Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	133	114	101	120
# contigs (>= 5000 bp)	93	88	49	89
# contigs (>= 10000 bp)	61	66	31	65
# contigs (>= 25000 bp)	23	28	13	28
# contigs (>= 50000 bp)	4	12	3	6
Total length (>= 1000 bp)	1991024	2478326	1148076	2109769
Total length (>= 5000 bp)	1892713	2415863	1032731	2044896
Total length (>= 10000 bp)	1656049	2251815	906101	1868303
Total length (>= 25000 bp)	1004334	1599649	625578	1271834
Total length (>= 50000 bp)	309692	1007527	282557	534356
# contigs	182	126	158	147
Largest contig	128273	128291	162453	128587
Total length	2024323	2486621	1188649	2128990
Reference length	2615003	2615003	2615003	2615003
GC (%)	27.97	27.96	27.81	28.04
Reference GC (%)	27.37	27.37	27.37	27.37
N50	24388	40495	26233	30338
NG50	19469	38494	-	24063
N75	14864	19975	11094	16678
NG75	2098	17469		7843
L50	24	18	12	21
LG50	37	19	-	30
L75	50	40	30	45
LG75	113	46		76
# misassemblies	48	53	13	32
# misassembled contigs	25	23	9	19
Misassembled contigs length	244486	252753	83888	187803
# local misassemblies	12	8	10	4
# structural variations	1	1	1	1
# unaligned contigs	0 + 122 part	0 + 89 part	0 + 103 part	0 + 115 part
Unaligned length	1411223	1798843	790301	1561955
Genome fraction (%)	19.830	21.250	13.654	18.878
Duplication ratio	1.182	1.238	1.116	1.149
# N's per 100 kbp	0.00	107.25	982.54	126.21
# mismatches per 100 kbp	3475.67	3526.87	3301.73	3505.21
# indels per 100 kbp	111.66	113.38	98.30	110.60
Largest alignment	19542	19316	19356	19316
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).
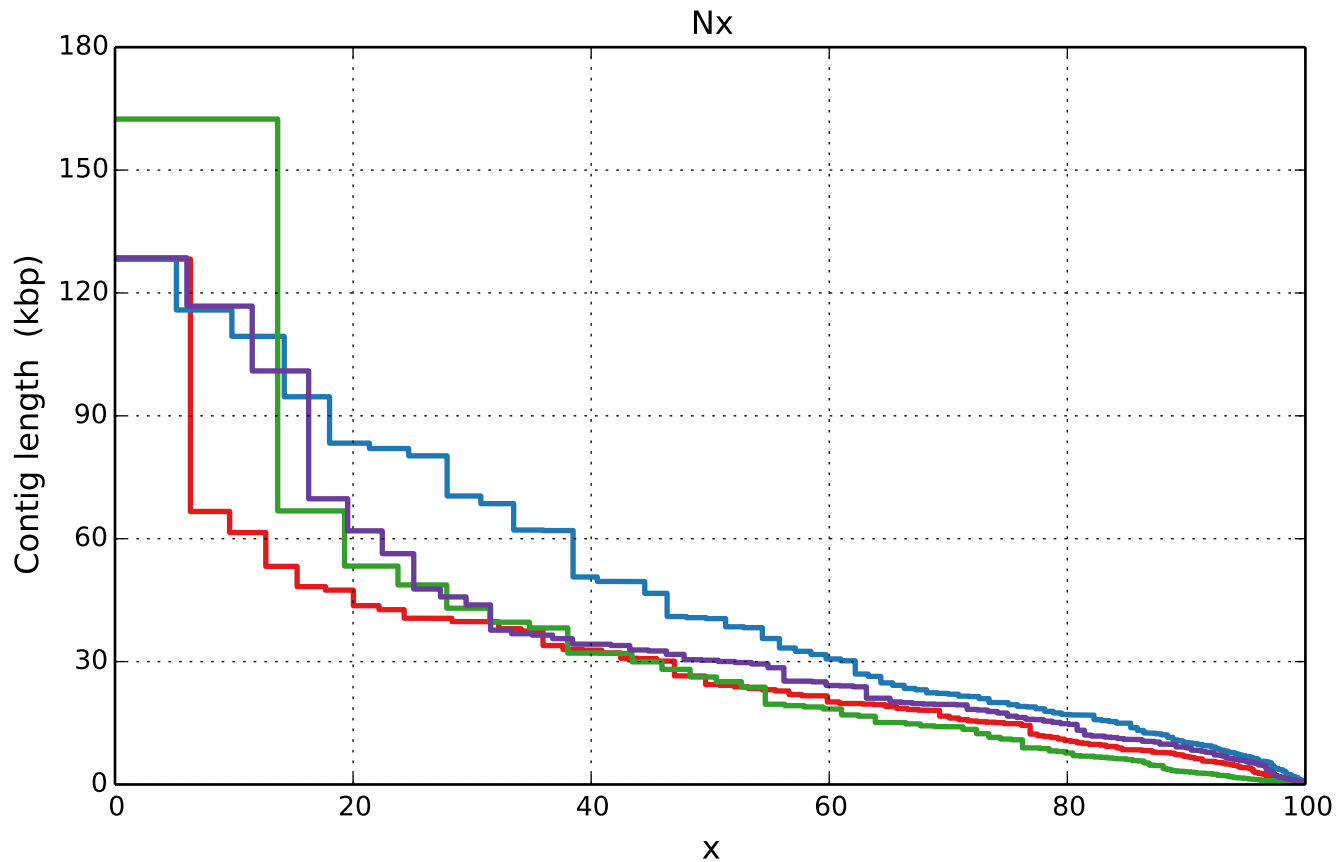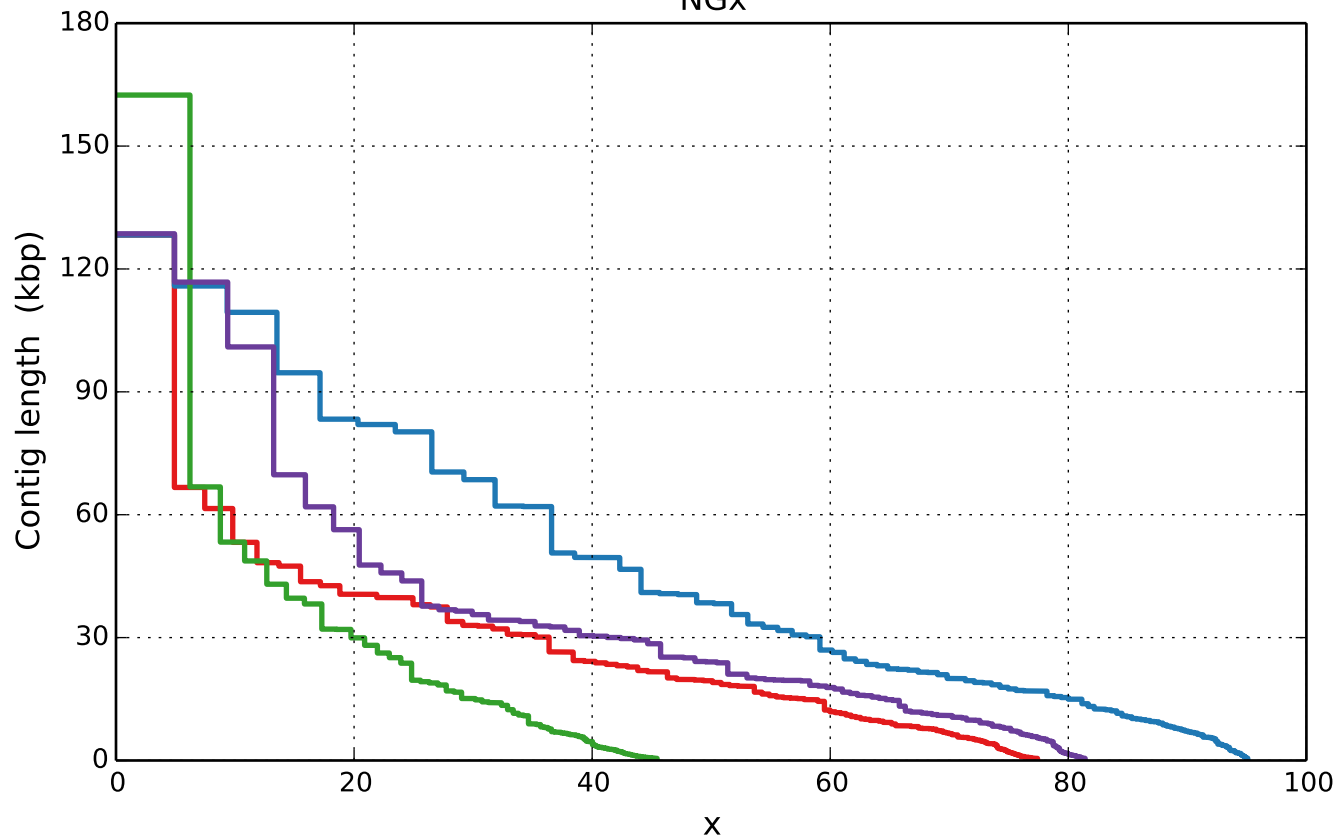
Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	48	53	13	32
# relocations	19	14	6	8
# translocations	29	39	7	24
# inversions	0	0	0	0
# possibly misassembled contigs	69	79	47	70
# misassembled contigs	25	23	9	19
Misassembled contigs length	244486	252753	83888	187803
# local misassemblies	12	8	10	4
# structural variations	1	1	1	1
# mismatches	18023	19598	11789	17304
# indels	579	630	351	546
# short indels	541	589	318	519
# long indels	38	41	33	27
Indels length	1217	1210	1178	952

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	122	89	103	115
# with misassembly	61	61	20	56
# both parts are significant	52	60	39	59
Partially unaligned length	1411223	1798843	790301	1561955
# N's	0	2667	11679	2687

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).

NGx

Cumulative length

GC content

windows vs GC (%)
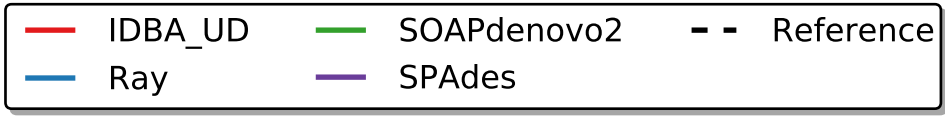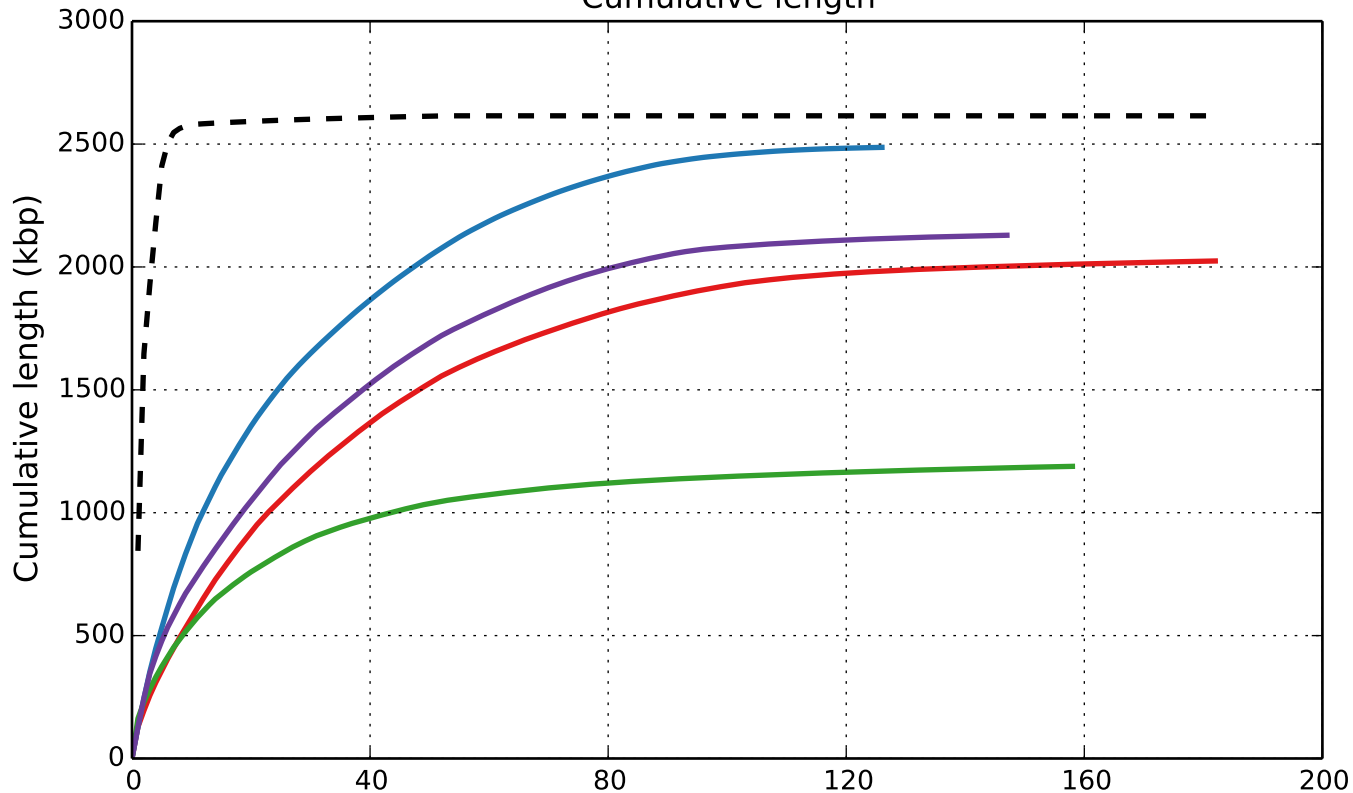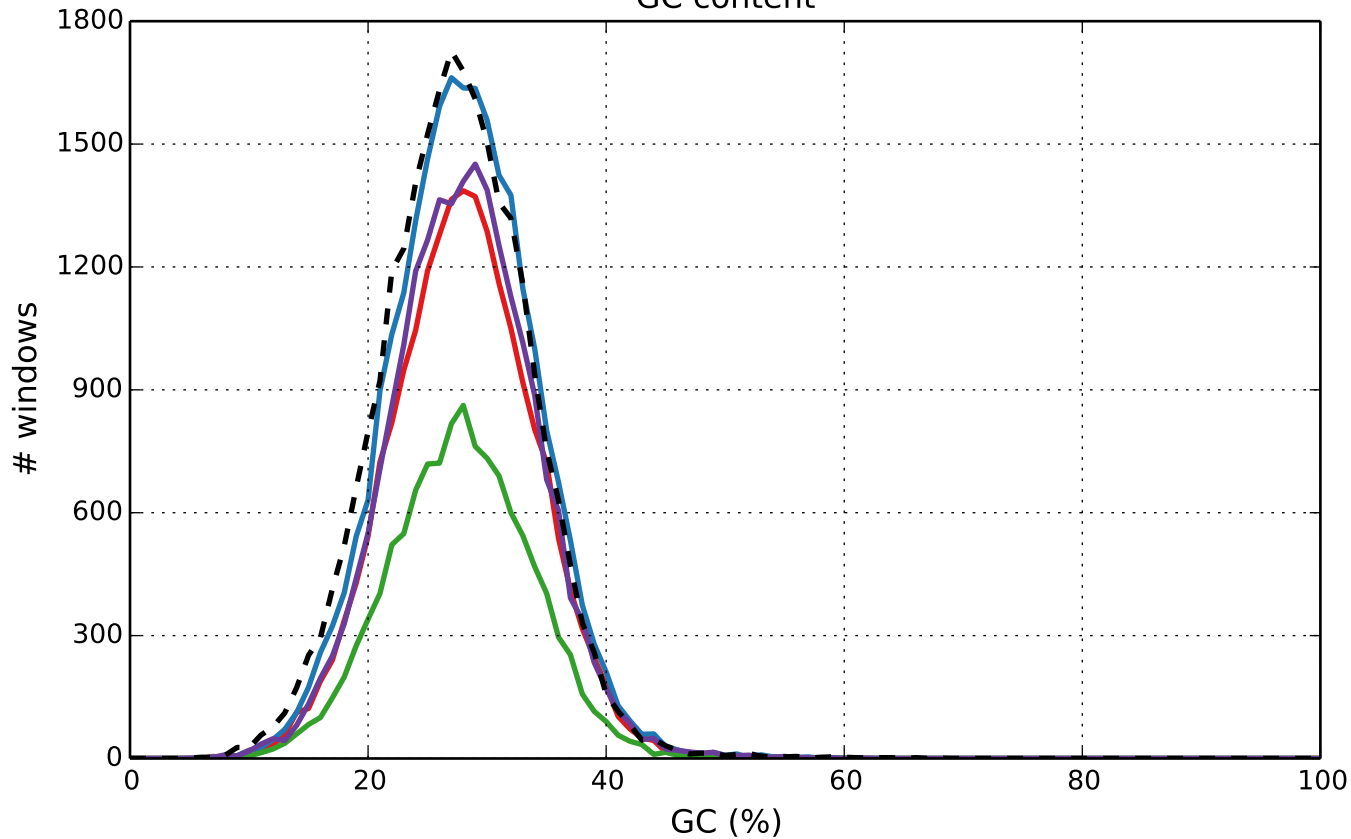
Misassemblies
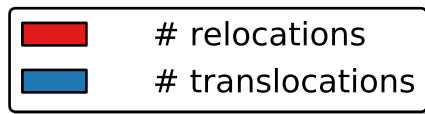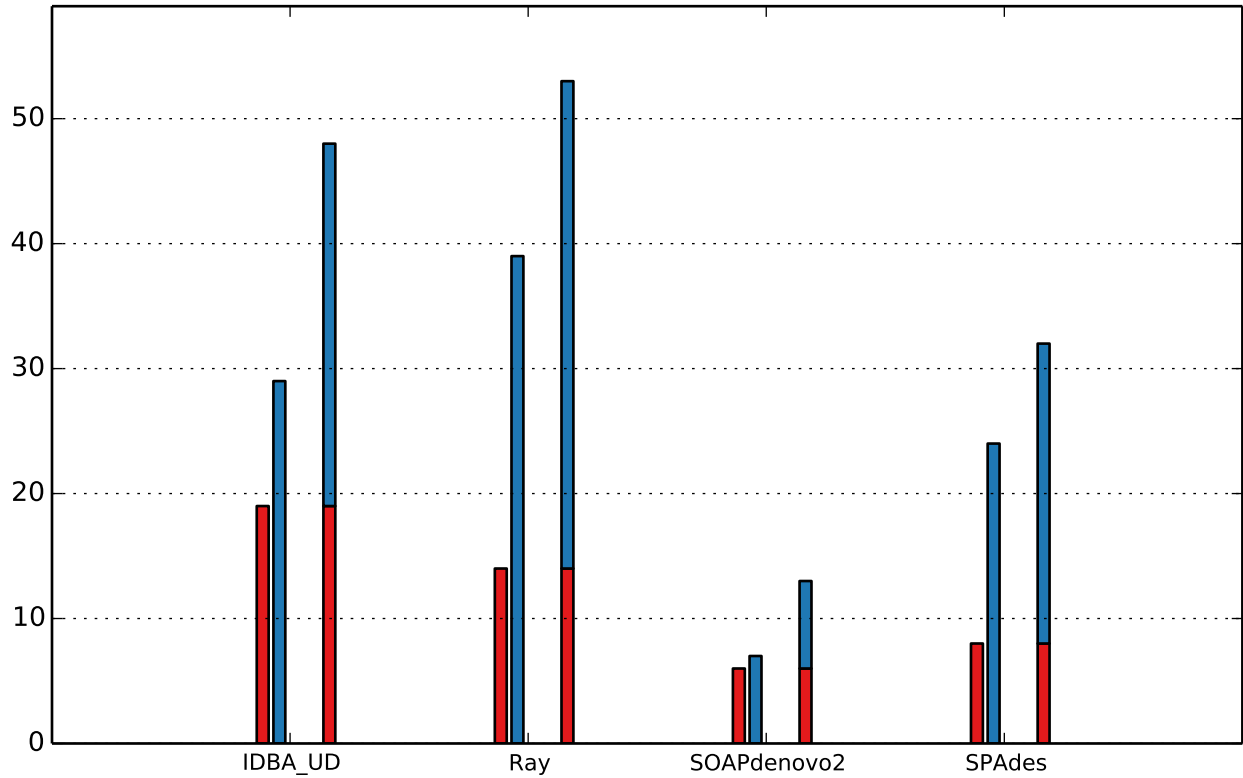
Cumulative length (aligned contigs)

Genome fraction, %