Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	67	43	80	66
# contigs (>= 5000 bp)	17	13	5	18
# contigs (>= 10000 bp)	11	4	1	9
# contigs (>= 25000 bp)	4	0	0	5
# contigs (>= 50000 bp)	2	0	0	3
Total length (>= 1000 bp)	451265	182753	175909	477822
Total length (>= 5000 bp)	345023	117624	34793	369363
Total length (>= 10000 bp)	297867	50106	10184	301618
Total length (>= 25000 bp)	194440	0	0	241521
Total length (>= 50000 bp)	118155	0	0	171043
# contigs	109	72	202	101
Largest contig	67479	14202	10184	63252
Total length	482208	202751	259033	501602
Reference length	5493117	5493117	5493117	5493117
GC (%)	45.86	46.00	47.08	44.73
Reference GC (%)	42.83	42.83	42.83	42.83
N50	14202	5593	1537	22352
N75	3978	2689	840	3915
L50	7	11	44	6
L75	21	23	101	20
# misassemblies	5	1	1	2
# misassembled contigs	4	1	1	2
Misassembled contigs length	44229	4199	10184	73370
# local misassemblies	4	21	122	2
# structural variations	0	0	0	0
# unaligned contigs	0 + 32 part	0 + 18 part	0 + 51 part	0 + 47 part
Unaligned length	174361	43655	31991	198300
Genome fraction (%)	5.343	2.643	3.928	5.138
Duplication ratio	1.049	1.096	1.052	1.075
# N's per 100 kbp	204.68	2629.83	3626.18	725.28
# mismatches per 100 kbp	1289.56	1266.71	1181.37	1290.70
# indels per 100 kbp	57.24	35.82	36.15	68.73
Largest alignment	22513	14187	5467	36125
NA50	1448	1804	1185	973
NGA50	-	-	-	-
NA75	-	-	539	-
LA50	44	22	53	52
LA75	-	-	139	-

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).
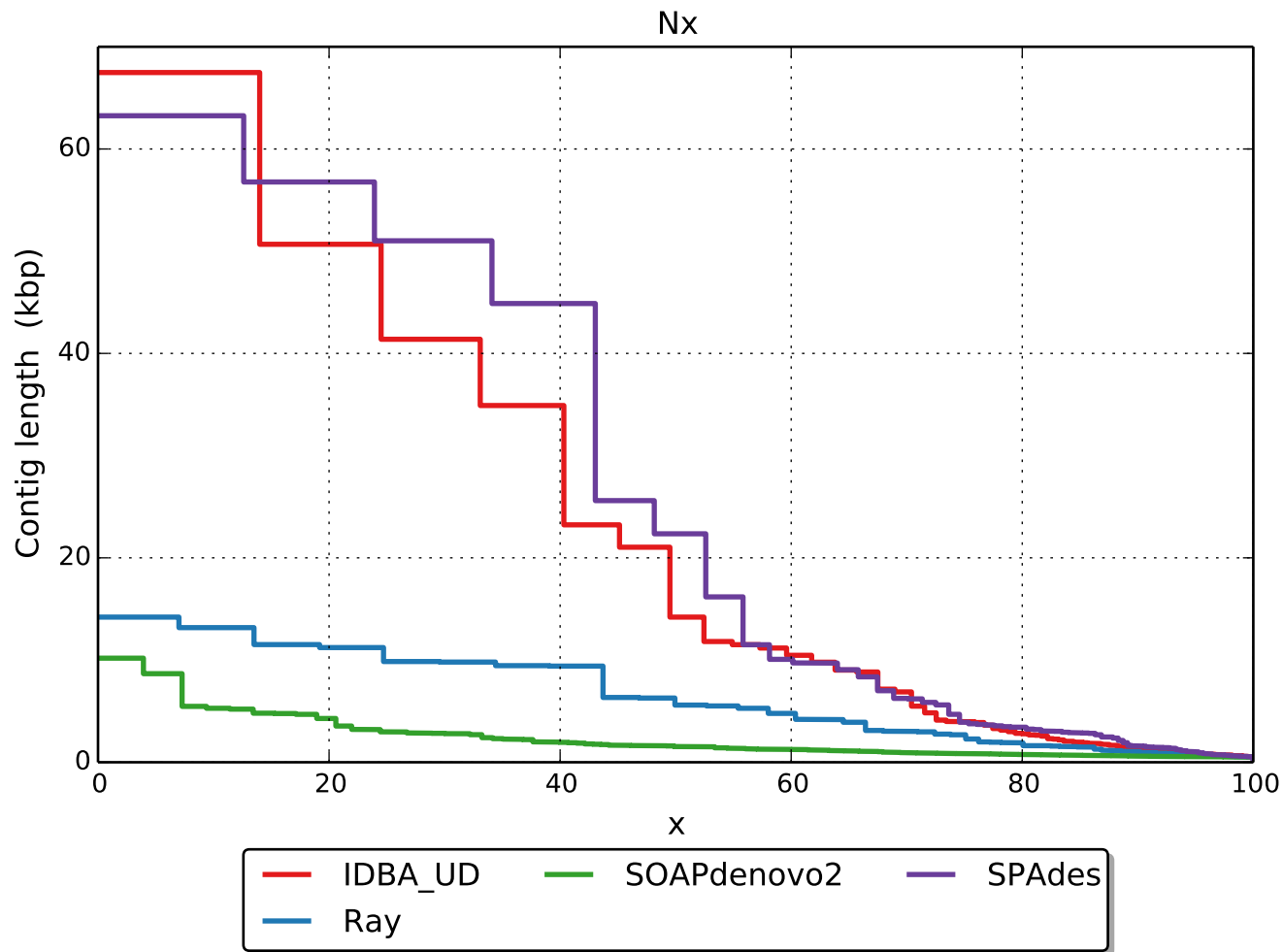
Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	5	1	1	2
# relocations	2	1	1	2
# translocations	0	0	0	0
# inversions	3	0	0	0
# possibly misassembled contigs	15	14	9	23
# misassembled contigs	4	1	1	2
Misassembled contigs length	44229	4199	10184	73370
# local misassemblies	4	21	122	2
# structural variations	0	0	0	0
# mismatches	3785	1839	2549	3643
# indels	168	52	78	194
# short indels	146	50	73	164
# long indels	22	2	5	30
Indels length	502	87	157	620

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).
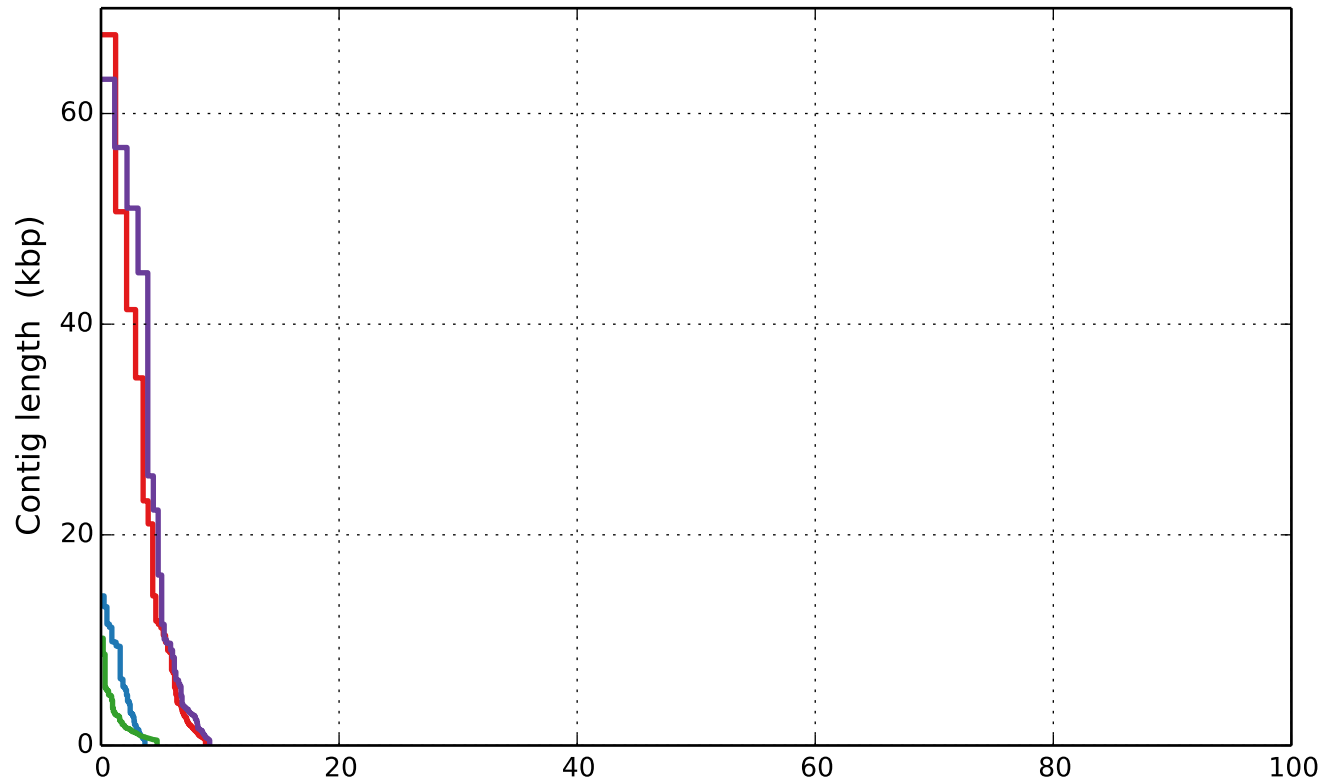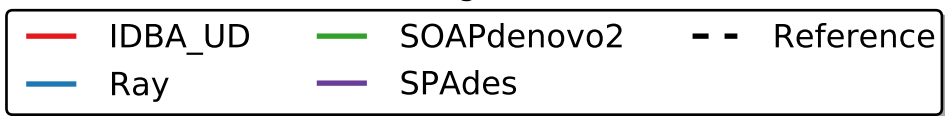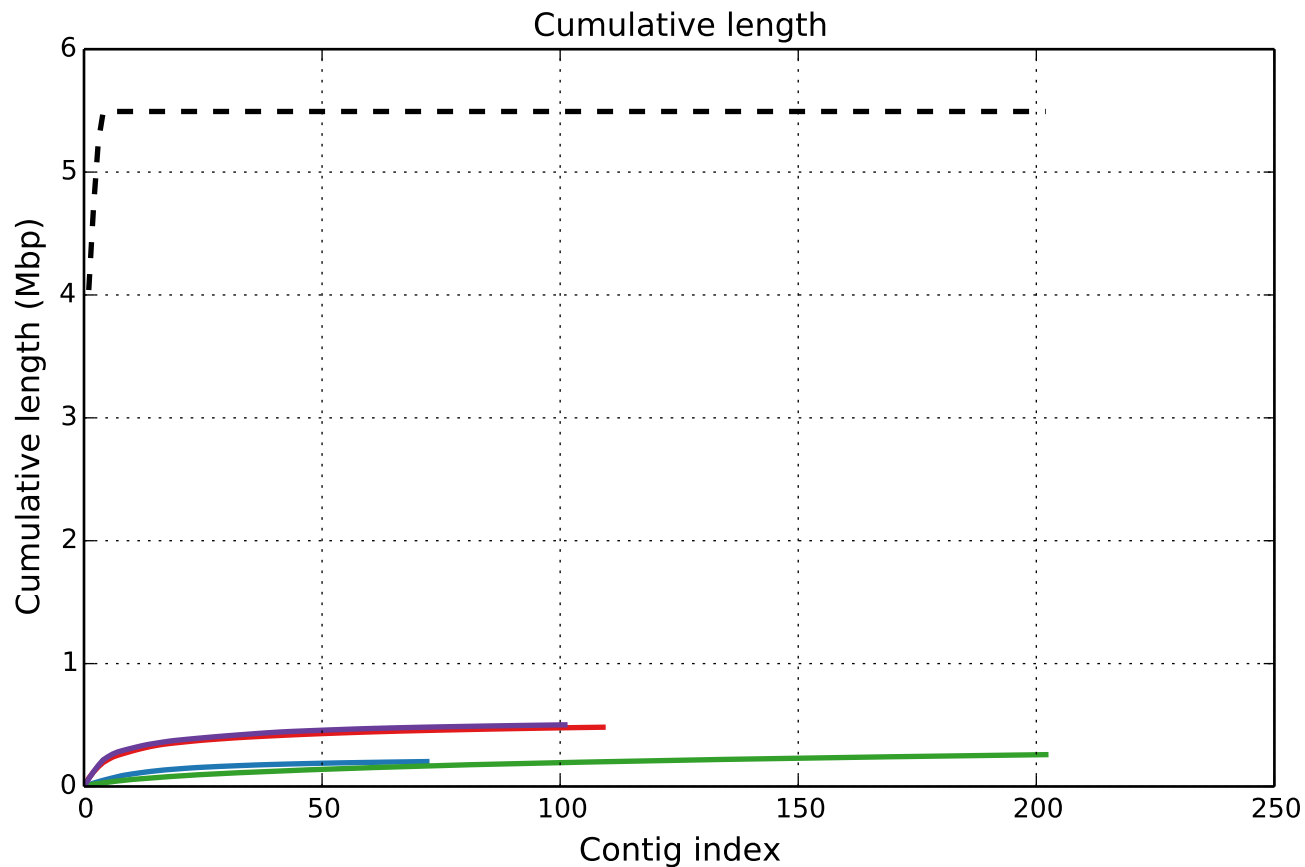
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	32	18	51	47
# with misassembly	1	3	2	2
# both parts are significant	12	10	8	20
Partially unaligned length	174361	43655	31991	198300
# N's	987	5332	9393	3638

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

Cumulative length (aligned contigs)

Genome fraction, %

- IDBA_UD
- Ray
- SOAPdenovo2
- SPAdes