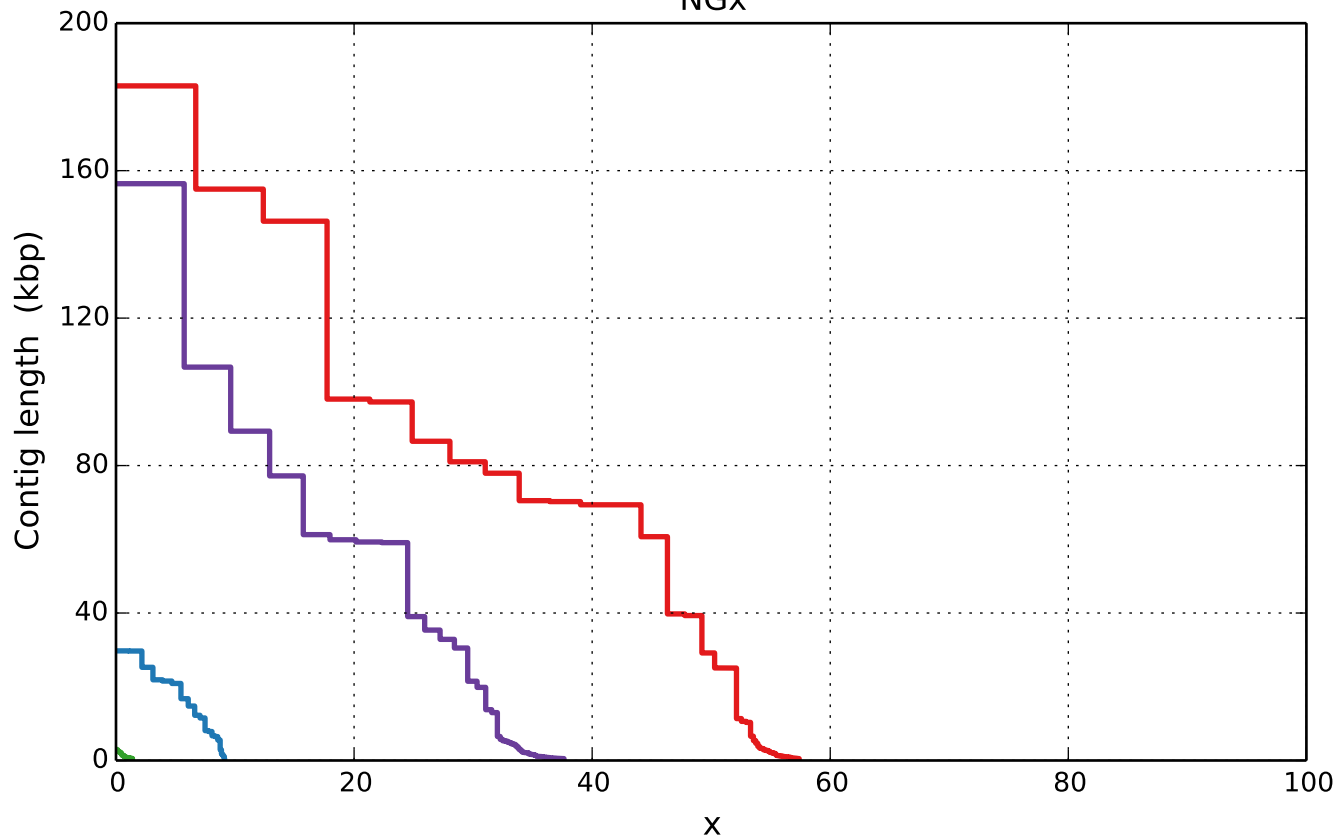
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	69	17	14	88
# with misassembly	5	0	4	3
# both parts are significant	9	2	3	7
Partially unaligned length	1489887	234620	10695	947634
# N's	1026	5924	2634	4471

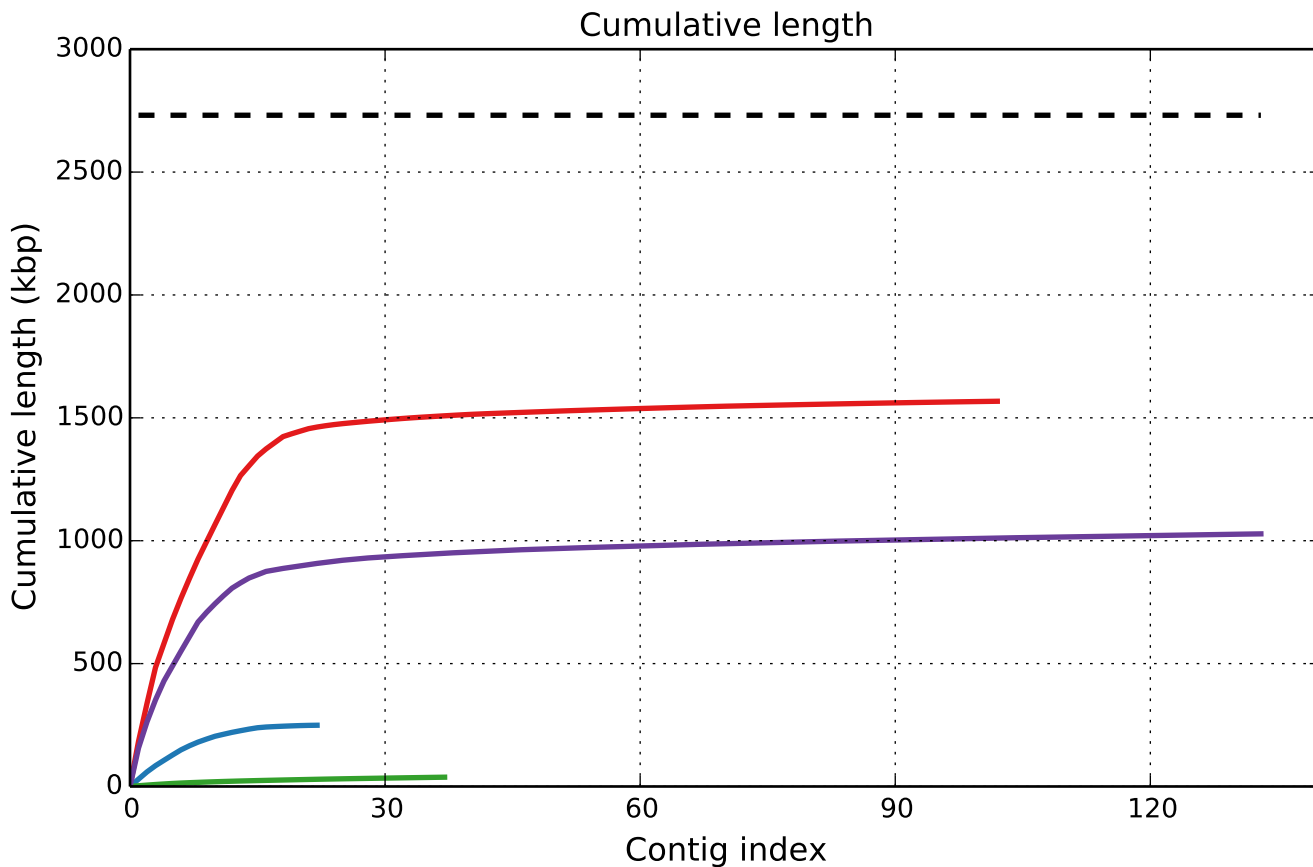
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



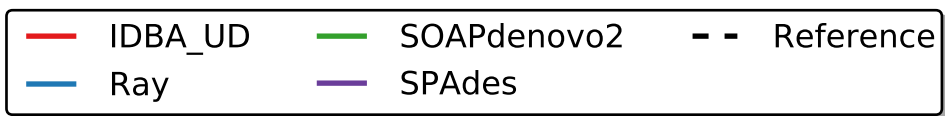
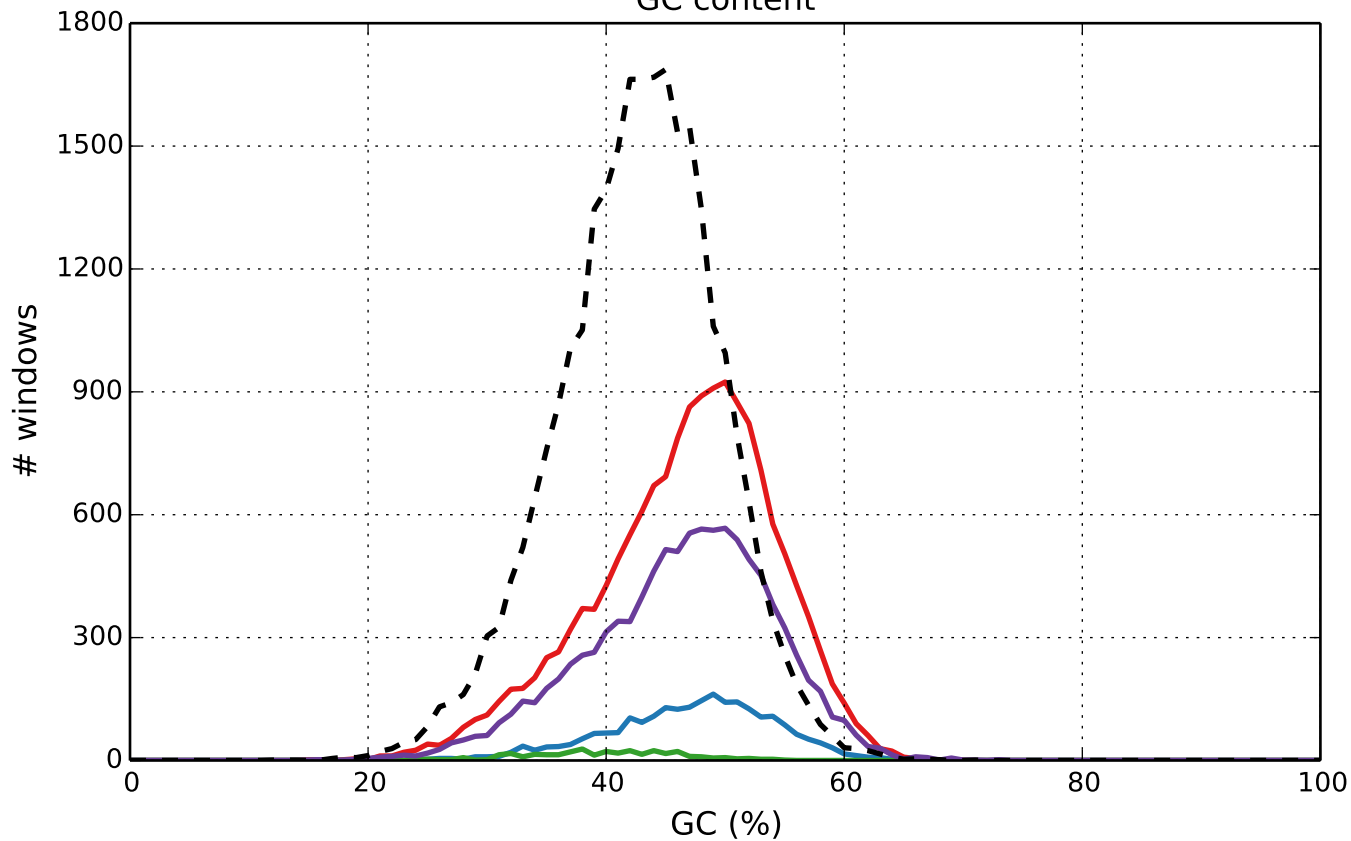
NGx

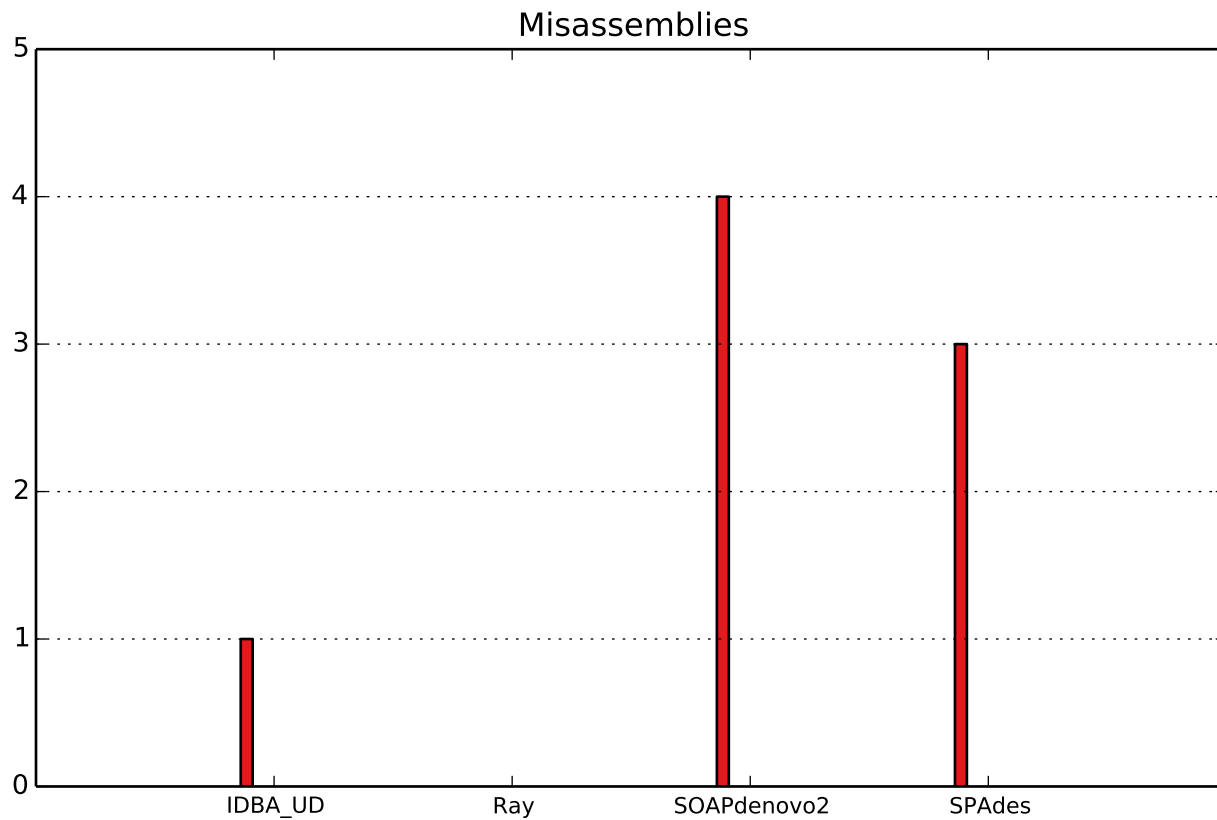


— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



GC content





Cumulative length (aligned contigs)

