

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	133	16	1	3	25
# contigs (>= 5000 bp)	2	1	1	0	5
# contigs (>= 10000 bp)	2	1	1	0	3
# contigs (>= 25000 bp)	2	1	1	0	1
# contigs (>= 50000 bp)	2	1	1	0	1
Total length (>= 1000 bp)	964024	262329	242734	3650	303624
Total length (>= 5000 bp)	798310	241774	242734	0	266578
Total length (>= 10000 bp)	798310	241774	242734	0	255712
Total length (>= 25000 bp)	798310	241774	242734	0	235338
Total length (>= 50000 bp)	798310	241774	242734	0	235338
# contigs	886	234	2	23	247
Largest contig	556320	241774	242734	1346	235338
Total length	1475374	398410	243292	16796	443371
Reference length	3842594	3842594	3842594	3842594	3842594
GC (%)	44.98	44.76	41.02	49.27	45.76
Reference GC (%)	50.11	50.11	50.11	50.11	50.11
N50	241990	241774	242734	776	235338
N75	791	713	242734	562	727
L50	2	1	1	9	1
L75	295	62	1	15	60
# misassemblies	21	4	0	0	4
# misassembled contigs	21	4	0	0	4
Misassembled contigs length	18151	3874	0	0	3628
# local misassemblies	10	4	0	0	1
# structural variations	2	0	0	0	0
# unaligned contigs	0 + 45 part	0 + 28 part	0 + 2 part	0 + 6 part	0 + 45 part
Unaligned length	761977	226733	215255	912	268727
Genome fraction (%)	17.808	4.445	0.729	0.413	4.524
Duplication ratio	1.043	1.005	1.001	1.001	1.005
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	629.13	1179.03	1935.78	1467.99	1672.96
# indels per 100 kbp	46.18	62.64	167.86	56.70	64.43
Largest alignment	9283	9283	9283	1346	9283
NA50	-	-	-	749	-
NGA50	-	-	-	-	-
NA75	-	-	-	521	-
LA50	-	-	-	9	-
LA75	-	-	-	17	-

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

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	21	4	0	0	4
# relocations	4	0	0	0	1
# translocations	17	4	0	0	3
# inversions	0	0	0	0	0
# possibly misassembled contigs	7	3	1	0	4
# misassembled contigs	21	4	0	0	4
Misassembled contigs length	18151	3874	0	0	3628
# local misassemblies	10	4	0	0	1
# structural variations	2	0	0	0	0
# mismatches	4305	2014	542	233	2908
# indels	316	107	47	9	112
# short indels	297	100	43	9	106
# long indels	19	7	4	0	6
Indels length	555	199	104	14	185

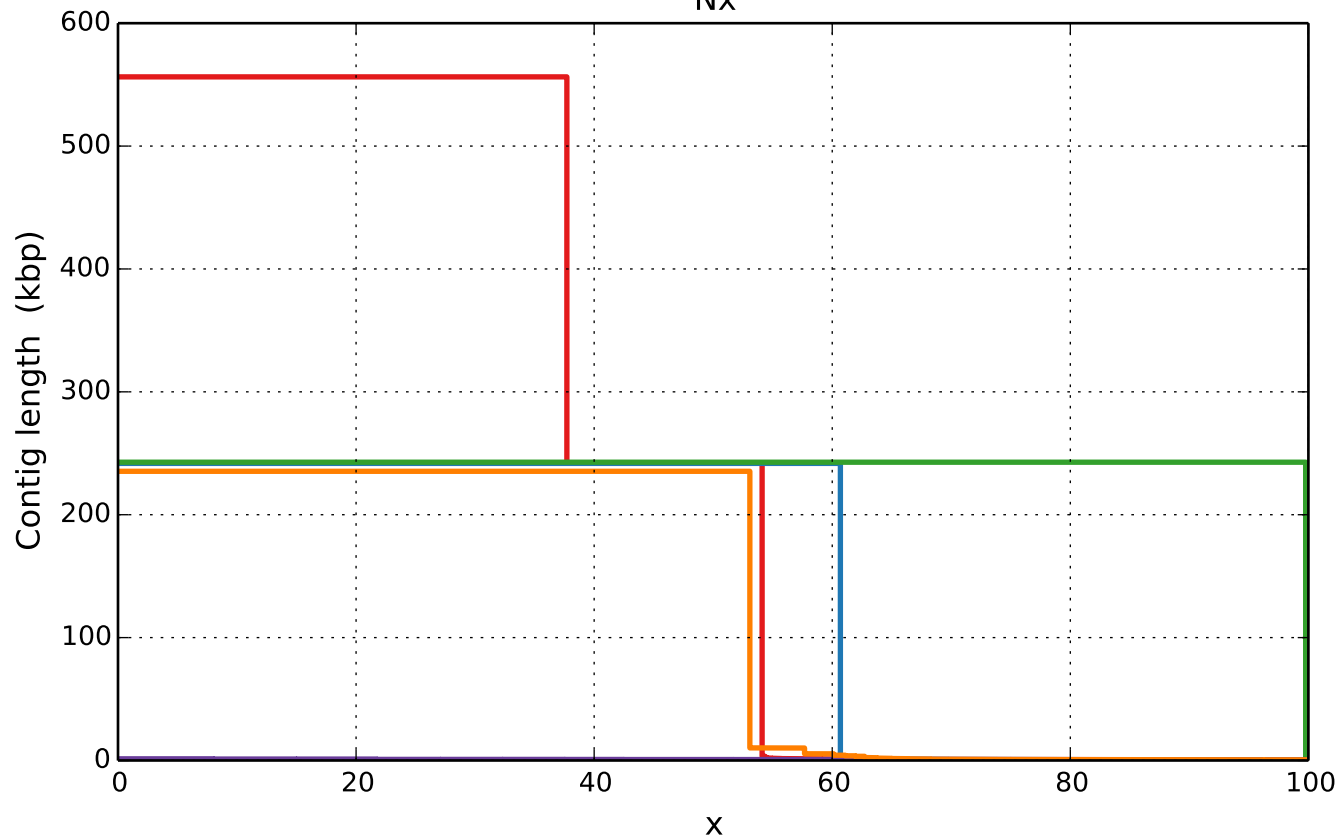
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	45	28	2	6	45
# with misassembly	2	1	1	0	1
# both parts are significant	7	3	1	0	4
Partially unaligned length	761977	226733	215255	912	268727
# N's	0	0	0	0	0

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



Gold_Assembly

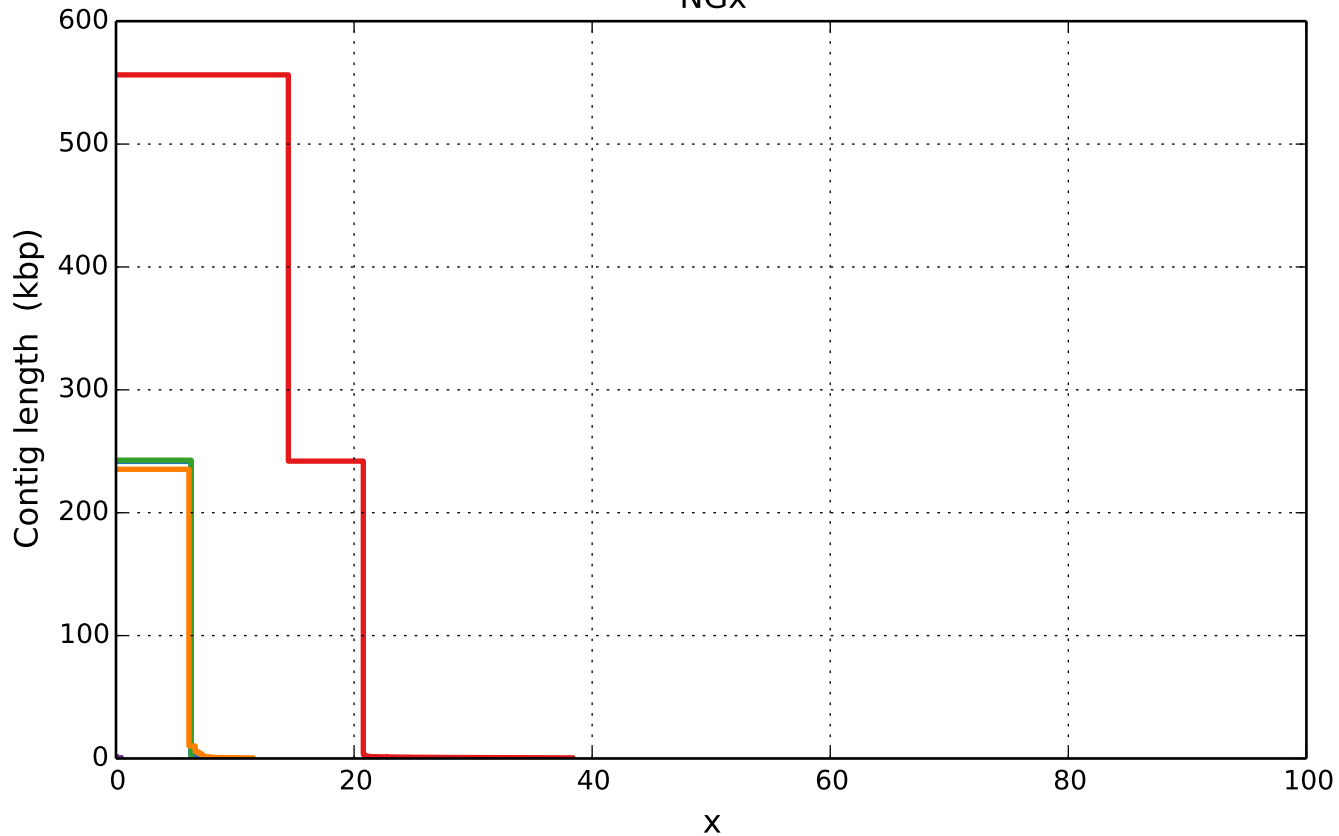
Ray

SPAdes

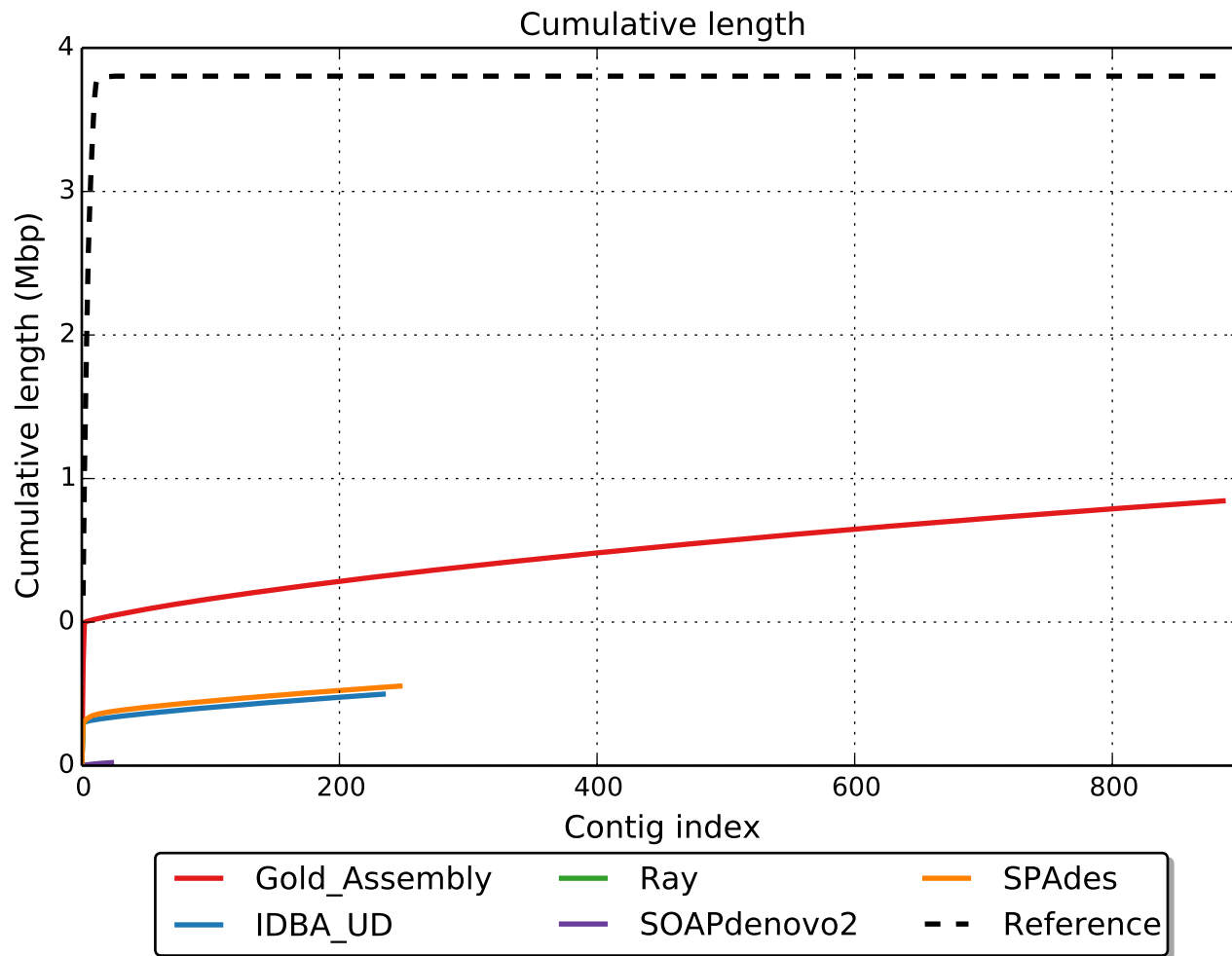
IDBA_UD

SOAPdenovo2

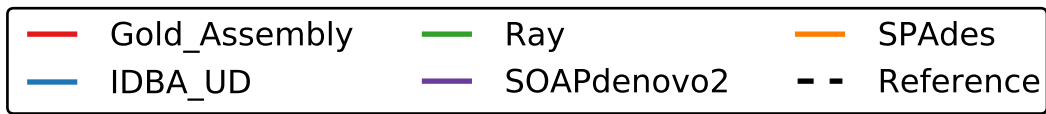
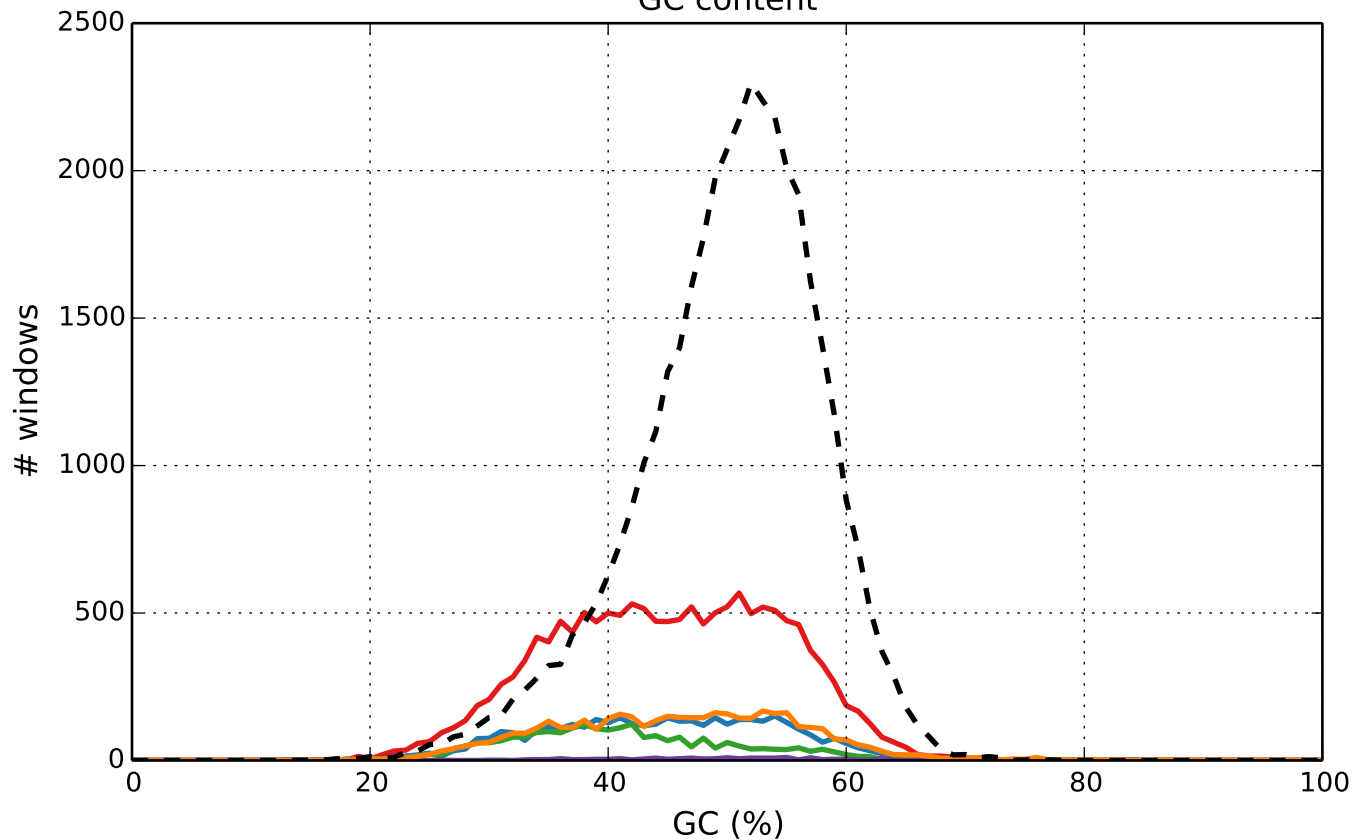
NGx



Gold_Assembly Ray SPAdes
IDBA_UD SOAPdenovo2



GC content



Misassemblies

