Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	5	4	4	3
# contigs (>= 5000 bp)	3	1	0	1
# contigs (>= 10000 bp)	3	1	0	0
# contigs (>= 25000 bp)	2	0	0	0
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 1000 bp)	258599	24997	5521	12319
Total length (>= 5000 bp)	254076	16529	0	7151
Total length (>= 10000 bp)	254076	16529	0	0
Total length (>= 25000 bp)	242948	0	0	0
Total length (>= 50000 bp)	215617	0	0	0
# contigs	8	6	6	3
Largest contig	215617	16529	1640	7151
Total length	260656	26343	6651	12319
Reference length	3478423	3478423	3478423	3478423
GC (%)	43.88	44.84	45.21	52.00
Reference GC (%)	51.82	51.82	51.82	51.82
N50	215617	16529	1219	7151
N75	215617	3721	1198	3811
L50	1	1	3	1
L75	1	2	4	2
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	1	5	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 7 part	0 + 3 part	0 + 1 part	0 + 2 part
Unaligned length	255720	20648	913	7123
Genome fraction (%)	0.140	0.147	0.160	0.143
Duplication ratio	1.016	1.114	1.031	1.042
# N's per 100 kbp	0.00	1746.19	2059.84	681.87
# mismatches per 100 kbp	617.67	547.73	772.55	1463.51
# indels per 100 kbp	102.94	19.56	0.00	80.19
Largest alignment	2698	3333	1640	3727
NA50	-	-	1131	-
NGA50	-	-	-	-
NA75	-	-	482	-
LA50	-	-	3	-
LA75	-	-	5	-

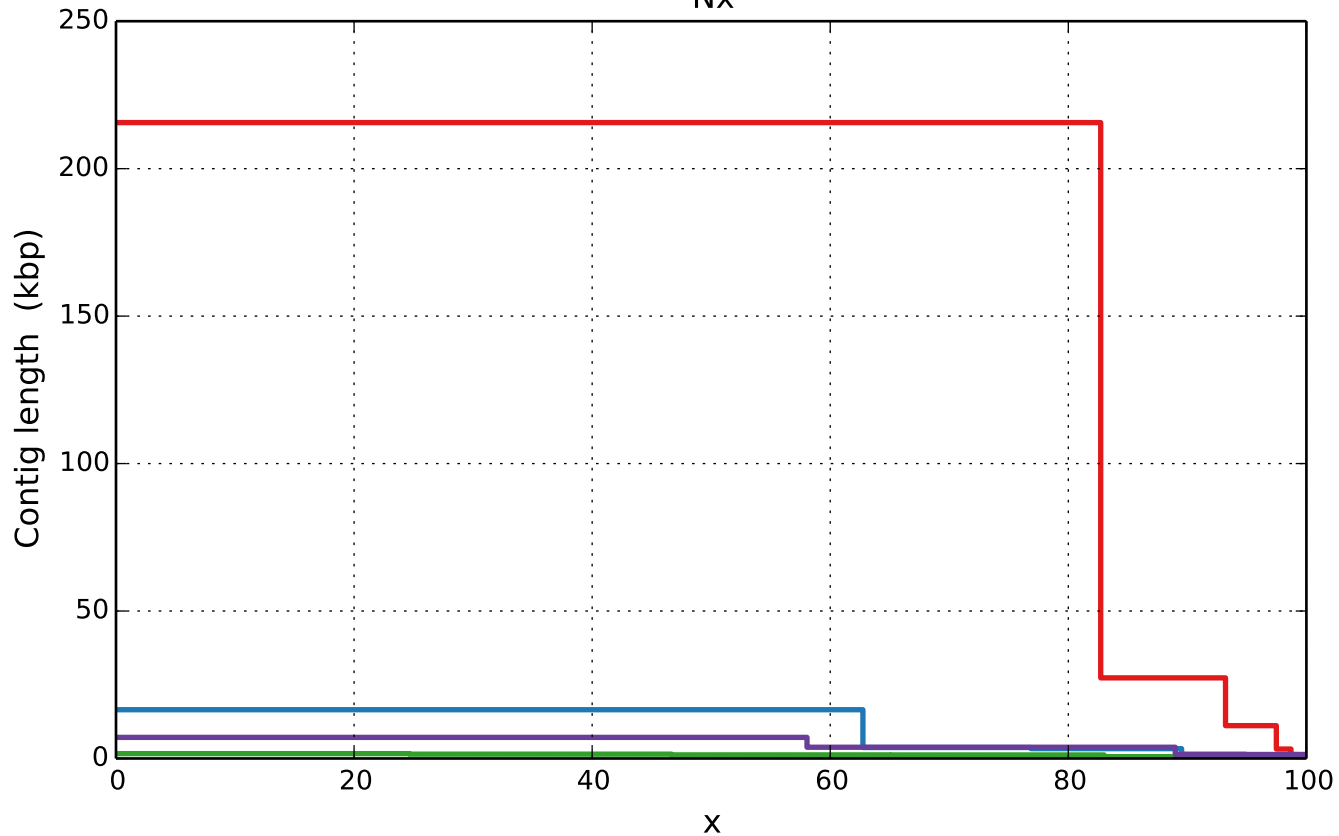All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	1	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	1	5	0
# structural variations	0	0	0	0
# mismatches	30	28	43	73
# indels	5	1	0	4
# short indels	5	1	0	3
# long indels	0	0	0	1
Indels length	7	1	0	15

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

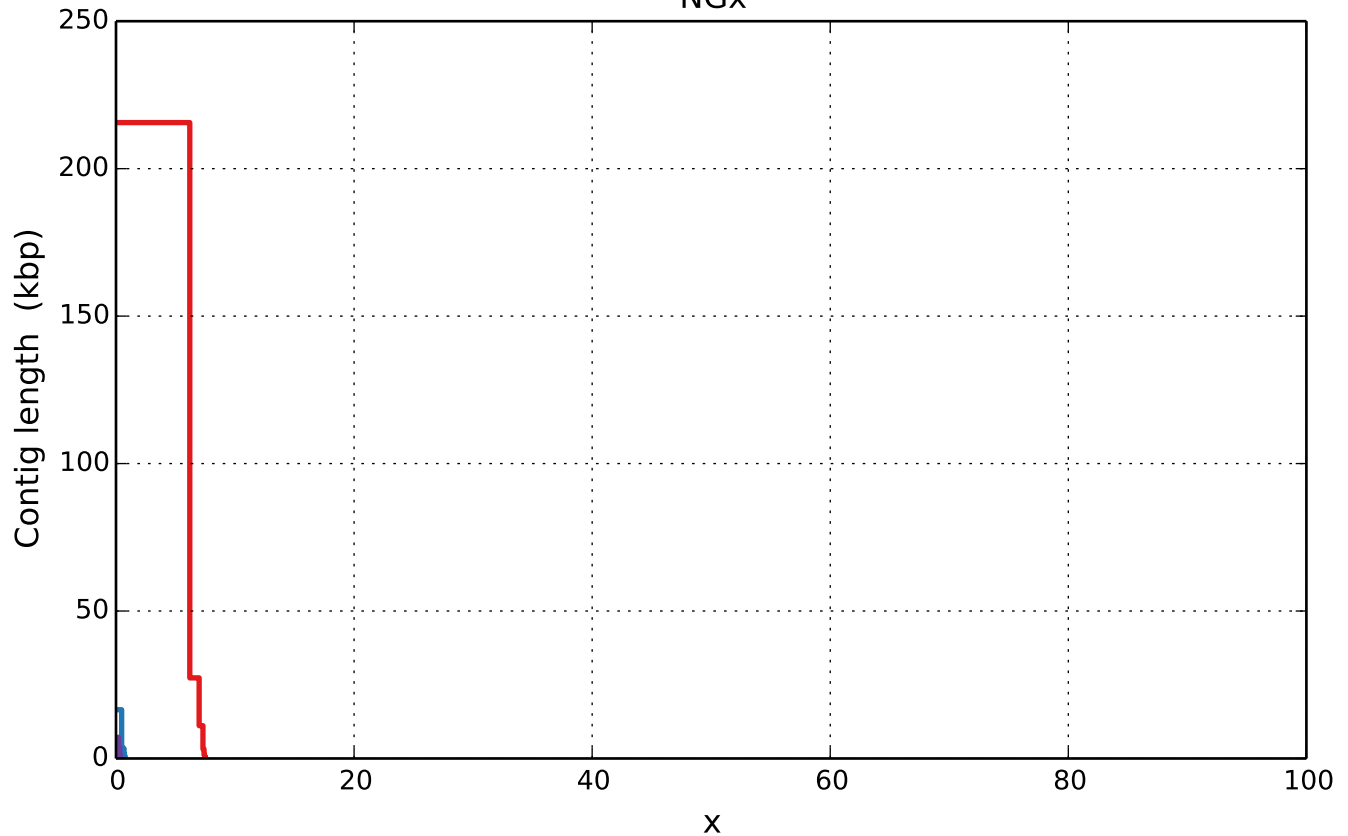|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	7	3	1	2
# with misassembly	0	0	0	0
# both parts are significant	1	0	0	0
Partially unaligned length	255720	20648	913	7123
# N's	0	460	137	84

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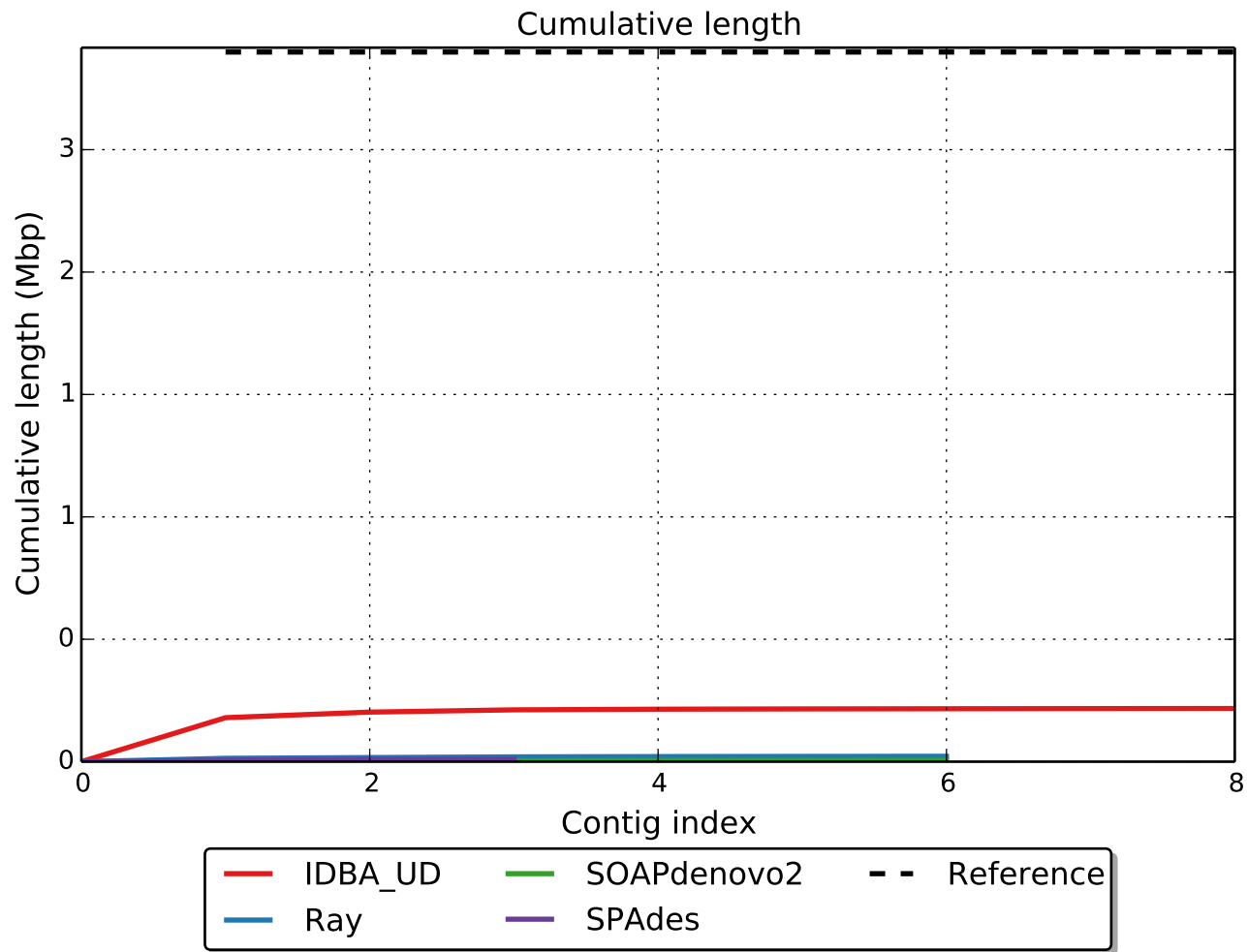(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

IDBA_UD   SOAPdenovo2   SPAdes

Ray

Genome fraction, %

IDBA_UD   SOAPdenovo2   SPAdes
Ray