Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	12	12	7	7
# contigs (>= 5000 bp)	10	7	2	7
# contigs (>= 10000 bp)	8	1	0	5
# contigs (>= 25000 bp)	7	0	0	4
# contigs (>= 50000 bp)	4	0	0	1
Total length (>= 1000 bp)	534551	73412	30348	207638
Total length (>= 5000 bp)	529653	63789	13985	207638
Total length (>= 10000 bp)	517271	21121	0	193586
Total length (>= 25000 bp)	497220	0	0	182334
Total length (>= 50000 bp)	375640	0	0	74266
# contigs	14	12	8	8
Largest contig	136589	21121	7887	74266
Total length	536059	73412	31014	208277
Reference length	3512473	3512473	3512473	3512473
GC (%)	50.78	44.22	45.29	49.89
Reference GC (%)	44.85	44.85	44.85	44.85
N50	80521	8025	4868	45577
N75	47332	5623	3441	36845
L50	3	3	3	2
L75	5	6	5	3
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	2	3	2	3
# structural variations	0	0	0	0
# unaligned contigs	0 + 12 part	0 + 11 part	0 + 6 part	0 + 6 part
Unaligned length	519260	56450	17985	192230
Genome fraction (%)	0.419	0.405	0.327	0.403
Duplication ratio	1.143	1.191	1.133	1.133
# N's per 100 kbp	18.47	1551.52	0.00	45.13
# mismatches per 100 kbp	3135.84	3075.63	3408.70	3099.41
# indels per 100 kbp	217.67	210.66	243.48	225.92
Largest alignment	3643	4935	3643	4935
NGA50	-	-	-	-

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).
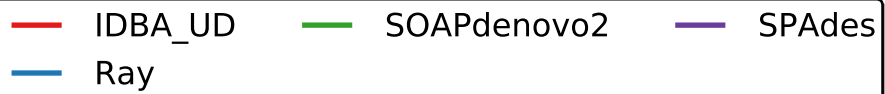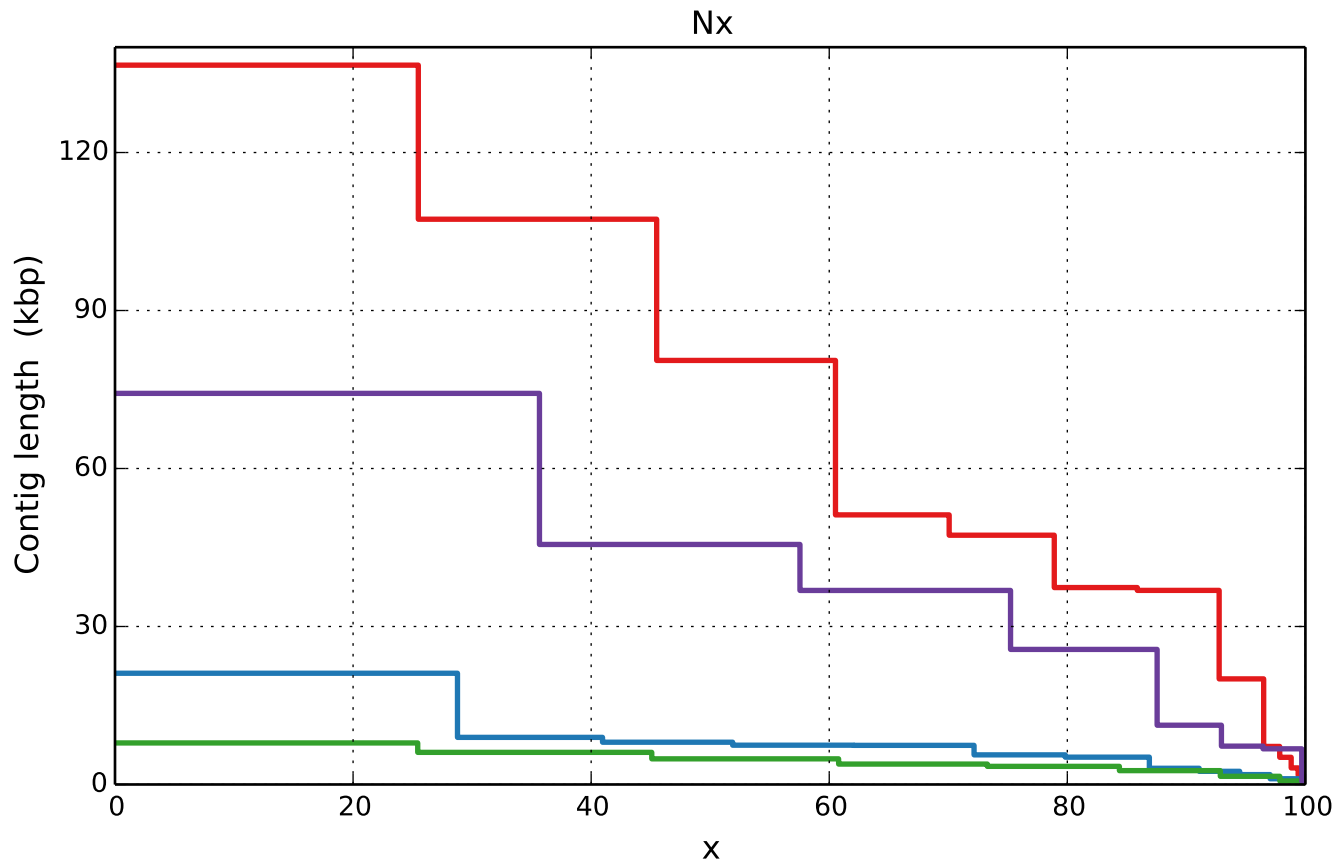
Misassemblies report

	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	4	7	4	4
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	2	3	2	3
# structural variations	0	0	0	0
# mismatches	461	438	392	439
# indels	32	30	28	32
# short indels	30	28	26	30
# long indels	2	2	2	2
Indels length	58	56	54	58

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).
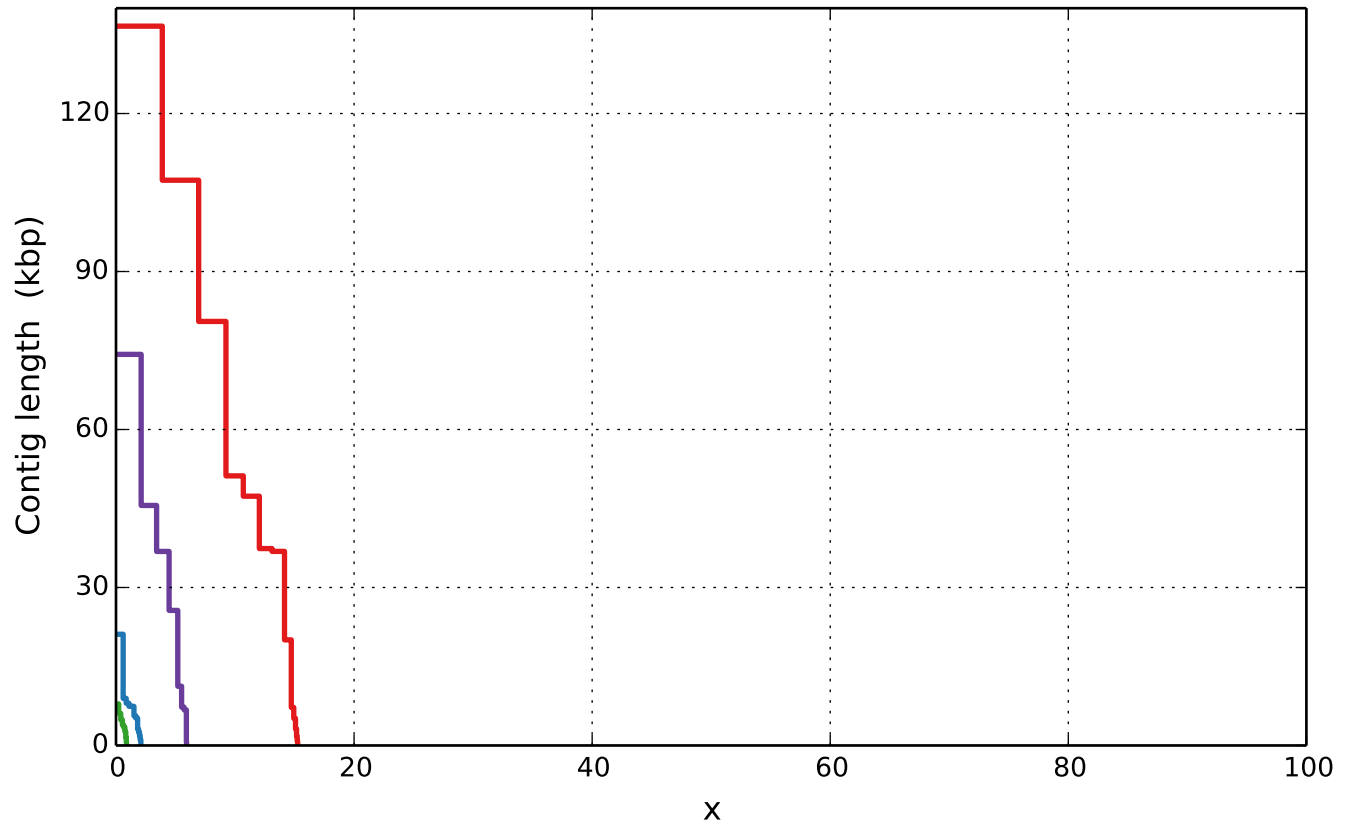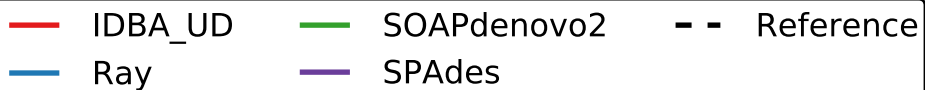
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	12	11	6	6
# with misassembly	4	6	2	2
# both parts are significant	3	6	3	3
Partially unaligned length	519260	56450	17985	192230
# N's	99	1139	0	94

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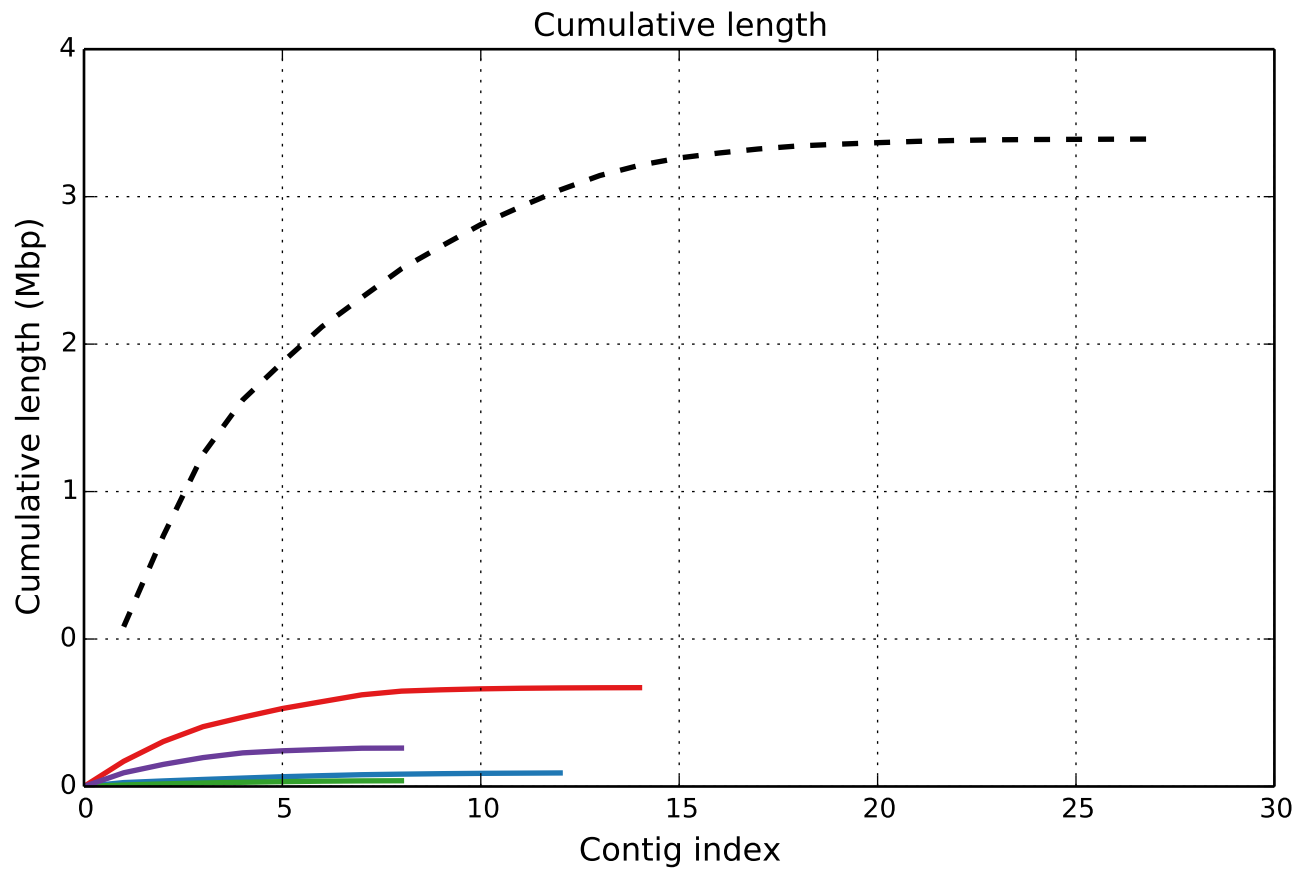(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

| | IDBA_UD | Ray | SOAPdenovo2 | SPAdes |

Cumulative length (aligned contigs)

Genome fraction, %

100 —

50 ···

■ IDBA_UD ■ SOAPdenovo2 ■ SPAdes
■ Ray