Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	18	10	13	11
# contigs (>= 5000 bp)	4	2	0	3
# contigs (>= 10000 bp)	1	1	0	1
# contigs (>= 25000 bp)	1	0	0	1
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	88018	43886	25405	62139
Total length (>= 5000 bp)	60982	24893	0	44548
Total length (>= 10000 bp)	40490	18364	0	28935
Total length (>= 25000 bp)	40490	0	0	28935
Total length (>= 50000 bp)	0	0	0	0
# contigs	35	12	24	24
Largest contig	40490	18364	4775	28935
Total length	100119	45140	33574	71518
Reference length	3058721	3058721	3058721	3058721
GC (%)	47.84	48.10	49.71	48.41
Reference GC (%)	38.99	38.99	38.99	38.99
N50	6765	6529	1846	9930
N75	1772	2673	1037	2878
L50	3	2	6	2
L75	10	5	13	6
# misassemblies	0	1	2	1
# misassembled contigs	0	1	1	1
Misassembled contigs length	0	18364	804	28935
# local misassemblies	1	3	3	3
# structural variations	0	0	0	0
# unaligned contigs	0 + 23 part	0 + 5 part	0 + 3 part	0 + 13 part
Unaligned length	52432	11170	2230	15368
Genome fraction (%)	1.504	1.040	1.005	1.586
Duplication ratio	1.036	1.068	1.020	1.158
# N's per 100 kbp	85.90	1165.26	1313.52	569.09
# mismatches per 100 kbp	2016.73	1885.61	1822.20	1830.81
# indels per 100 kbp	45.64	6.29	26.03	18.56
Largest alignment	8028	13683	3992	17898
NA50	-	2427	1307	2289
NGA50	-	-	-	-
NA75	-	-	865	-
LA50	-	4	7	5
LA75	-	-	14	-

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

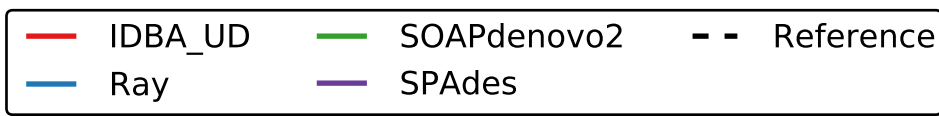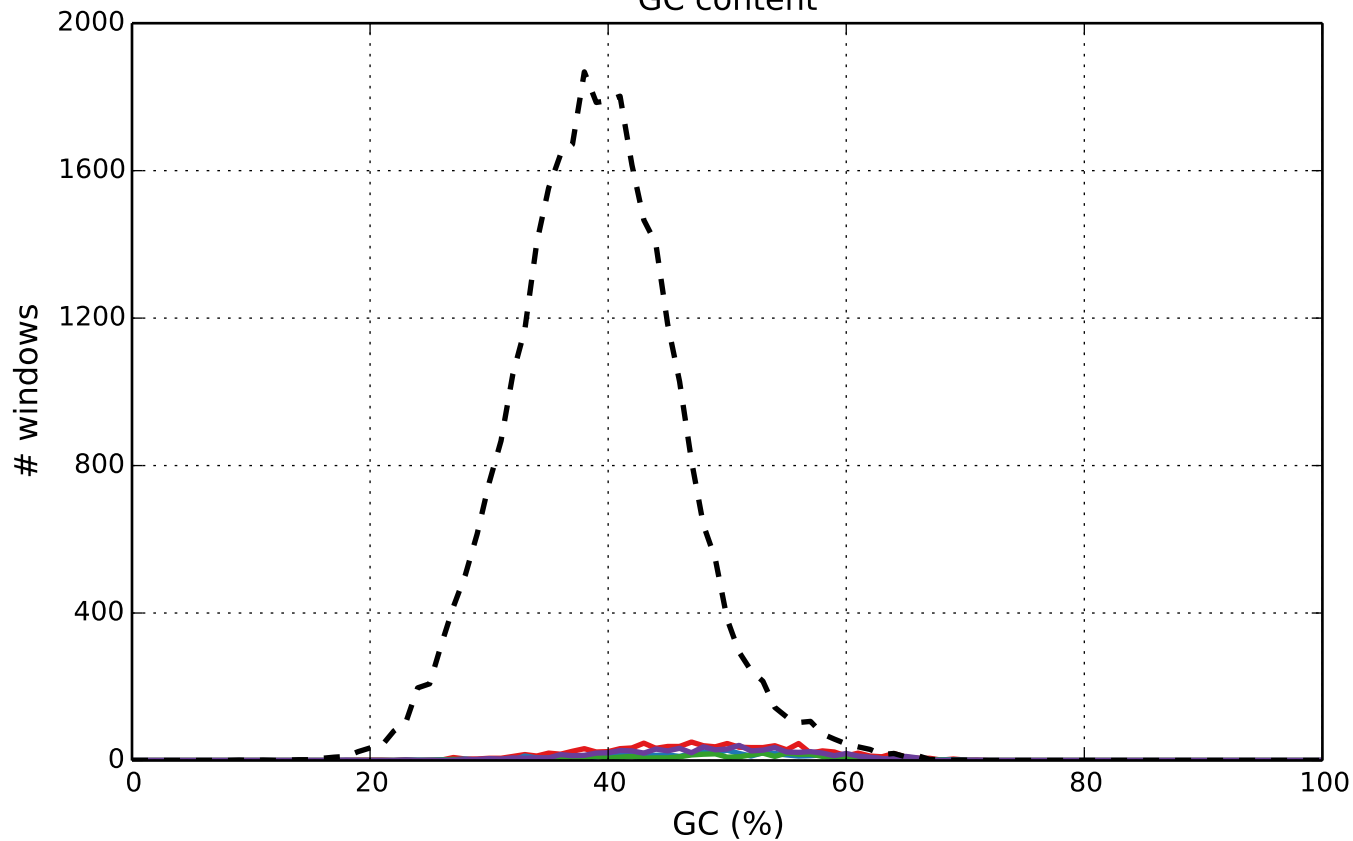|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	1	2	1
# relocations	0	1	2	1
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	4	2	1	4
# misassembled contigs	0	1	1	1
Misassembled contigs length	0	18364	804	28935
# local misassemblies	1	3	3	3
# structural variations	0	0	0	0
# mismatches	928	600	560	888
# indels	21	2	8	9
# short indels	21	2	8	8
# long indels	0	0	0	1
Indels length	32	6	10	35

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	23	5	3	13
# with misassembly	2	1	0	0
# both parts are significant	3	2	1	2
Partially unaligned length	52432	11170	2230	15368
# N's	86	526	441	407

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).
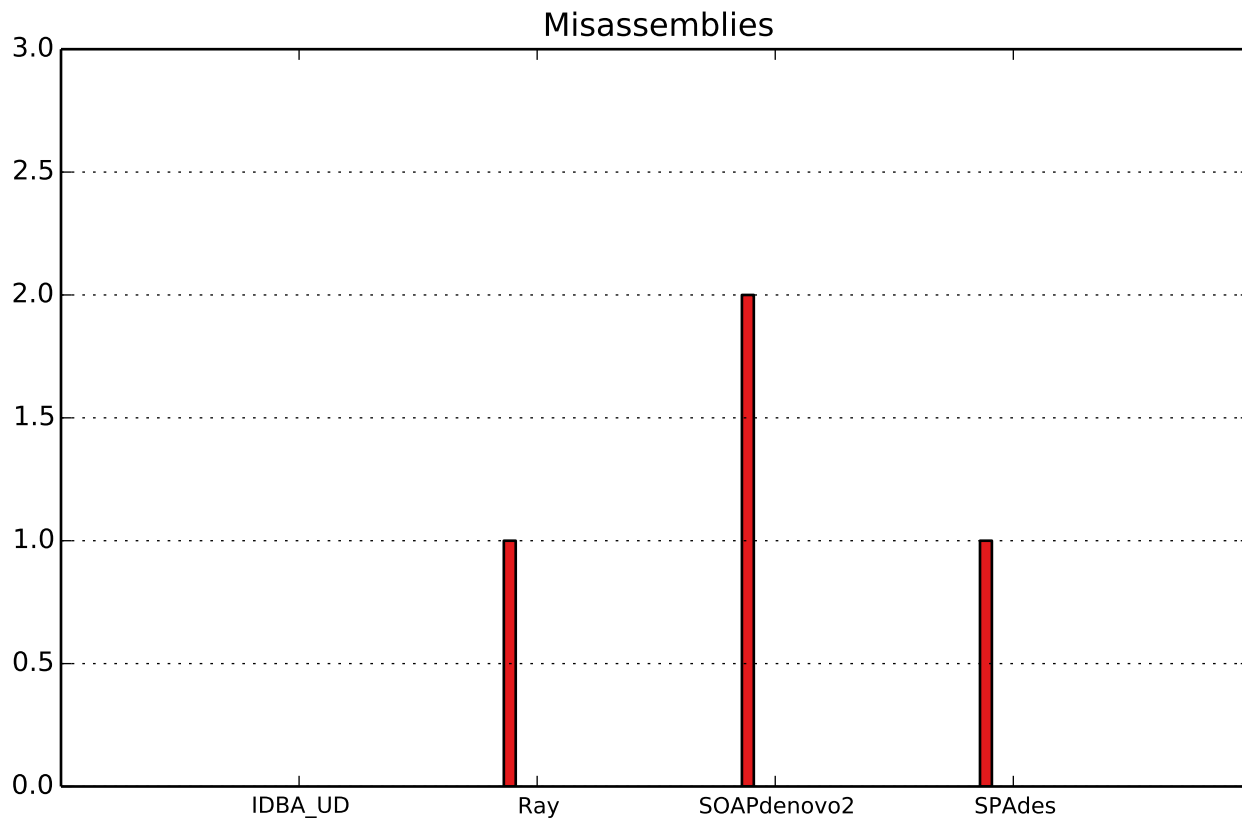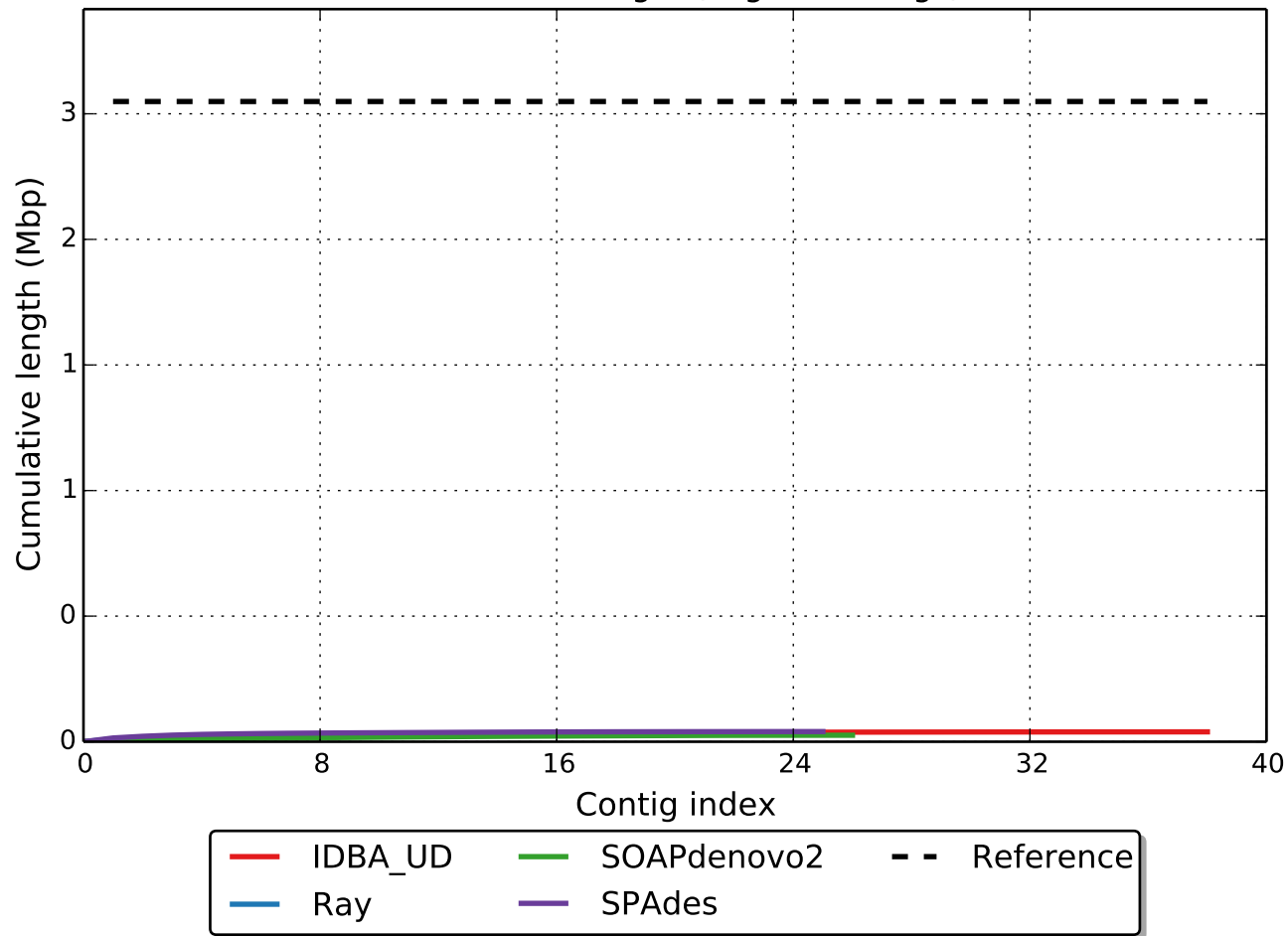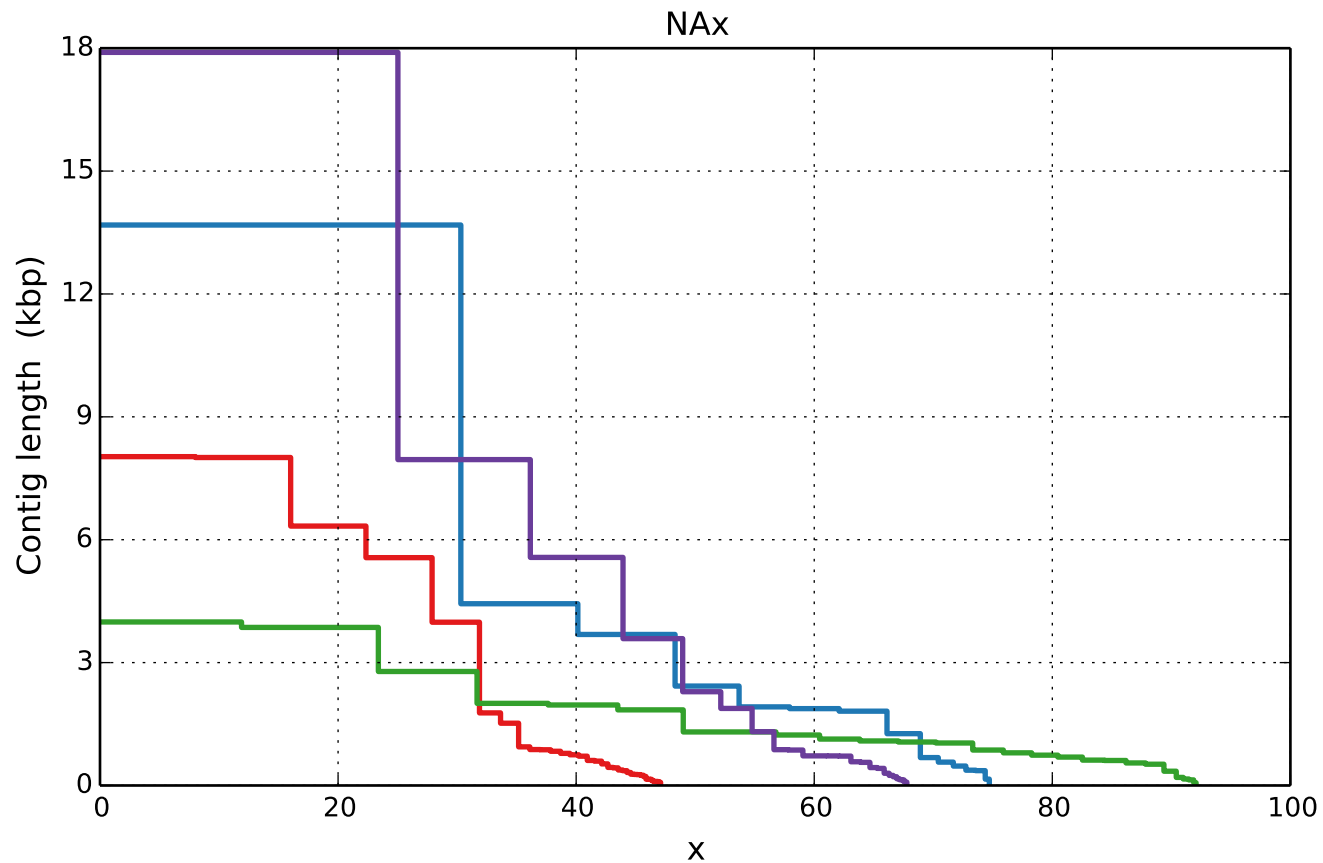
NGx

Cumulative length

GC content

Misassemblies
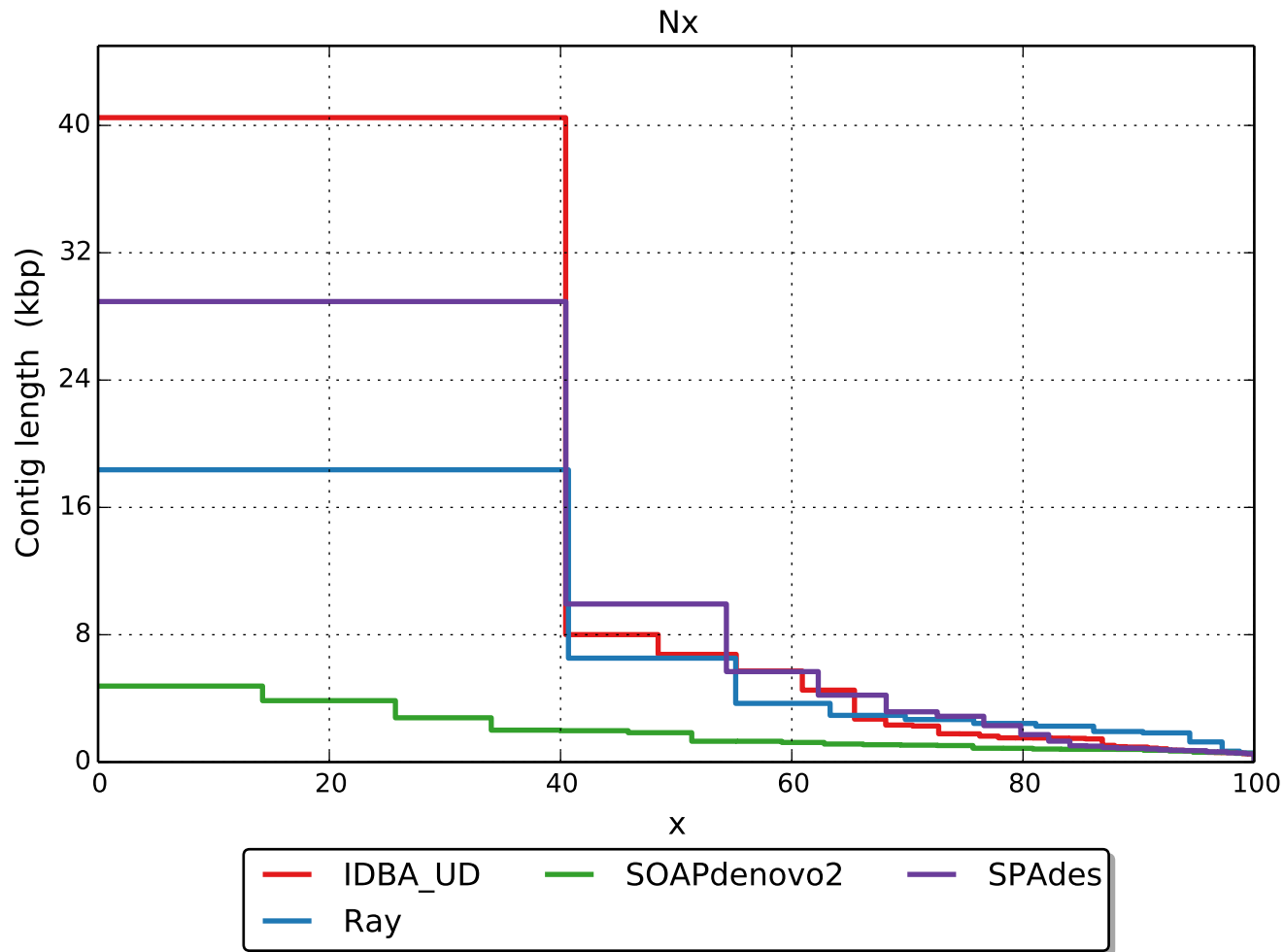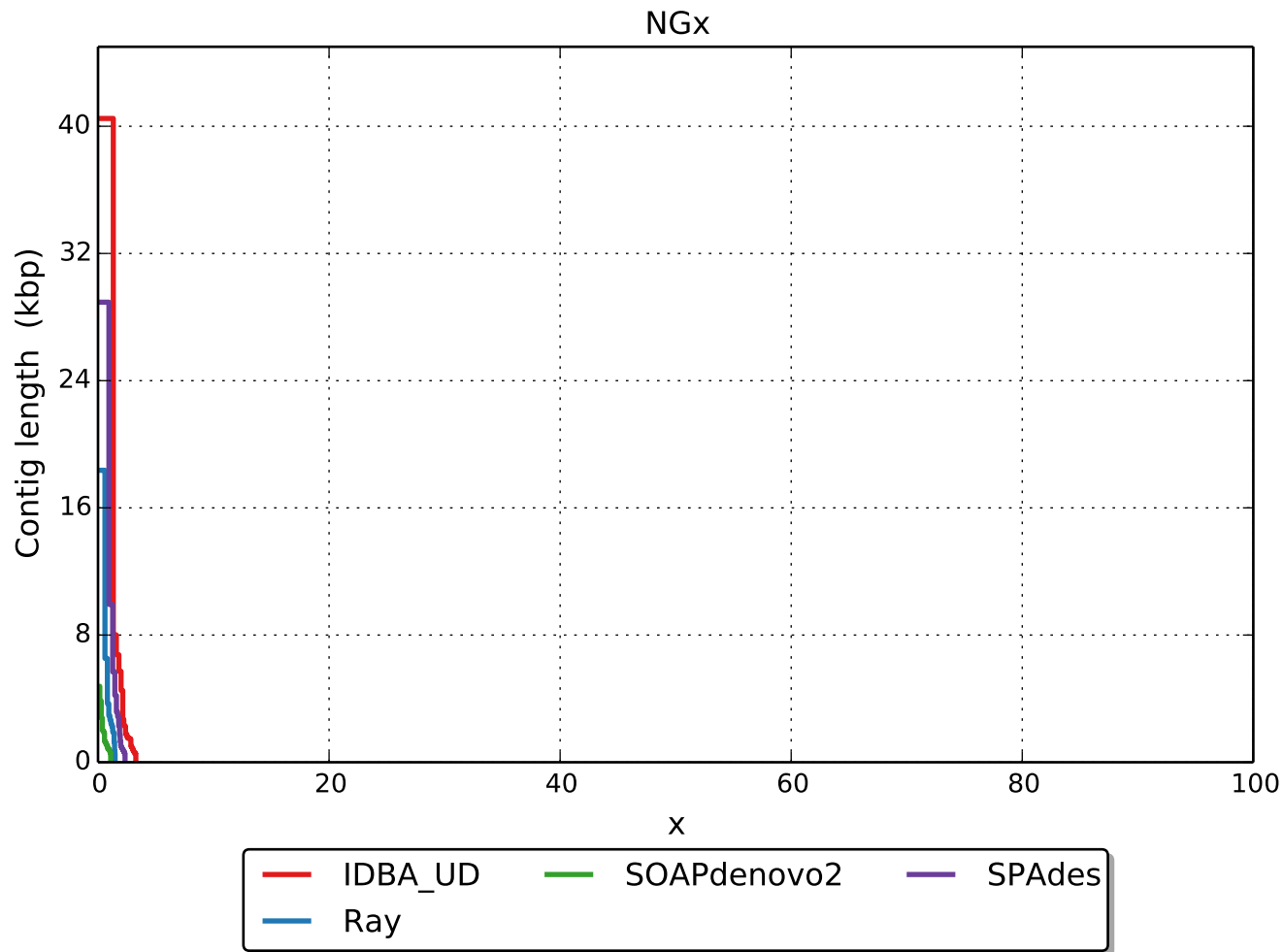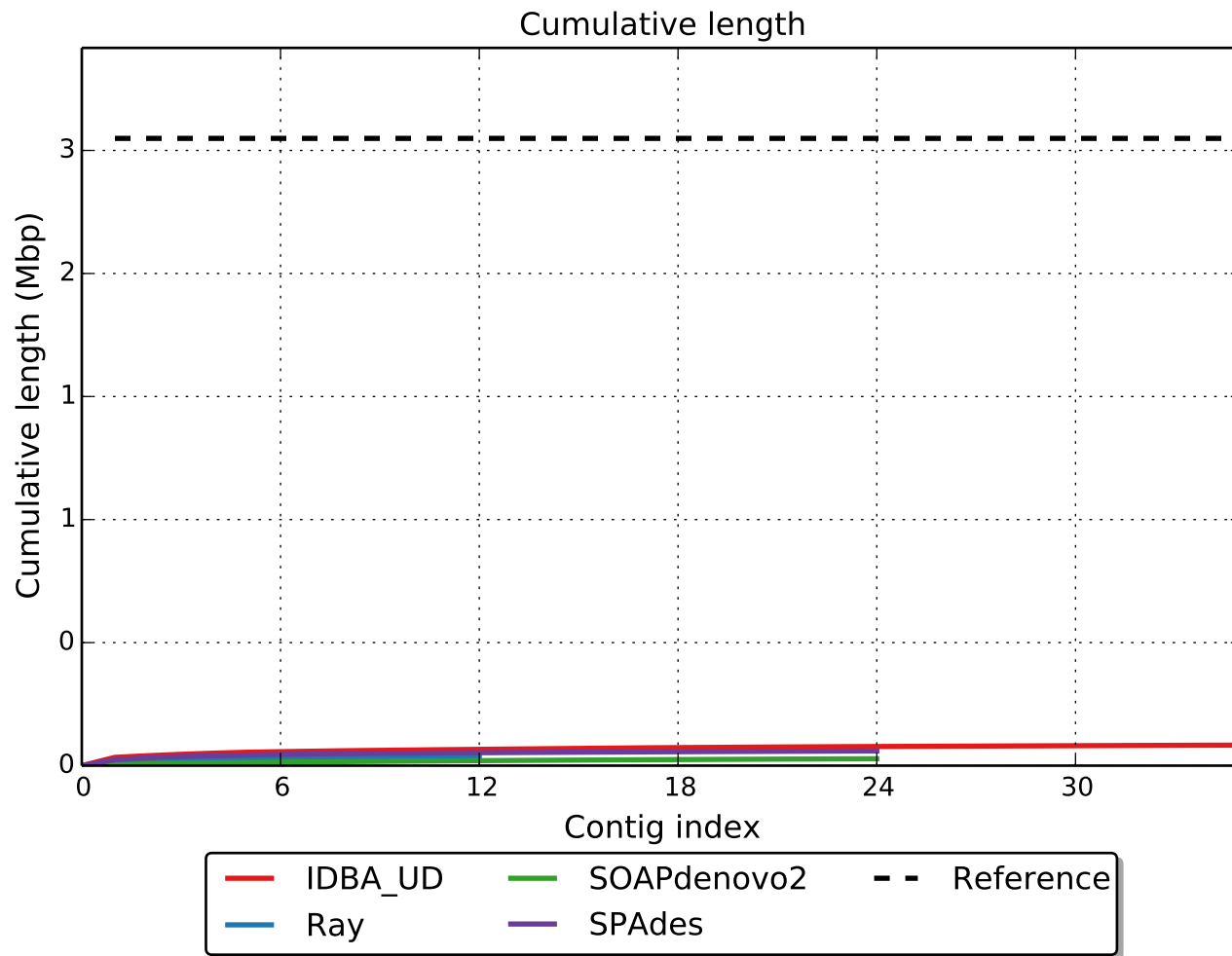
relocations

Cumulative length (aligned contigs)

Genome fraction, %

IDBA_UD
Ray
SOAPdenovo2
SPAdes