Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	29	24	57	26
# contigs (>= 5000 bp)	10	8	4	9
# contigs (>= 10000 bp)	10	5	0	8
# contigs (>= 25000 bp)	6	4	0	6
# contigs (>= 50000 bp)	4	1	0	3
Total length (>= 1000 bp)	497801	240884	126135	541414
Total length (>= 5000 bp)	463734	209645	23032	506413
Total length (>= 10000 bp)	463734	188786	0	499035
Total length (>= 25000 bp)	390447	177252	0	471151
Total length (>= 50000 bp)	318099	68072	0	362668
# contigs	40	31	107	51
Largest contig	126992	68072	7255	179778
Total length	505377	245838	162002	557173
Reference length	5530115	5530115	5530115	5530115
GC (%)	46.20	46.70	46.90	45.91
Reference GC (%)	43.62	43.62	43.62	43.62
N50	65305	36527	1818	116588
N75	35493	11534	1121	36189
L50	3	3	24	2
L75	6	5	53	5
# misassemblies	1	0	1	0
# misassembled contigs	1	0	1	0
Misassembled contigs length	65305	0	2299	0
# local misassemblies	0	10	7	0
# structural variations	1	0	0	0
# unaligned contigs	0 + 17 part	0 + 11 part	0 + 11 part	0 + 34 part
Unaligned length	357695	167086	8598	451829
Genome fraction (%)	2.292	1.346	2.732	1.860
Duplication ratio	1.165	1.058	1.015	1.024
# N's per 100 kbp	29.68	1173.13	416.04	268.68
# mismatches per 100 kbp	489.07	702.75	692.43	852.60
# indels per 100 kbp	14.99	8.06	17.87	35.00
Largest alignment	30990	36179	5375	49043
NA50	-	-	1532	-
NGA50	-	-	-	-
NA75	-	-	903	-
LA50	-	-	28	-
LA75	-	-	61	-

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).
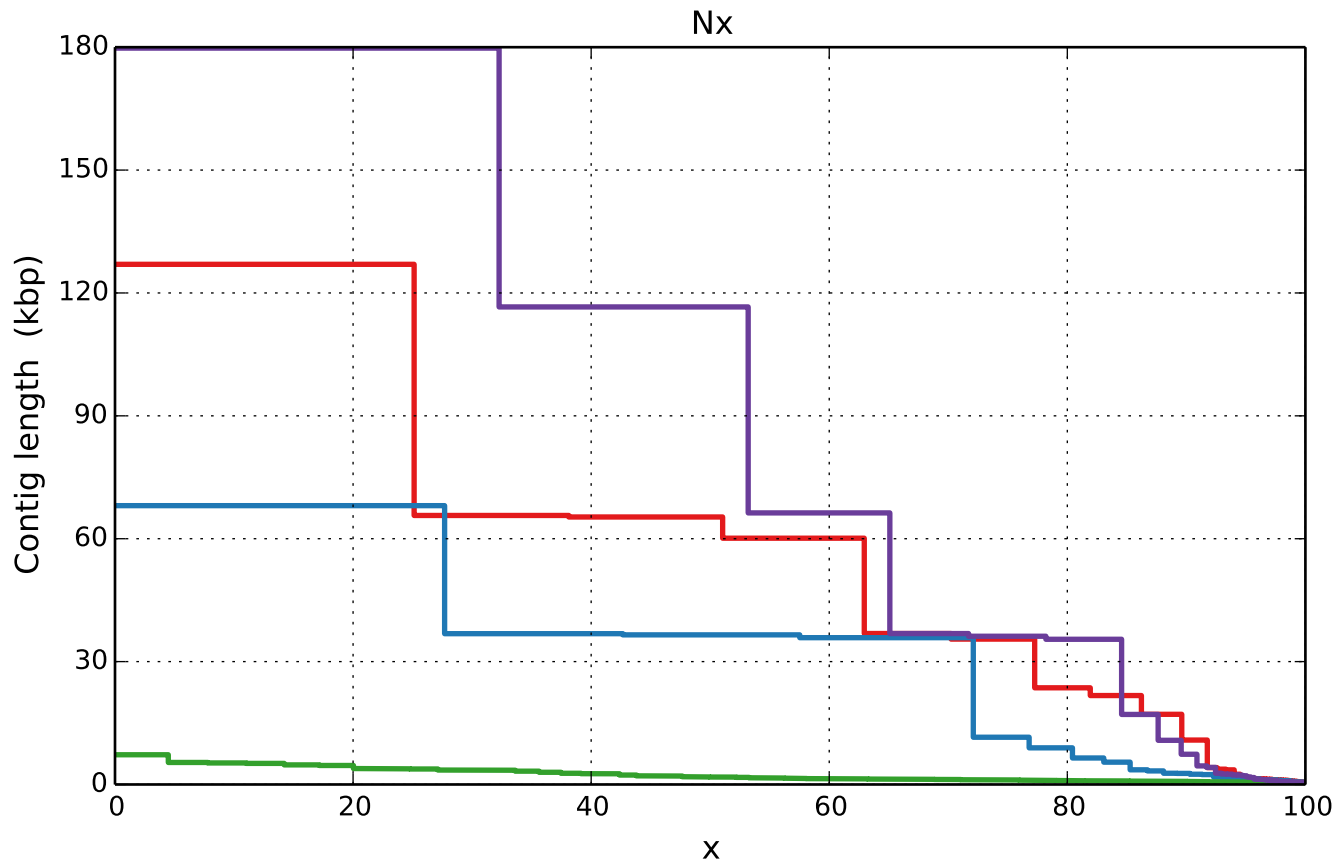
Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	1	0	1	0
# relocations	1	0	1	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	7	5	5	9
# misassembled contigs	1	0	1	0
Misassembled contigs length	65305	0	2299	0
# local misassemblies	0	10	7	0
# structural variations	1	0	0	0
# mismatches	620	523	1046	877
# indels	19	6	27	36
# short indels	17	6	26	33
# long indels	2	0	1	3
Indels length	54	12	74	95

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).
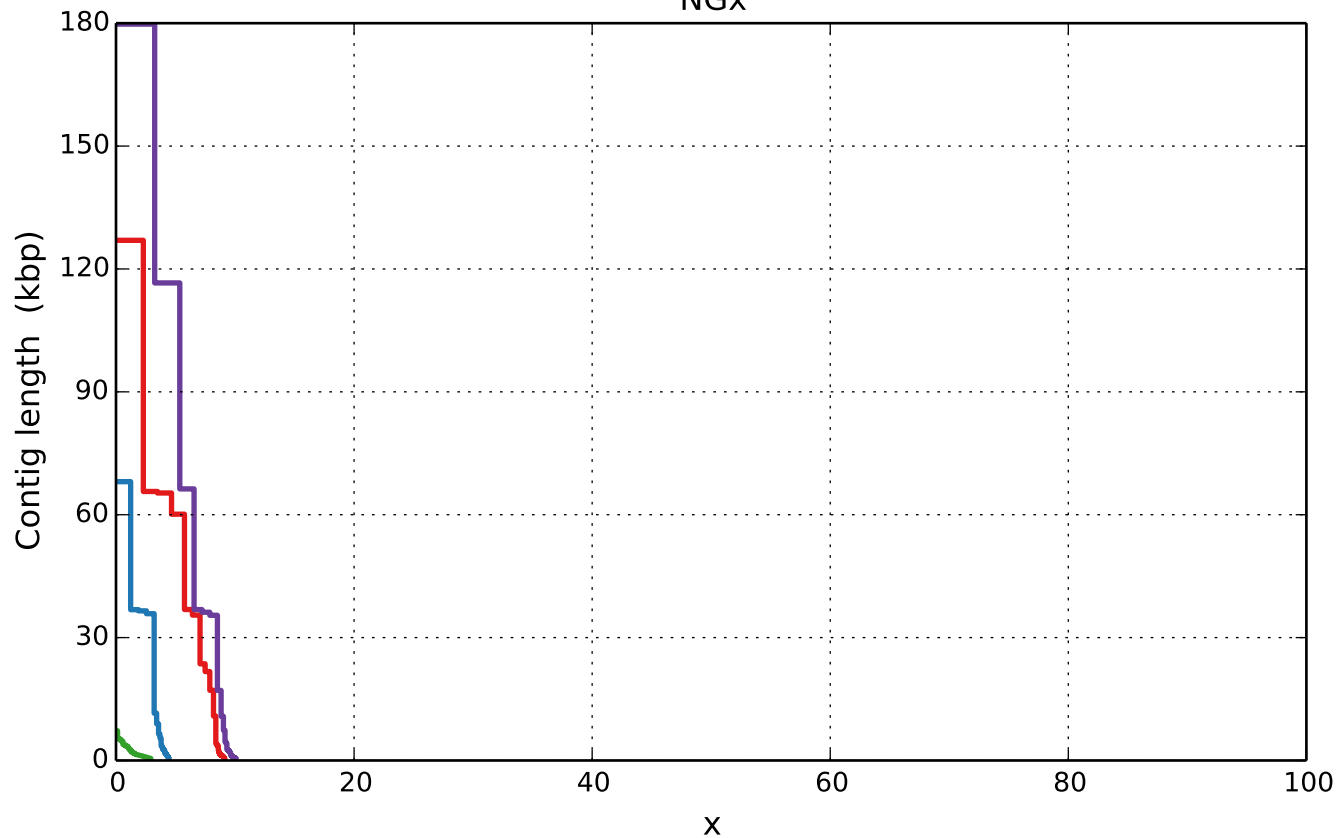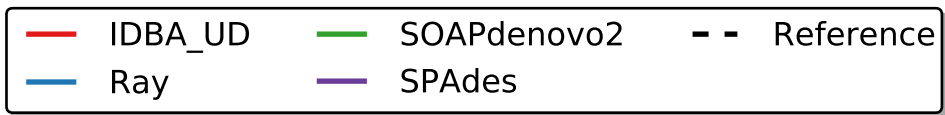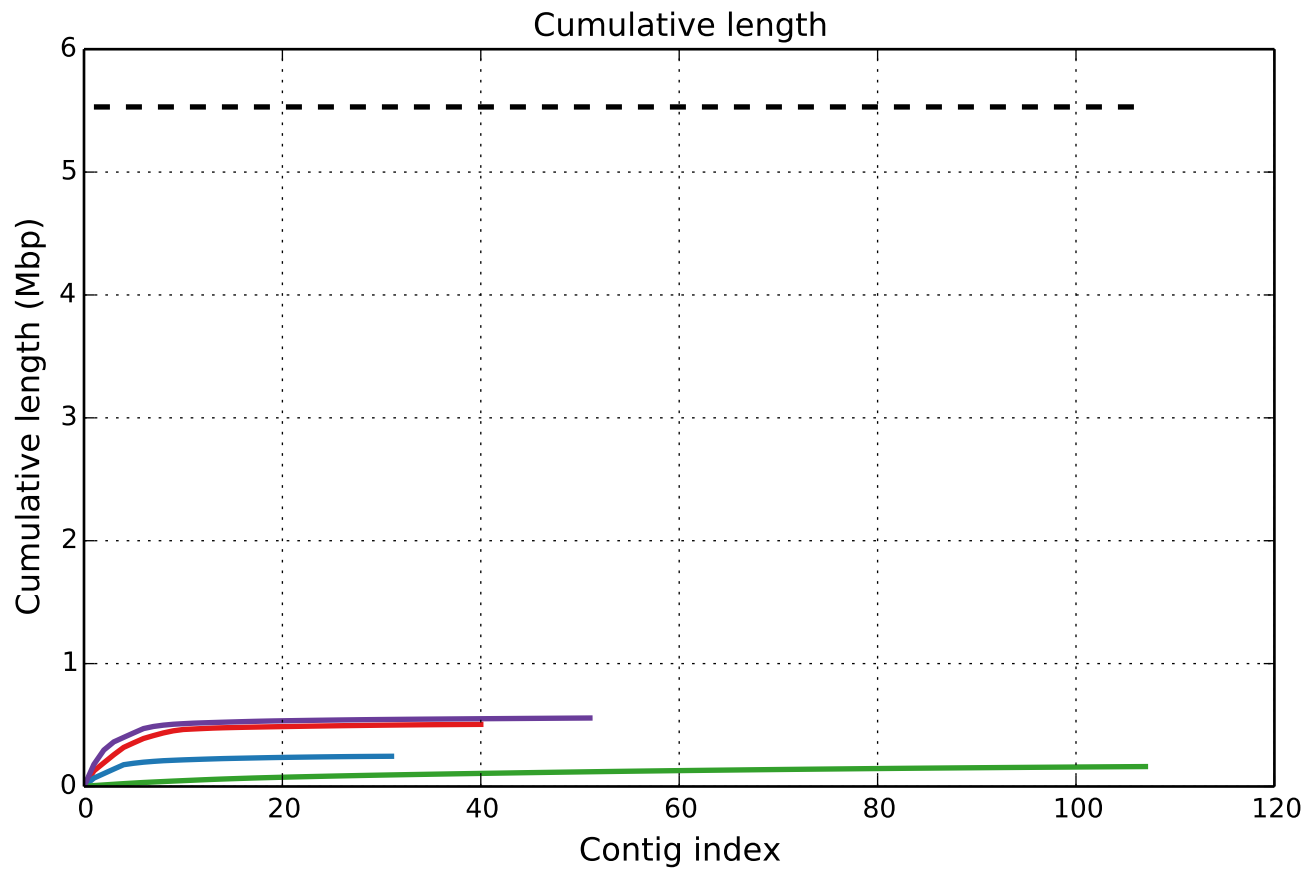
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	17	11	11	34
# with misassembly	1	0	1	1
# both parts are significant	6	4	4	9
Partially unaligned length	357695	167086	8598	451829
# N's	150	2884	674	1497

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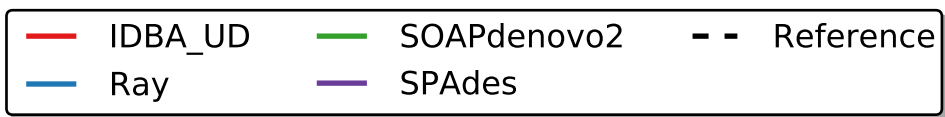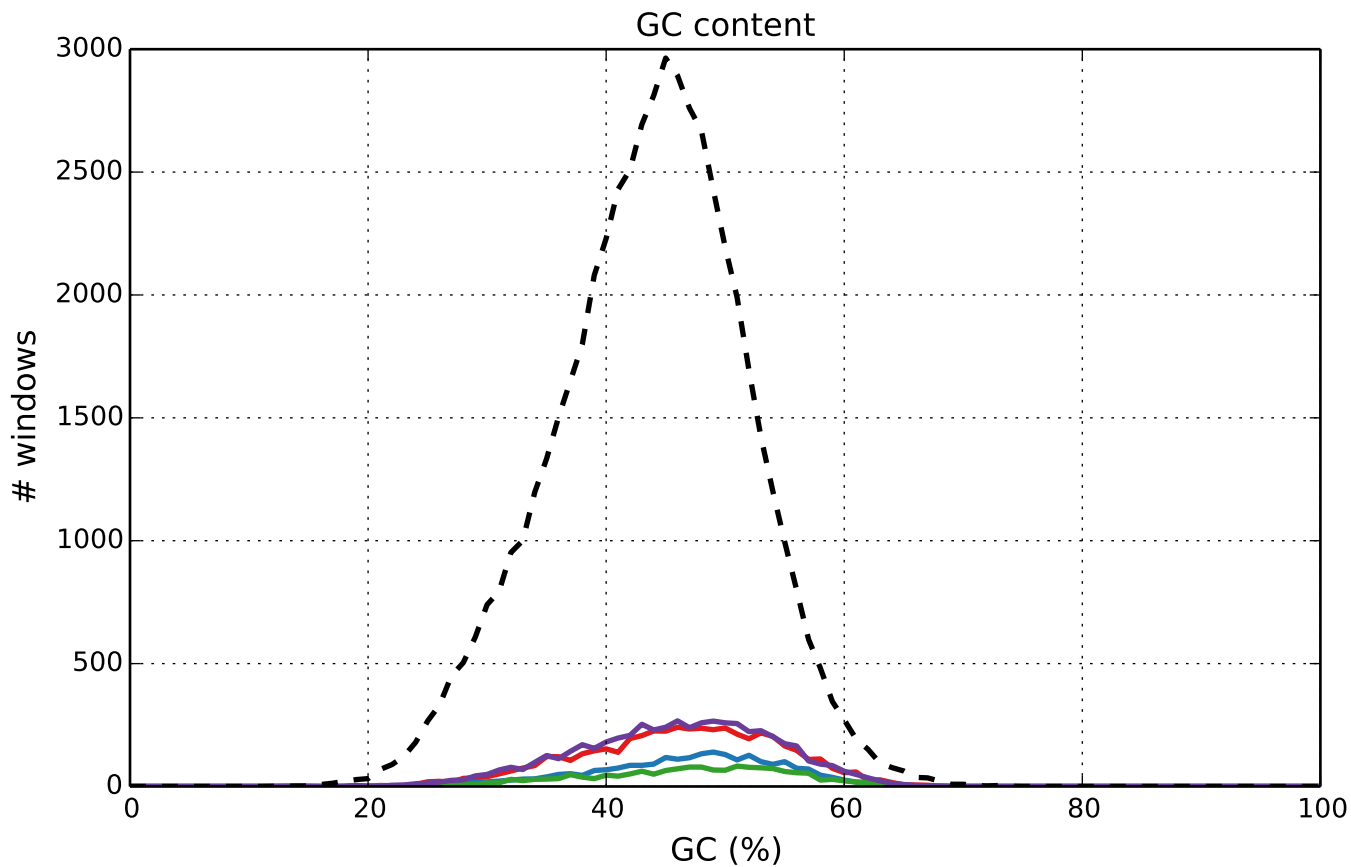(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

NGx

Cumulative length

GC content

windows

GC (%)

IDBA_UD   SOAPdenovo2   - - - Reference

Ray   SPAdes

Misassemblies

Cumulative length (aligned contigs)

NGAx

Genome fraction, %