Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	28	20	17	16
# contigs (>= 5000 bp)	8	6	1	7
# contigs (>= 10000 bp)	6	2	0	7
# contigs (>= 25000 bp)	4	0	0	1
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 1000 bp)	293468	93079	51801	168957
Total length (>= 5000 bp)	249733	57700	6085	142326
Total length (>= 10000 bp)	234202	24644	0	142326
Total length (>= 25000 bp)	212000	0	0	46093
Total length (>= 50000 bp)	94894	0	0	0
# contigs	46	24	32	30
Largest contig	94894	14241	6085	46093
Total length	306558	96050	62275	179129
Reference length	6538460	6538460	6538460	6538460
GC (%)	45.80	45.83	45.47	47.46
Reference GC (%)	49.39	49.39	49.39	49.39
N50	43793	8207	3106	14949
N75	10672	3182	1660	11227
L50	3	5	8	4
L75	6	11	14	7
# misassemblies	3	1	0	3
# misassembled contigs	2	1	0	2
Misassembled contigs length	47514	10403	0	34040
# local misassemblies	2	7	11	0
# structural variations	1	1	0	1
# unaligned contigs	0 + 23 part	0 + 10 part	0 + 13 part	0 + 17 part
Unaligned length	208768	26588	10067	79859
Genome fraction (%)	1.245	0.927	0.775	1.285
Duplication ratio	1.201	1.146	1.031	1.182
# N's per 100 kbp	23.81	1383.65	1607.39	253.45
# mismatches per 100 kbp	1453.48	1314.73	1012.93	1912.75
# indels per 100 kbp	47.92	29.69	15.80	57.13
Largest alignment	26543	8088	4653	13743
NA50	-	2594	2414	-
NGA50	-	-	-	-
NA75	-	-	673	-
LA50	-	10	10	-
LA75	-	-	23	-

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).
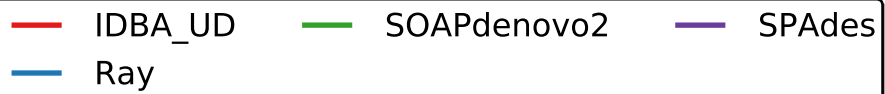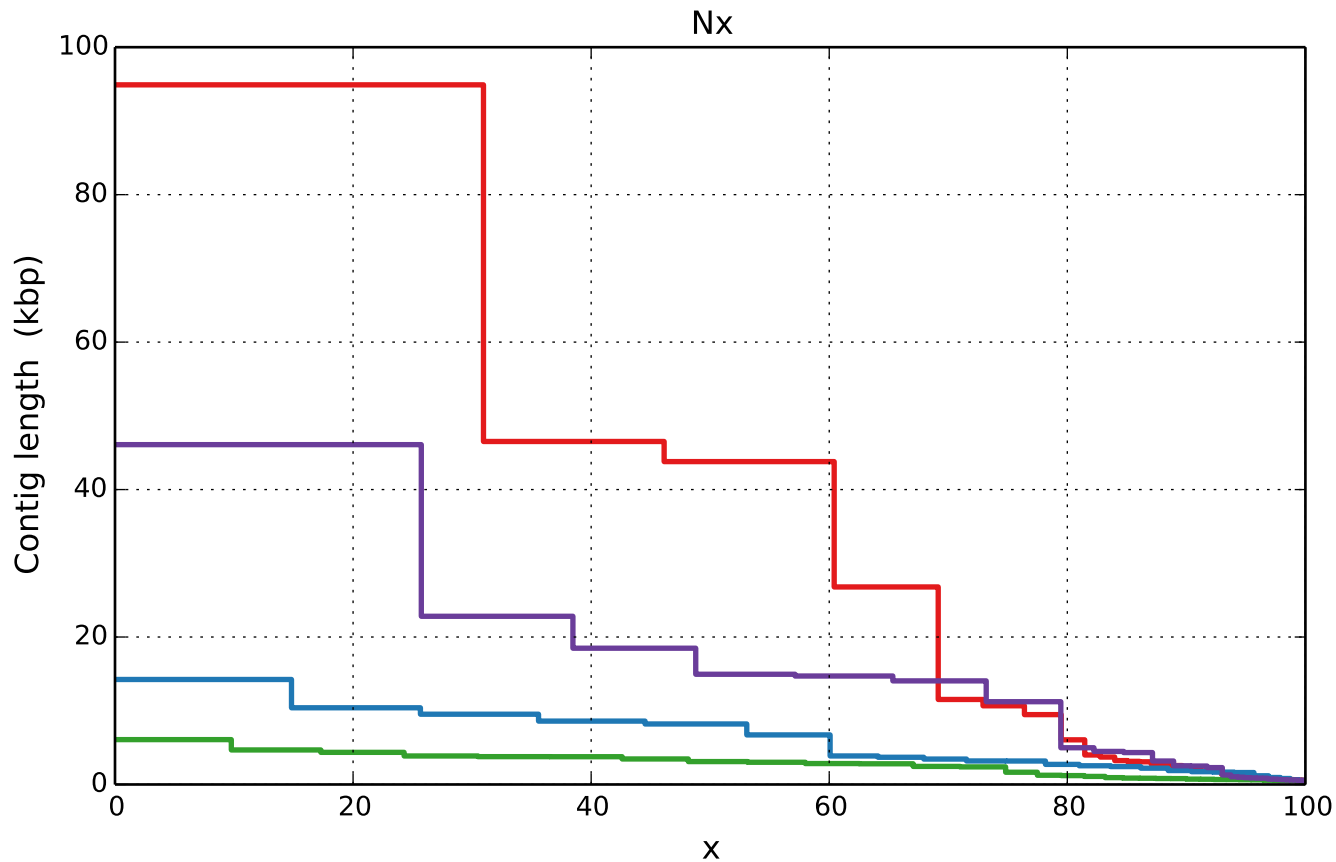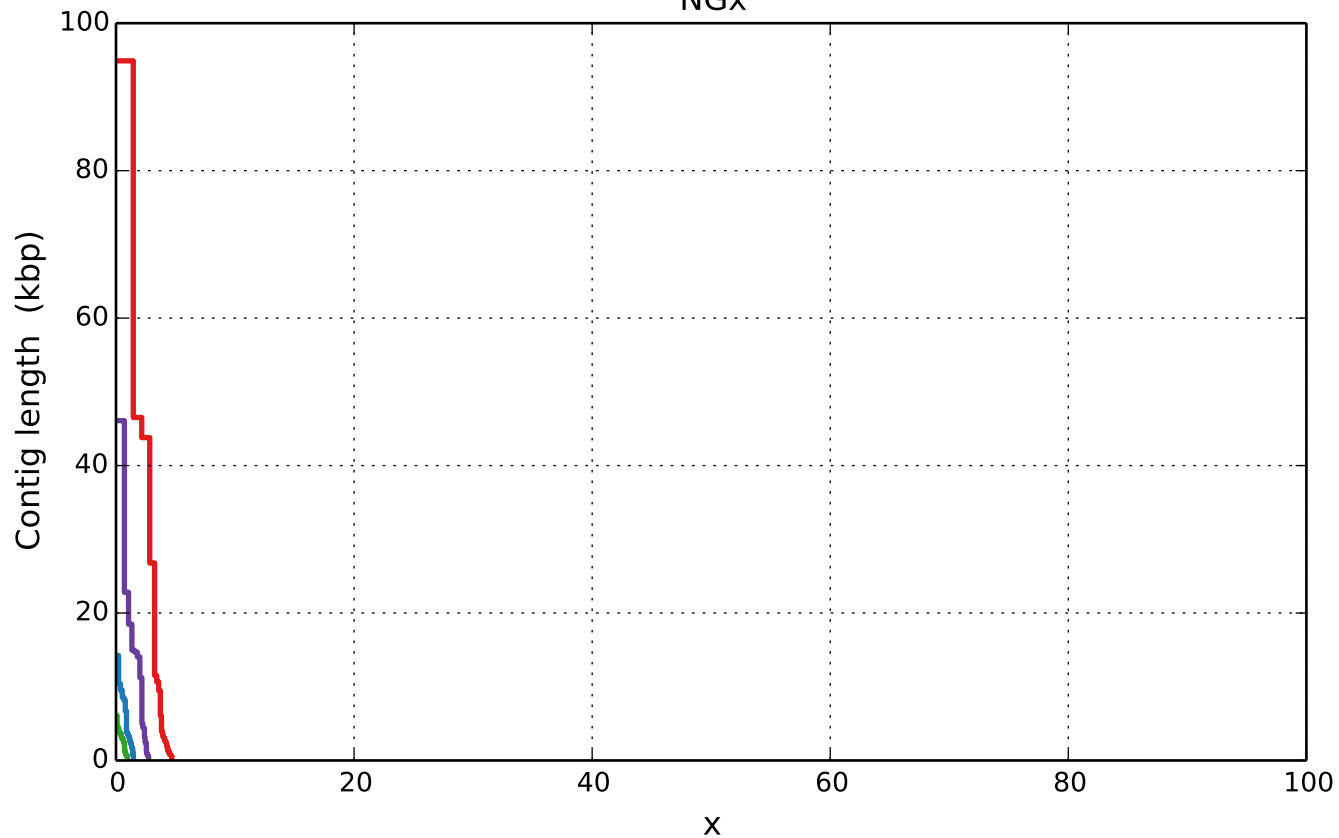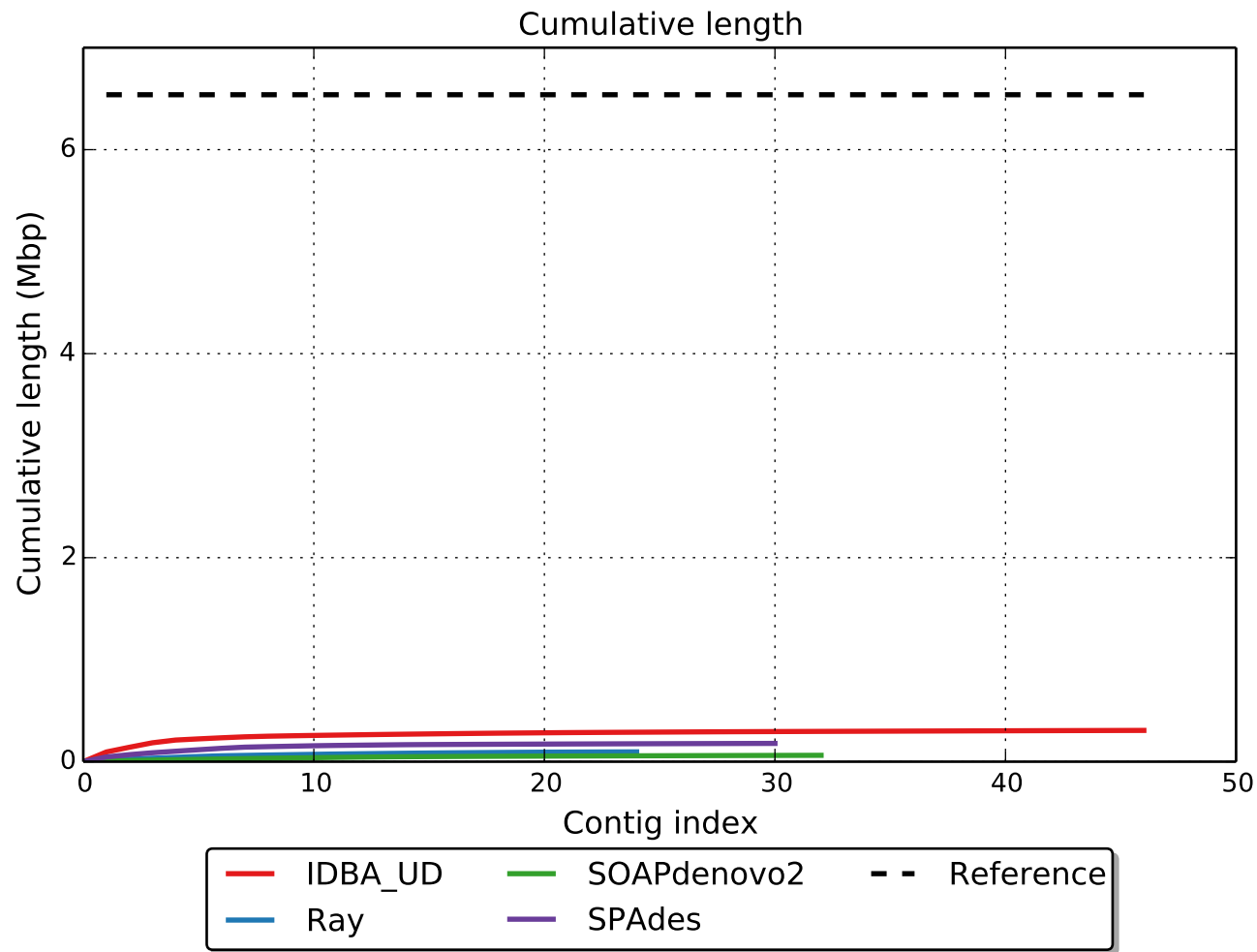
Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	3	1	0	3
# relocations	3	1	0	3
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	5	6	5	10
# misassembled contigs	2	1	0	2
Misassembled contigs length	47514	10403	0	34040
# local misassemblies	2	7	11	0
# structural variations	1	1	0	1
# mismatches	1183	797	513	1607
# indels	39	18	8	48
# short indels	37	18	8	44
# long indels	2	0	0	4
Indels length	85	19	12	95

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
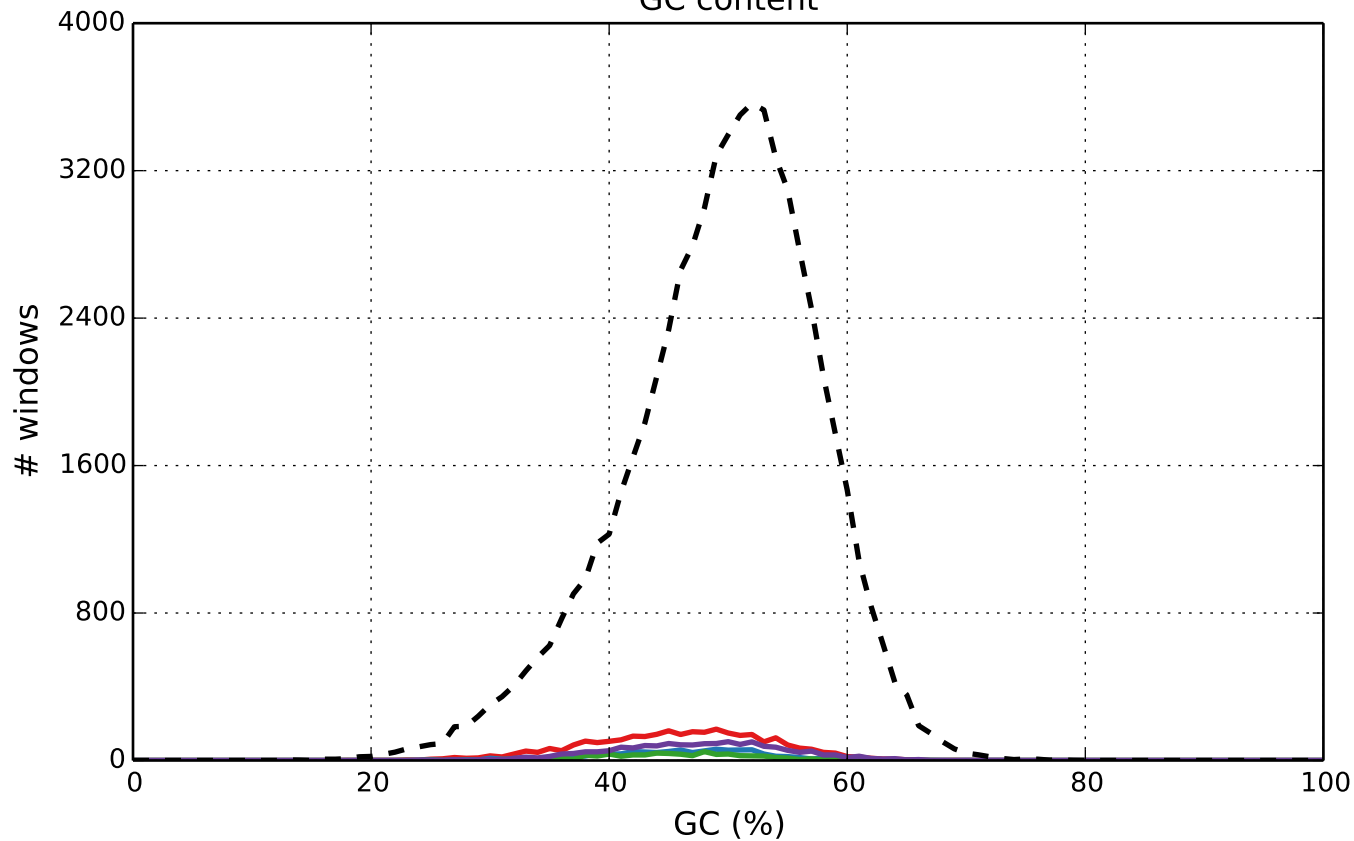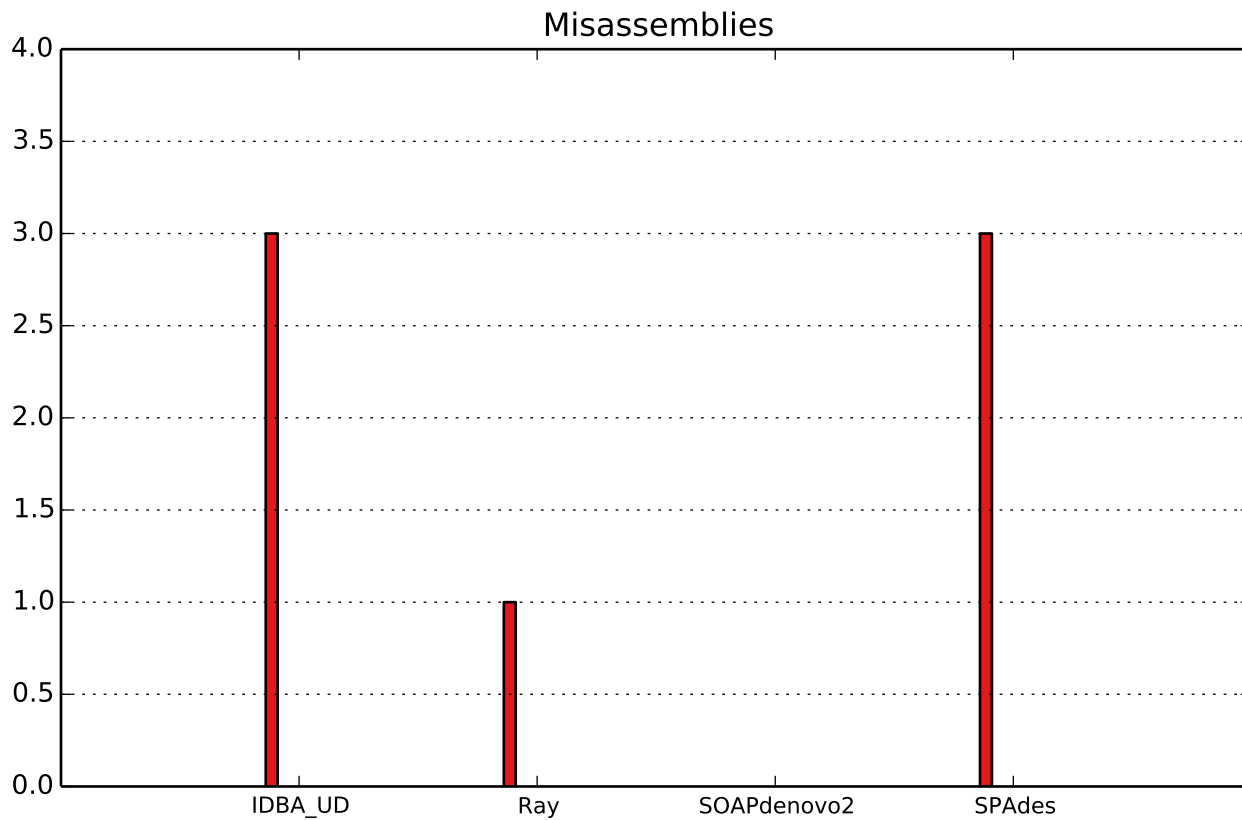
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	23	10	13	17
# with misassembly	2	1	0	1
# both parts are significant	3	3	5	7
Partially unaligned length	208768	26588	10067	79859
# N's	73	1329	1001	454

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).
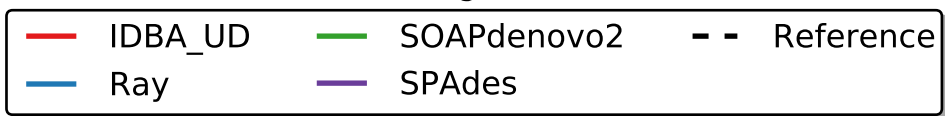
Cumulative length

GC content

Misassemblies

Cumulative length (aligned contigs)

NGAx

Genome fraction, %

IDBA_UD
Ray
SOAPdenovo2
SPAdes