Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	20	22	13	20
# contigs (>= 5000 bp)	5	8	6	7
# contigs (>= 10000 bp)	4	6	1	5
# contigs (>= 25000 bp)	1	1	0	3
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 1000 bp)	164051	147646	63131	171556
Total length (>= 5000 bp)	126382	116402	48425	144773
Total length (>= 10000 bp)	117385	100103	10762	132889
Total length (>= 25000 bp)	71408	34615	0	95269
Total length (>= 50000 bp)	71408	0	0	0
# contigs	35	29	24	22
Largest contig	71408	34615	10762	39677
Total length	174481	152644	70110	173026
Reference length	3719688	3719688	3719688	3719688
GC (%)	47.76	46.63	49.83	47.56
Reference GC (%)	54.18	54.18	54.18	54.18
N50	17341	11226	7126	27250
N75	4898	6837	4540	16096
L50	2	4	5	3
L75	6	8	7	5
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	6	8	0
# structural variations	1	1	1	2
# unaligned contigs	0 + 20 part	0 + 7 part	0 + 6 part	0 + 14 part
Unaligned length	80701	68495	1531	77684
Genome fraction (%)	2.466	2.067	1.768	2.320
Duplication ratio	1.022	1.094	1.043	1.105
# N's per 100 kbp	24.07	1479.91	735.99	284.93
# mismatches per 100 kbp	2331.69	1877.67	2384.72	2758.14
# indels per 100 kbp	61.04	29.91	36.50	59.10
Largest alignment	21525	14123	10762	31684
NA50	622	515	6232	-
NGA50	-	-	-	-
NA75	-	-	2034	-
LA50	18	26	5	-
LA75	-	-	9	-

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).
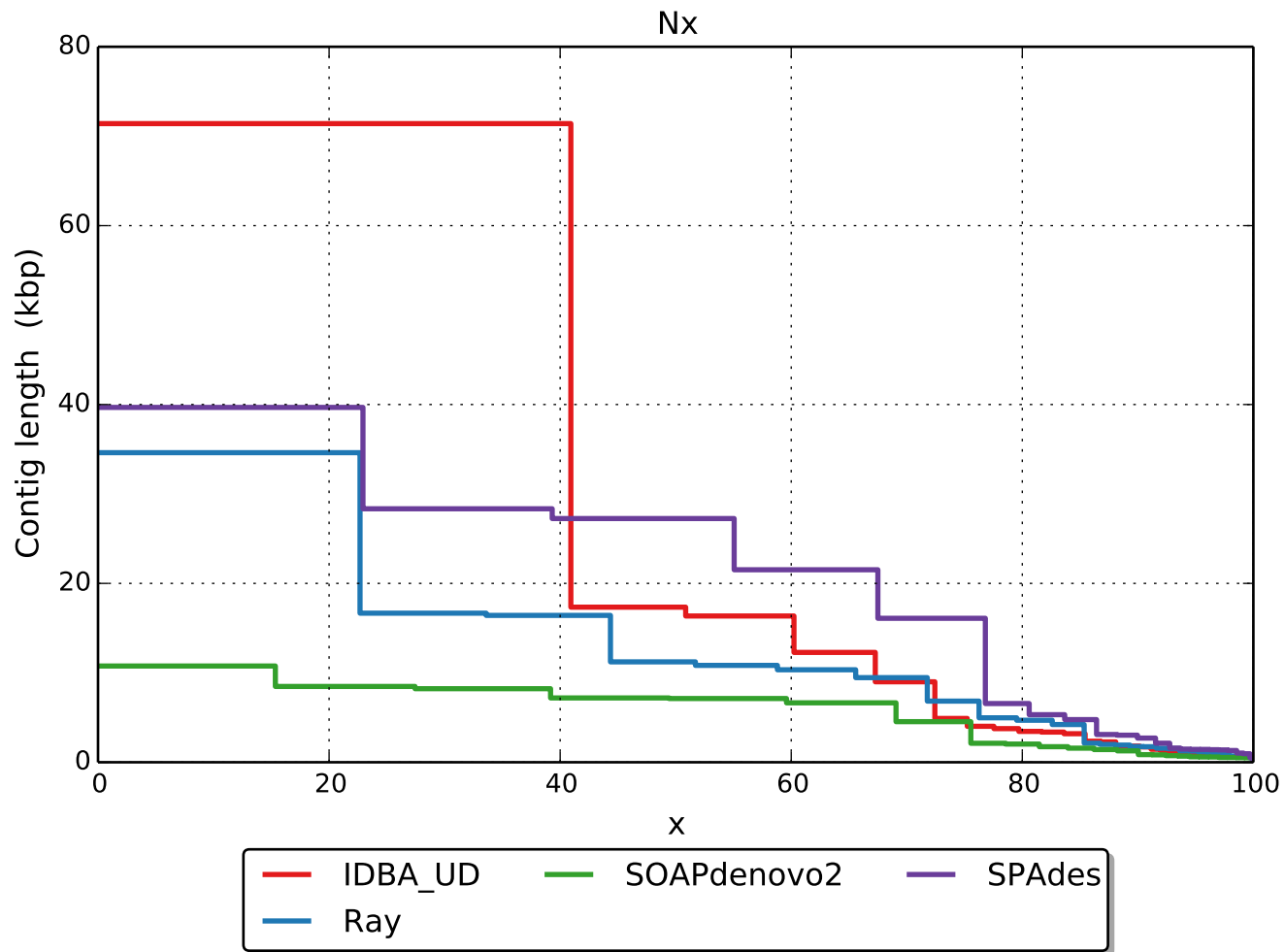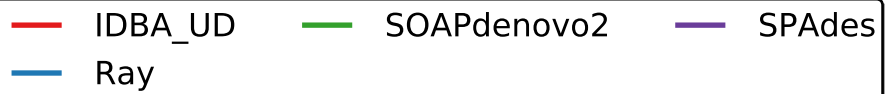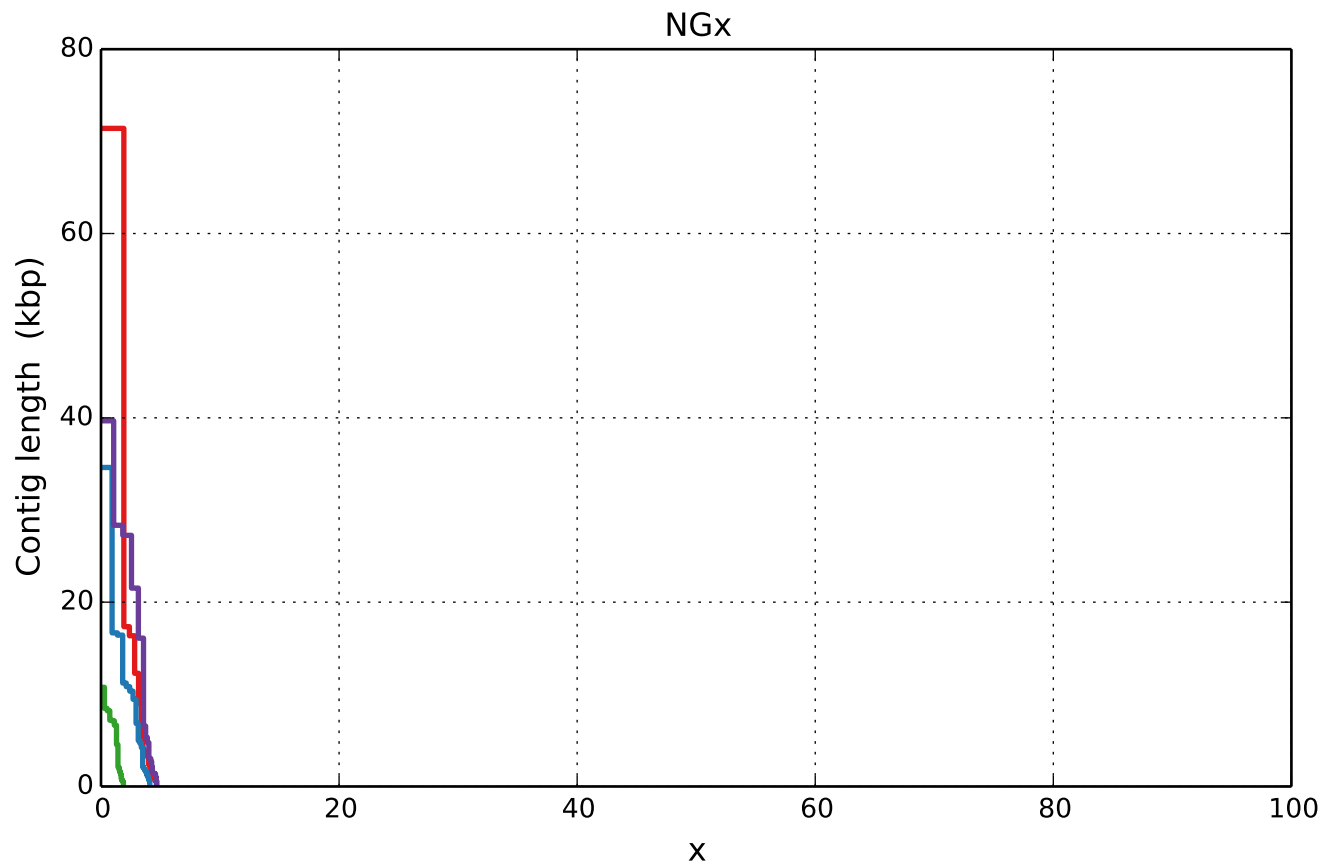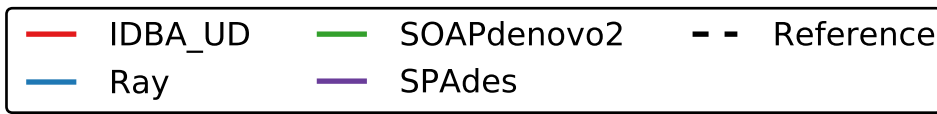
Misassemblies report

	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	5	5	1	6
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	0	6	8	0
# structural variations	1	1	1	2
# mismatches	2139	1444	1568	2380
# indels	56	23	24	51
# short indels	52	23	24	49
# long indels	4	0	0	2
Indels length	97	28	31	75

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).
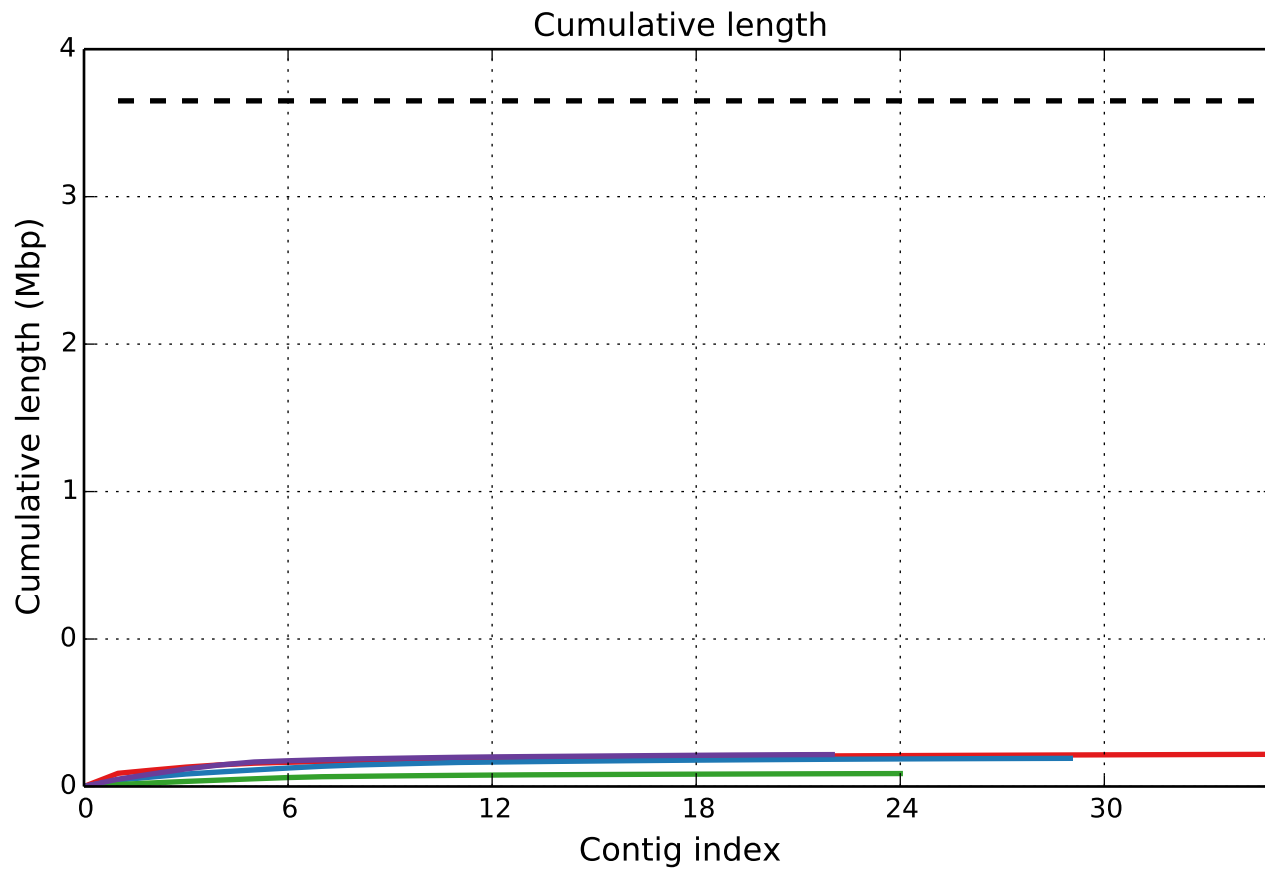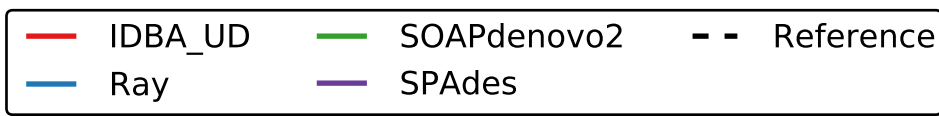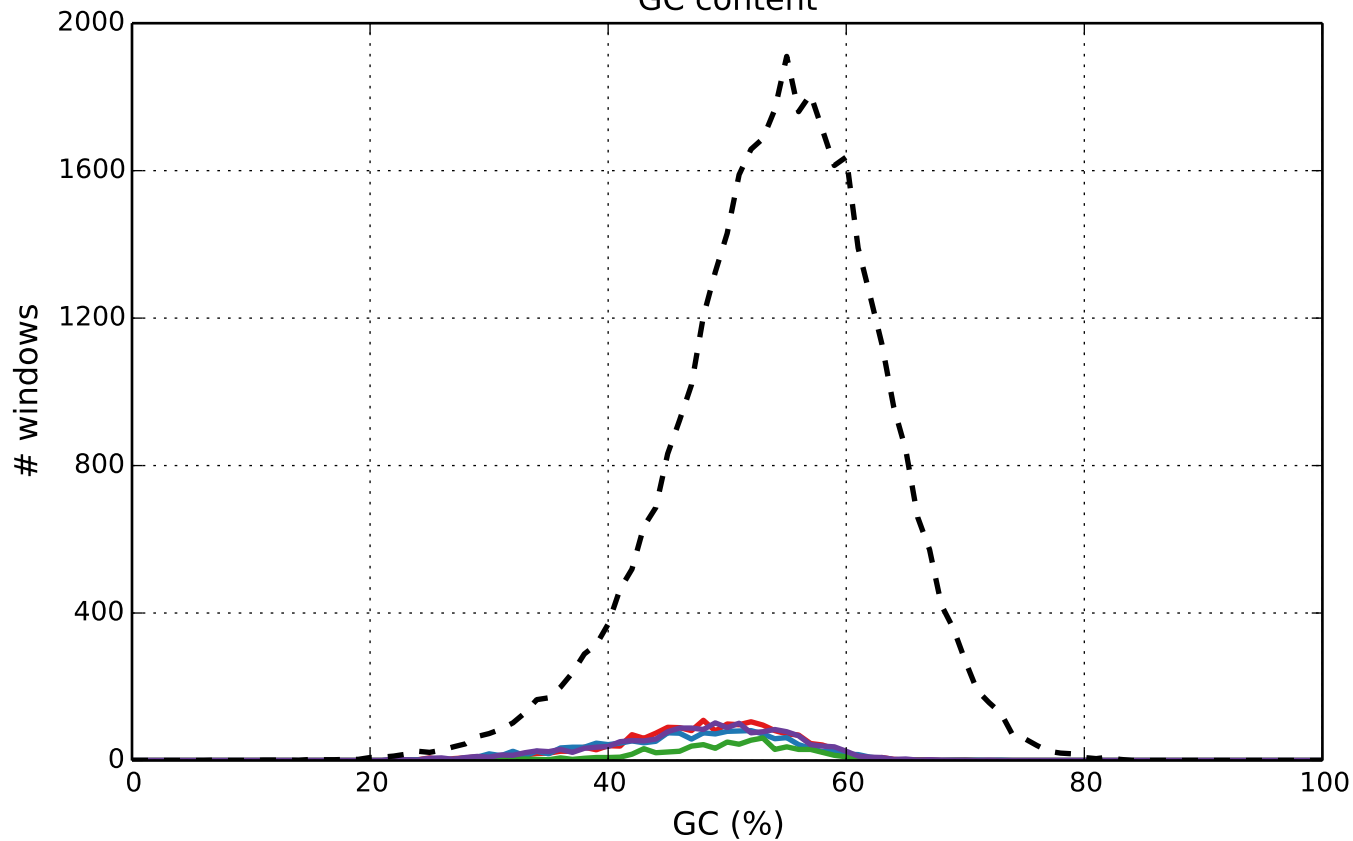
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	20	7	6	14
# with misassembly	1	1	0	0
# both parts are significant	4	2	0	4
Partially unaligned length	80701	68495	1531	77684
# N's	42	2259	516	493

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
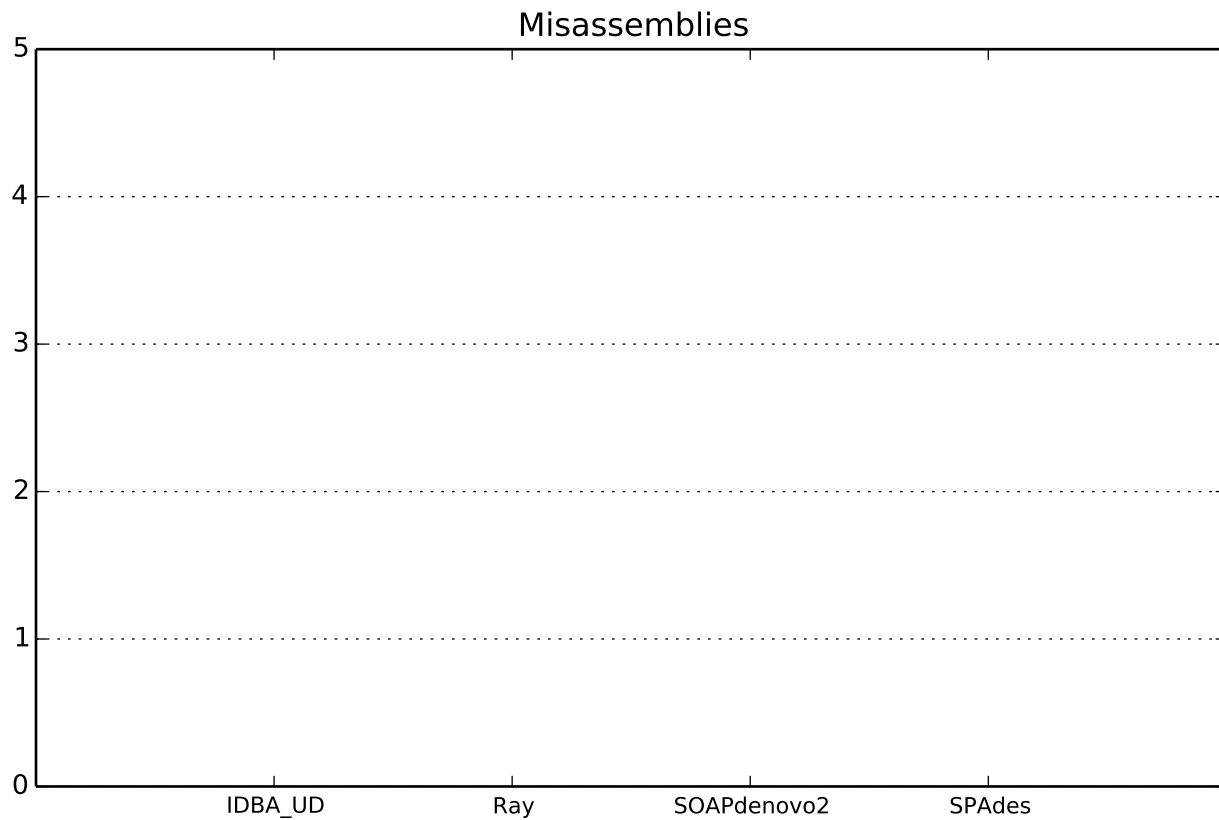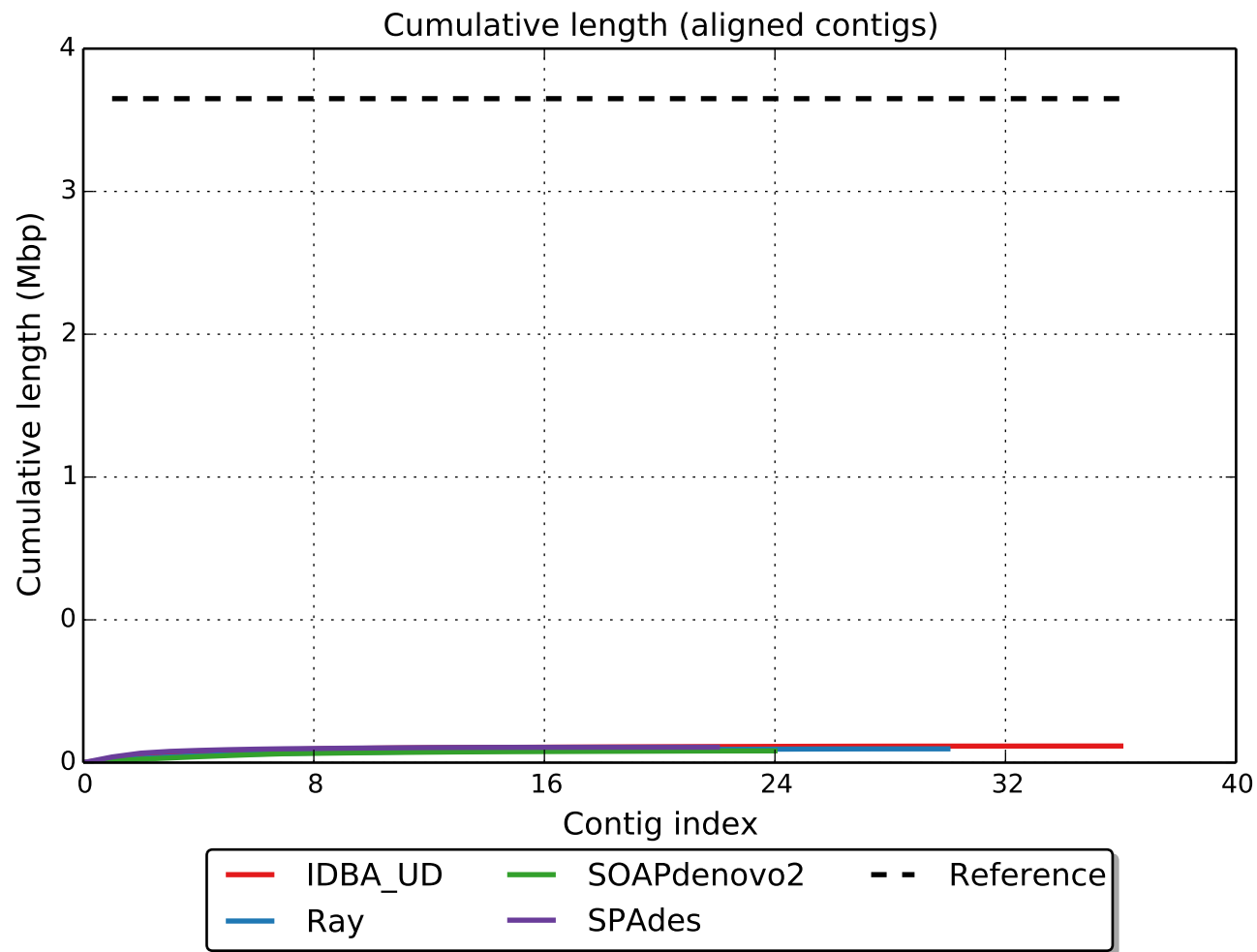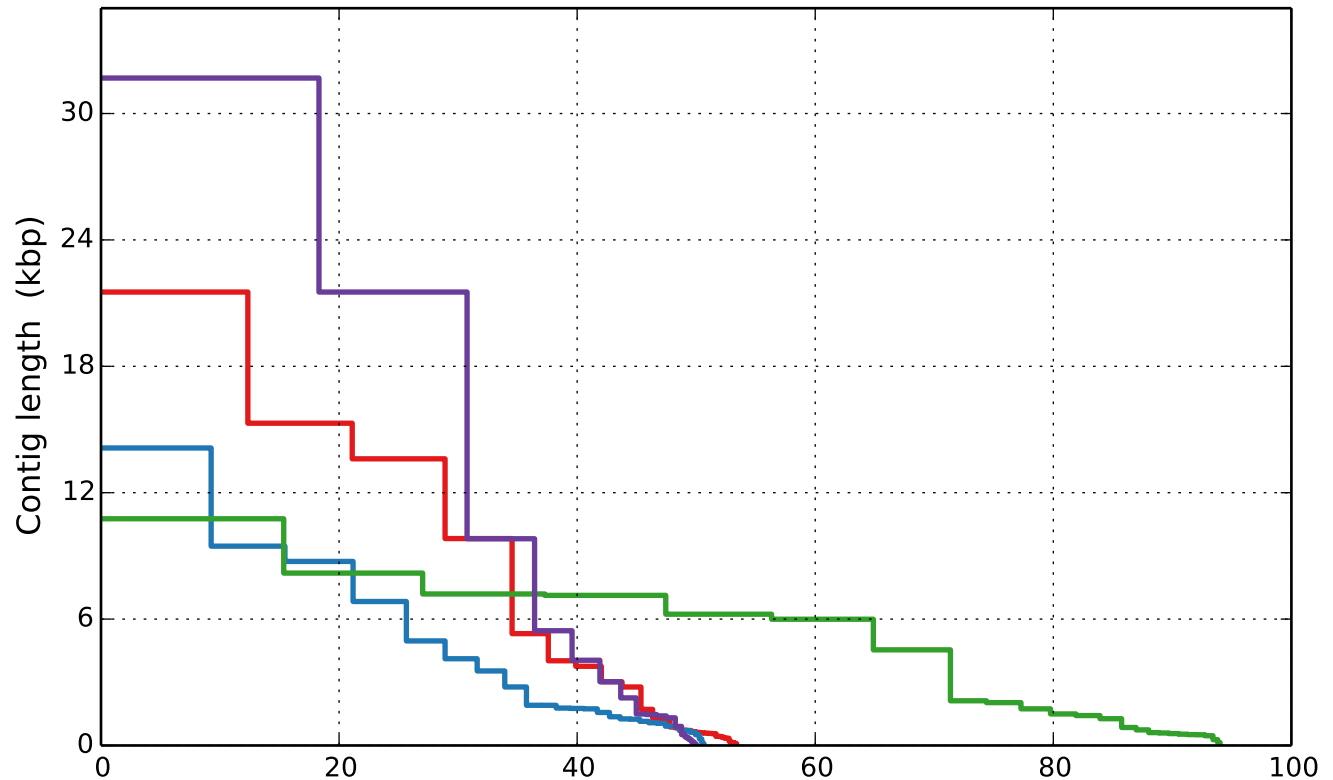
Misassemblies

IDBA_UD   Ray   SOAPdenovo2   SPAdes

Cumulative length (aligned contigs)

NGAx

Genome fraction, %

Legend: IDBA_UD, Ray, SOAPdenovo2, SPAdes