

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	33	18	44	32
# contigs (>= 5000 bp)	5	3	5	4
# contigs (>= 10000 bp)	1	3	0	2
# contigs (>= 25000 bp)	0	1	0	1
# contigs (>= 50000 bp)	0	1	0	1
Total length (>= 1000 bp)	94468	154528	106308	193321
Total length (>= 5000 bp)	37672	125447	35341	143867
Total length (>= 10000 bp)	11176	125447	0	129655
Total length (>= 25000 bp)	0	88128	0	118876
Total length (>= 50000 bp)	0	88128	0	118876
# contigs	65	30	100	52
Largest contig	11176	88128	9696	118876
Total length	118064	163447	145763	207743
Reference length	7694202	7694202	7694202	7694202
GC (%)	44.23	47.78	47.01	46.42
Reference GC (%)	43.05	43.05	43.05	43.05
N50	2830	88128	1734	118876
N75	1221	15847	935	3033
L50	11	1	21	1
L75	28	3	48	8
# misassemblies	0	1	0	0
# misassembled contigs	0	1	0	0
Misassembled contigs length	0	15847	0	0
# local misassemblies	0	9	22	0
# structural variations	0	1	0	0
# unaligned contigs	0 + 14 part	0 + 5 part	0 + 9 part	0 + 15 part
Unaligned length	17514	84812	3660	133001
Genome fraction (%)	1.278	0.952	1.824	0.960
Duplication ratio	1.022	1.073	1.013	1.012
# N's per 100 kbp	409.95	1119.02	818.45	831.32
# mismatches per 100 kbp	902.99	900.63	521.00	600.05
# indels per 100 kbp	44.74	20.47	20.67	79.92
Largest alignment	11140	21366	9696	8310
NA50	1740	-	1707	-
NGA50	-	-	-	-
NA75	789	-	860	-
LA50	15	-	21	-
LA75	41	-	49	-

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

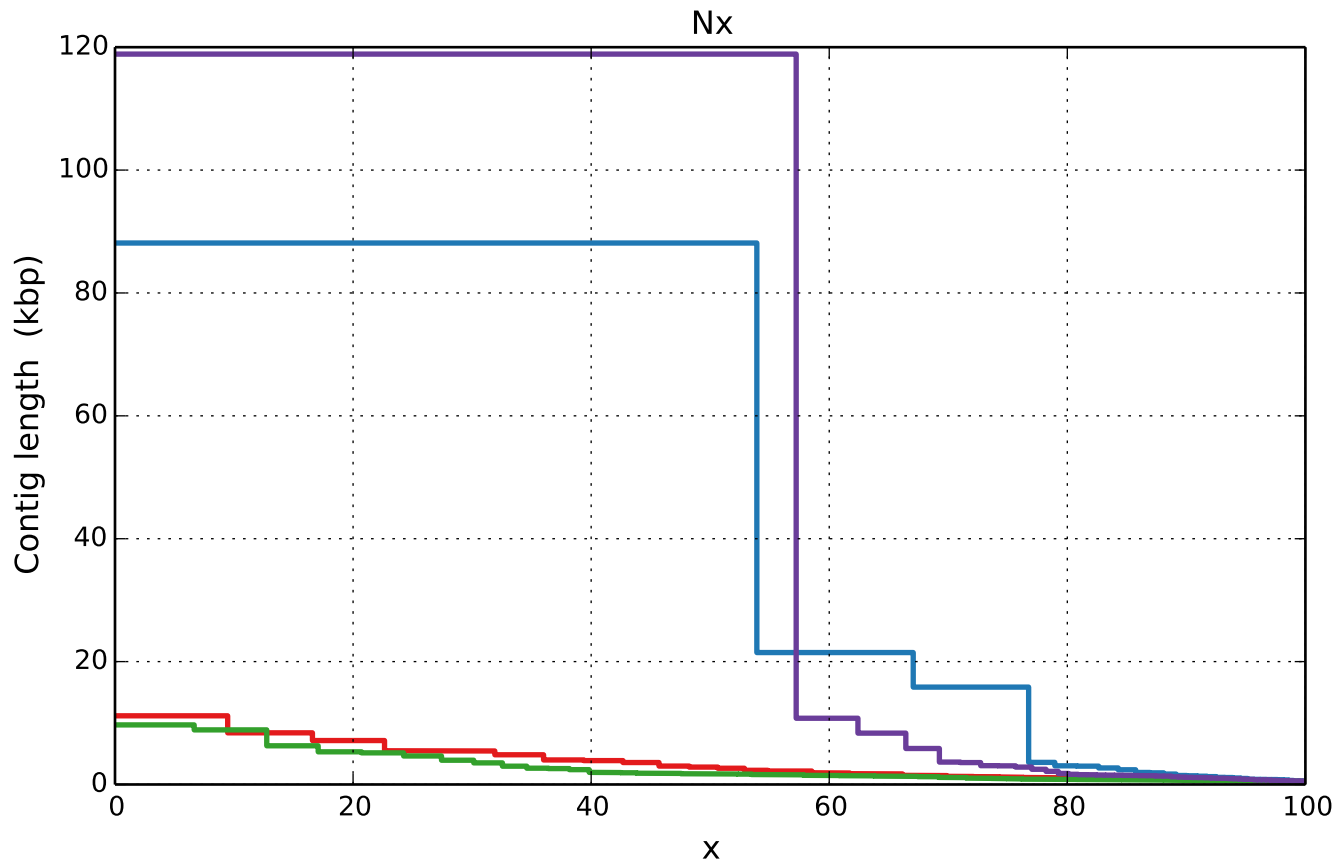
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	1	0	0
# relocations	0	1	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	1	2	1	2
# misassembled contigs	0	1	0	0
Misassembled contigs length	0	15847	0	0
# local misassemblies	0	9	22	0
# structural variations	0	1	0	0
# mismatches	888	660	731	443
# indels	44	15	29	59
# short indels	39	14	27	50
# long indels	5	1	2	9
Indels length	118	48	67	220

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

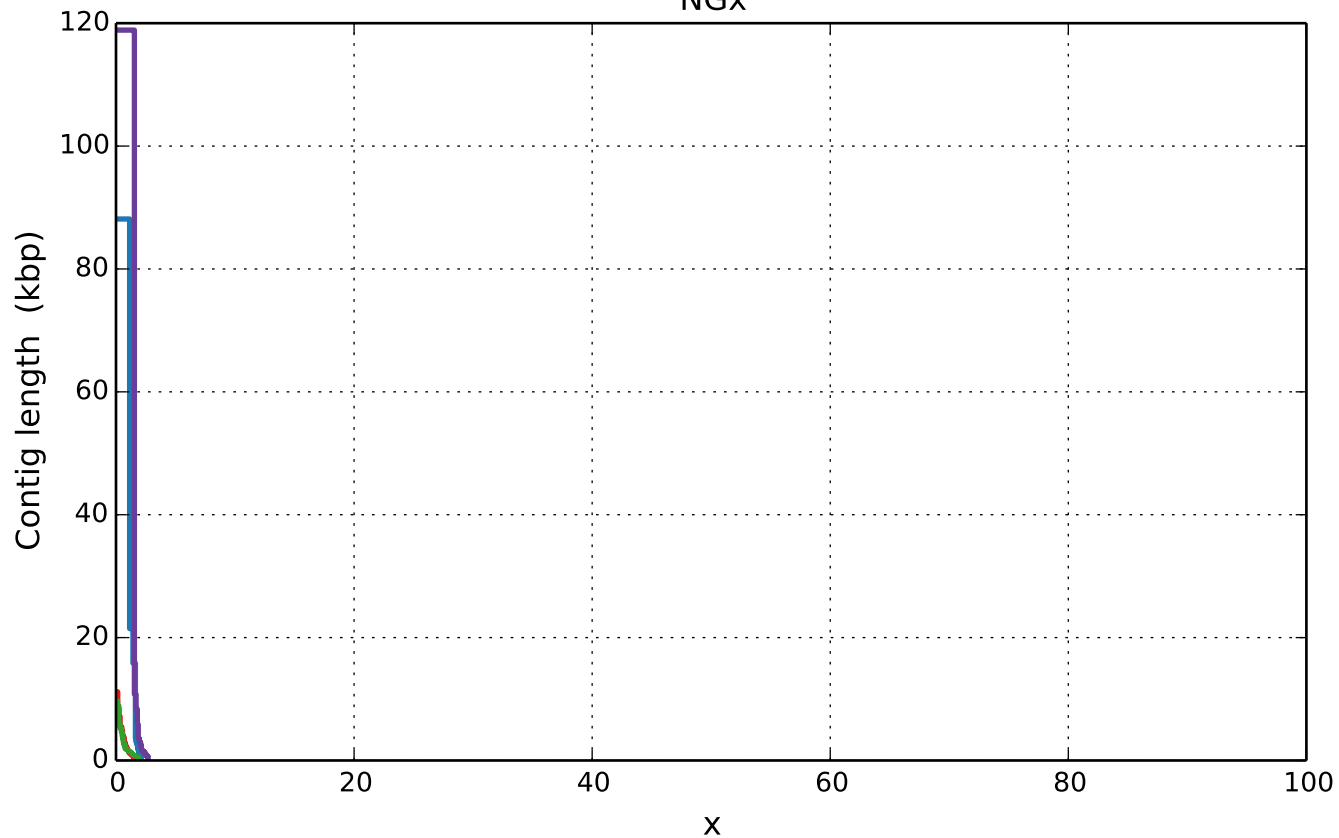
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	14	5	9	15
# with misassembly	1	0	0	0
# both parts are significant	1	1	1	2
Partially unaligned length	17514	84812	3660	133001
# N's	484	1829	1193	1727

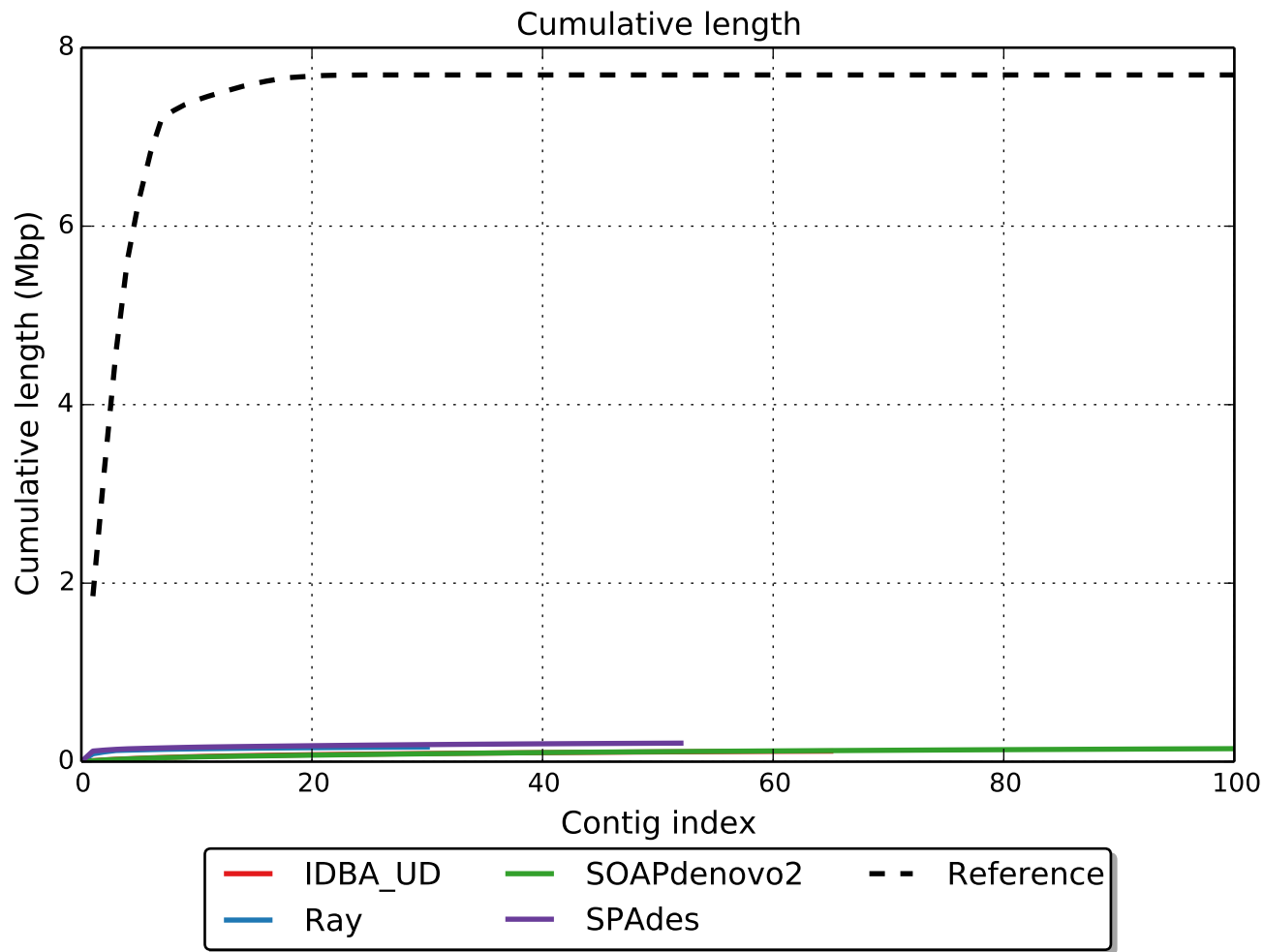
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



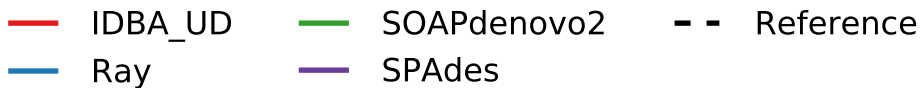
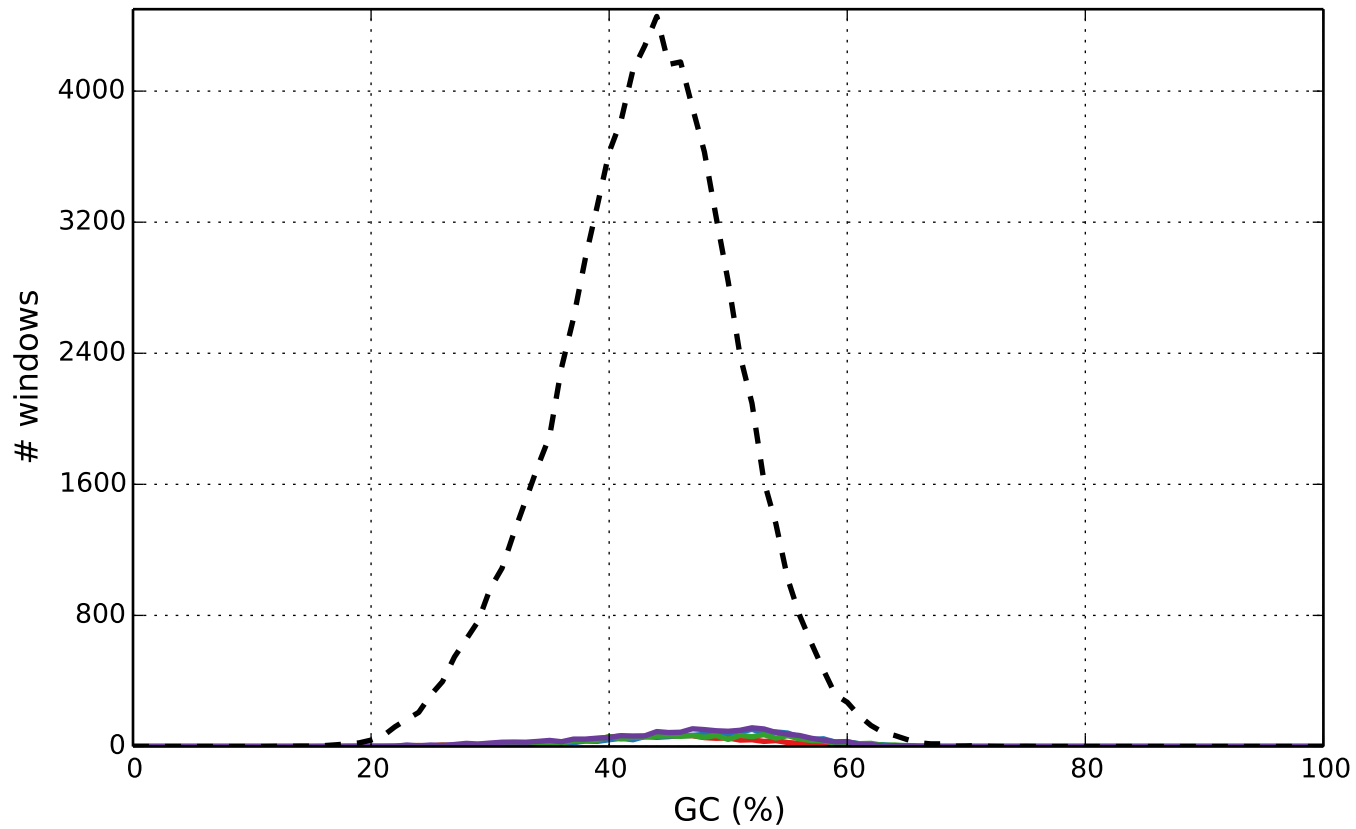
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

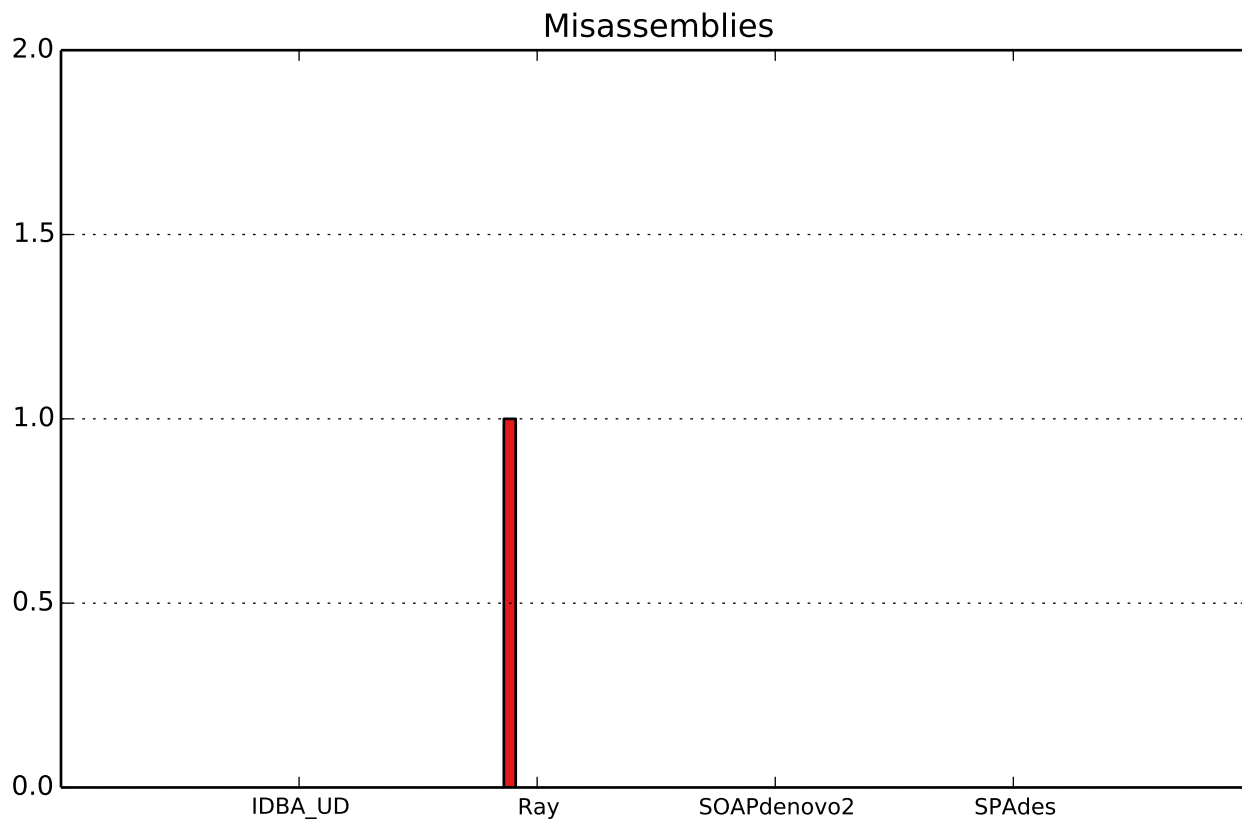
NGx





GC content





 # relocations

