Report

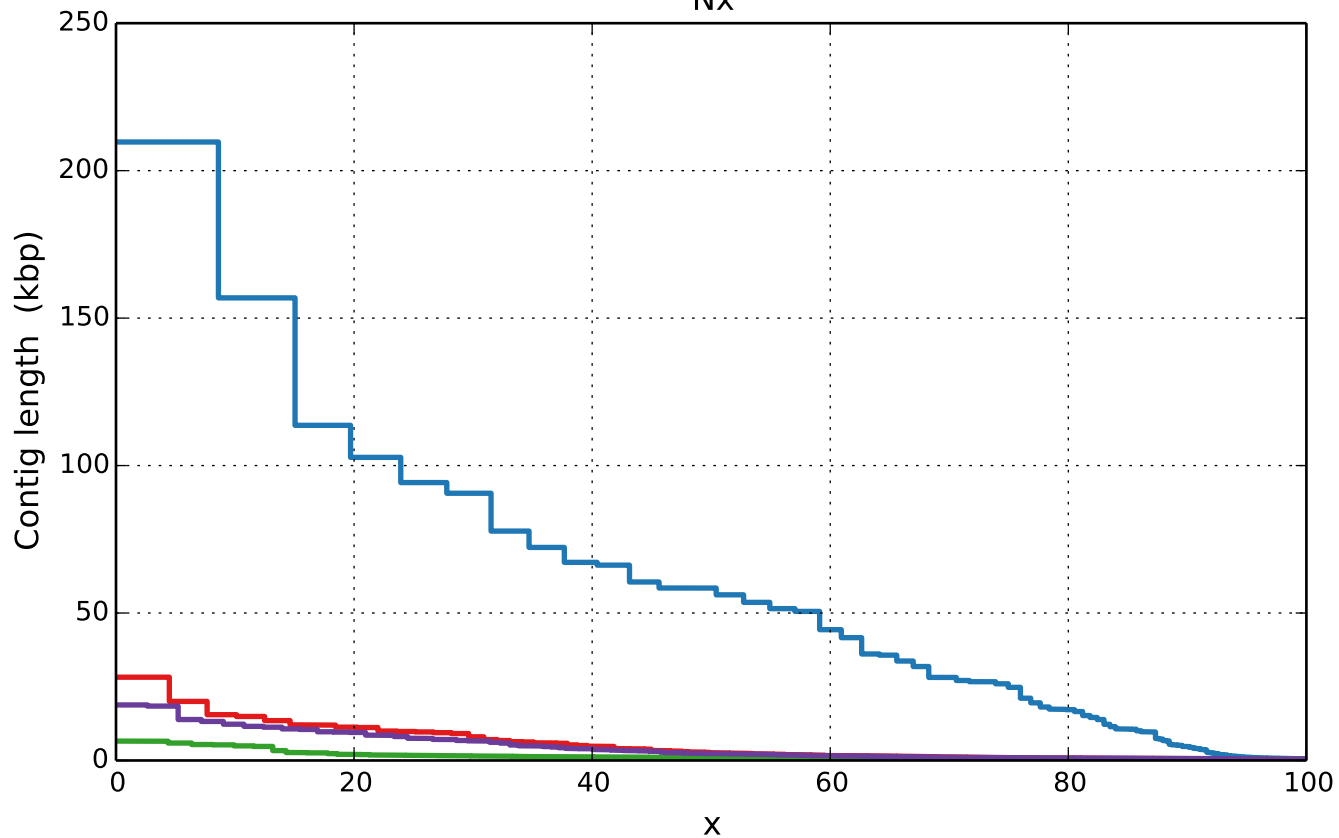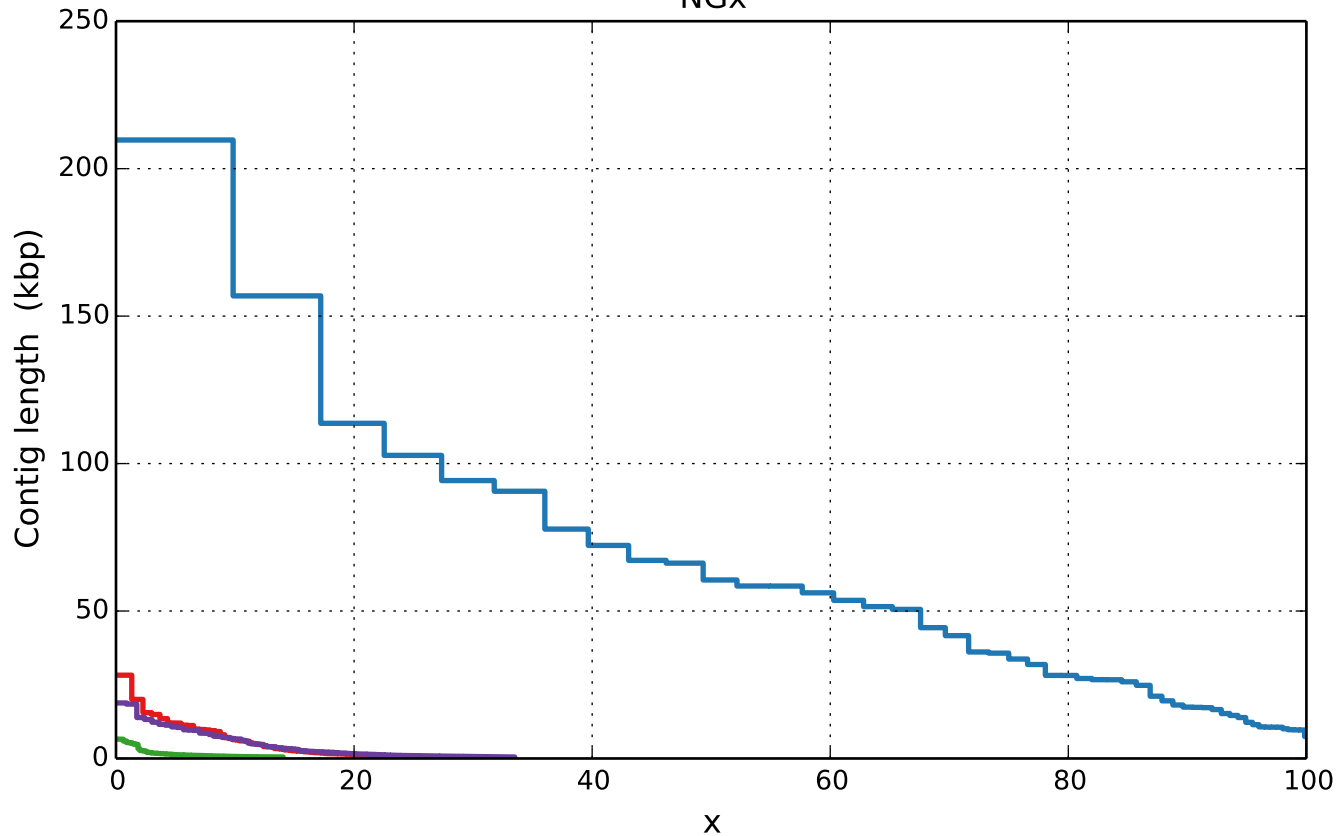|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	138	135	84	164
# contigs (>= 5000 bp)	24	59	5	25
# contigs (>= 10000 bp)	9	47	0	9
# contigs (>= 25000 bp)	1	29	0	0
# contigs (>= 50000 bp)	0	17	0	0
Total length (>= 1000 bp)	466424	2331746	151500	514785
Total length (>= 5000 bp)	249440	2182577	29709	241440
Total length (>= 10000 bp)	138779	2099047	0	120780
Total length (>= 25000 bp)	28239	1826835	0	0
Total length (>= 50000 bp)	0	1440574	0	0
# contigs	383	284	310	444
Largest contig	28239	209717	6577	18832
Total length	630541	2437114	299338	713862
Reference length	2131358	2131358	2131358	2131358
GC (%)	40.96	41.85	41.79	41.48
Reference GC (%)	41.97	41.97	41.97	41.97
N50	2638	58463	1006	2309
NG50	-	60528	-	-
N75	962	24801	642	937
NG75	-	33719	-	-
L50	43	13	83	60
LG50	-	11	-	-
L75	145	30	176	186
LG75	-	22	-	-
# misassemblies	1	13	0	6
# misassembled contigs	1	4	0	6
Misassembled contigs length	825	179866	0	30076
# local misassemblies	4	6	1	1
# structural variations	0	0	0	0
# unaligned contigs	0 + 50 part	0 + 77 part	0 + 15 part	0 + 49 part
Unaligned length	235173	1696945	28066	165766
Genome fraction (%)	16.899	27.876	12.594	21.586
Duplication ratio	1.098	1.246	1.011	1.191
# N's per 100 kbp	0.00	231.09	1213.68	151.29
# mismatches per 100 kbp	3158.52	3441.51	2475.11	3062.15
# indels per 100 kbp	50.25	77.26	45.08	64.34
Largest alignment	8026	30082	5910	13132
NA50	630	-	829	917
NGA50	-	-	-	-
NA75	-	-	561	181
LA50	231	-	104	162
LA75	-	-	216	440

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	1	13	0	6
# relocations	0	1	0	0
# translocations	1	12	0	6
# inversions	0	0	0	0
# possibly misassembled contigs	21	42	2	22
# misassembled contigs	1	4	0	6
Misassembled contigs length	825	179866	0	30076
# local misassemblies	4	6	1	1
# structural variations	0	0	0	0
# mismatches	11376	20447	6644	14088
# indels	181	459	121	296
# short indels	162	440	109	287
# long indels	19	19	12	9
Indels length	621	754	289	549

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	50	77	15	49
# with misassembly	18	39	6	9
# both parts are significant	19	39	1	20
Partially unaligned length	235173	1696945	28066	165766
# N's	0	5632	3633	1080

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).
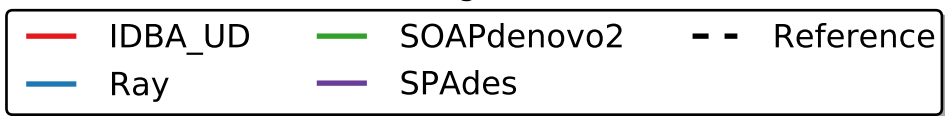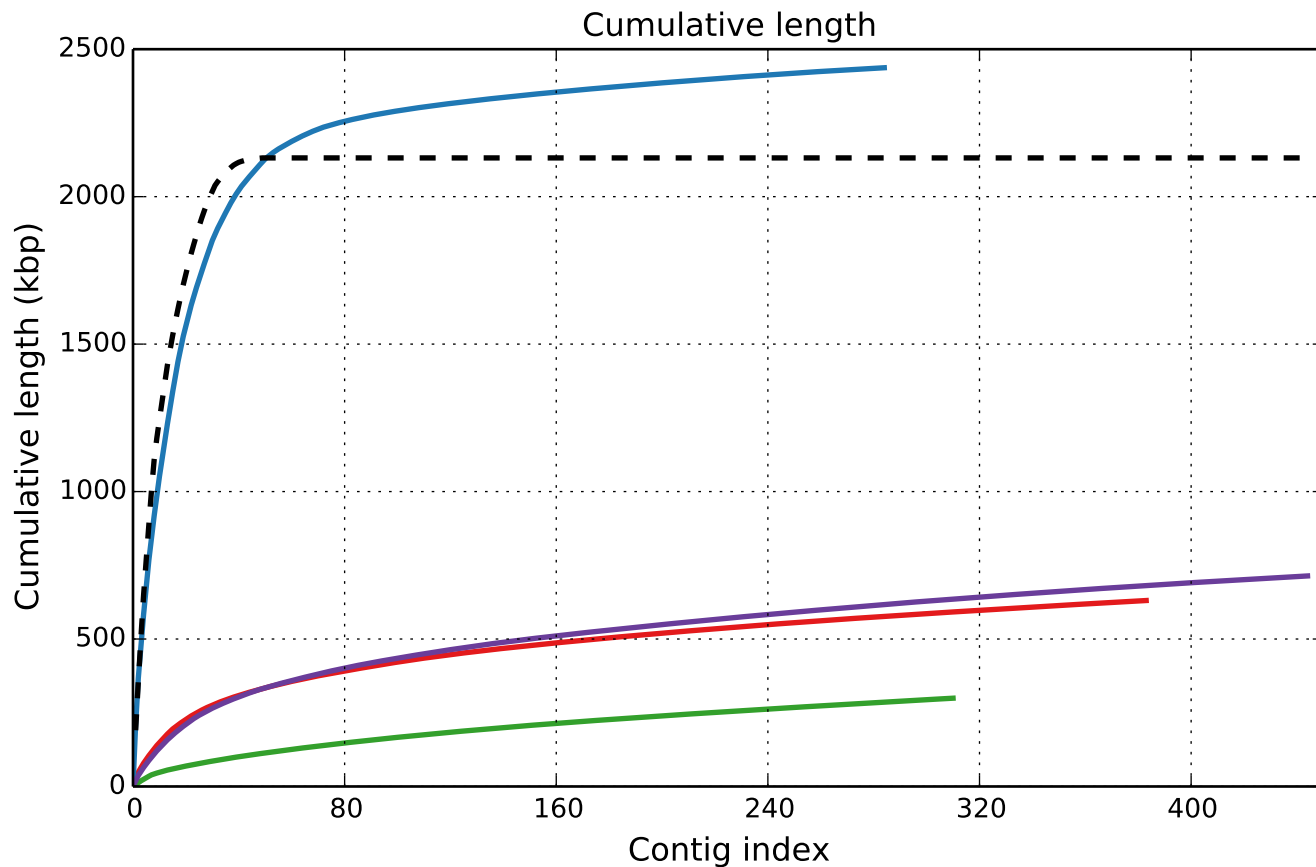
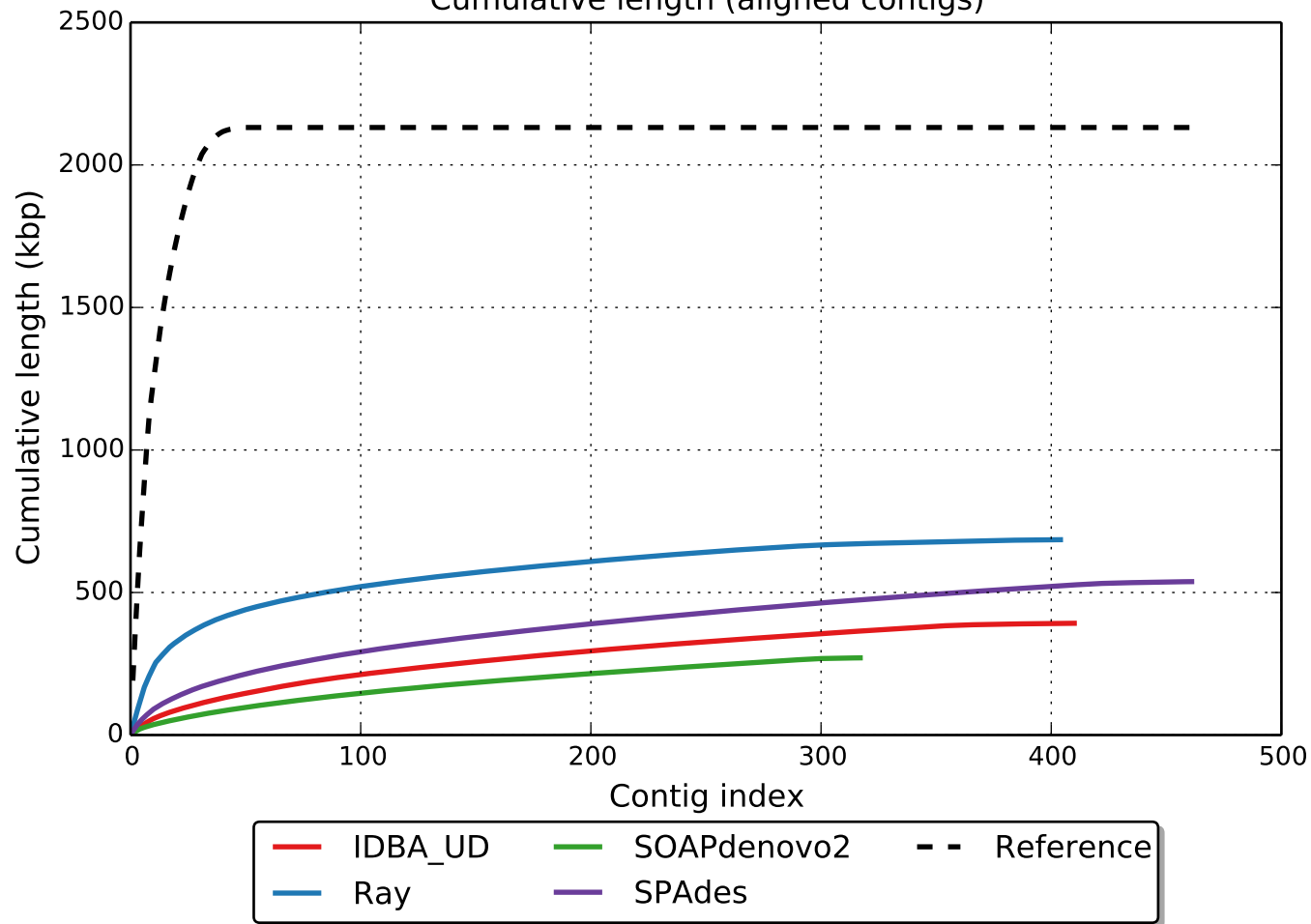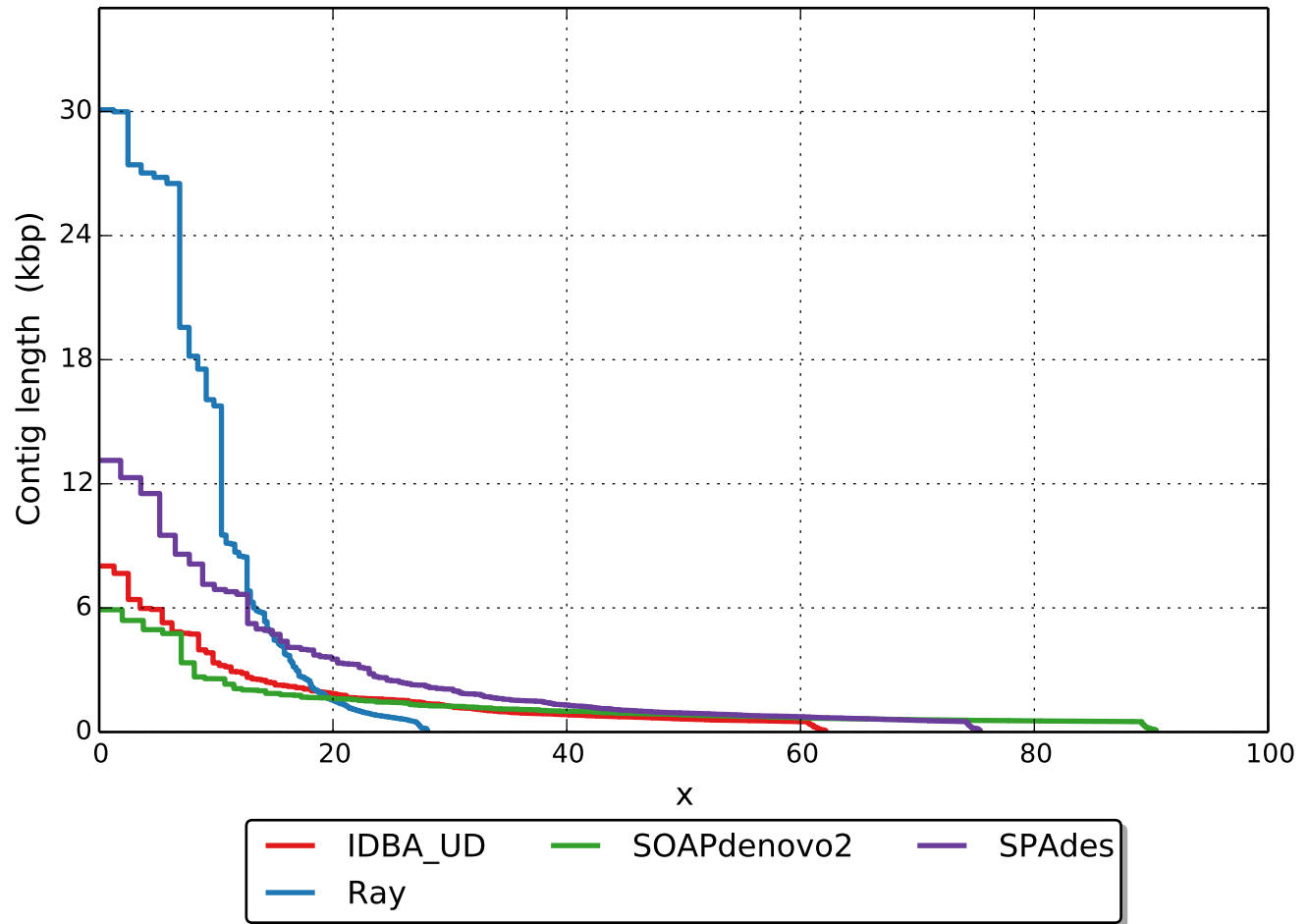Cumulative length

GC content
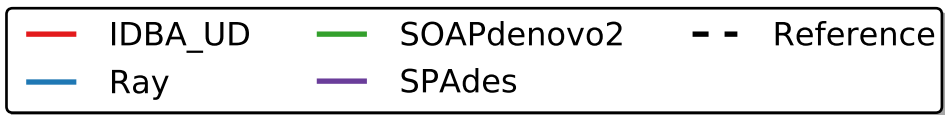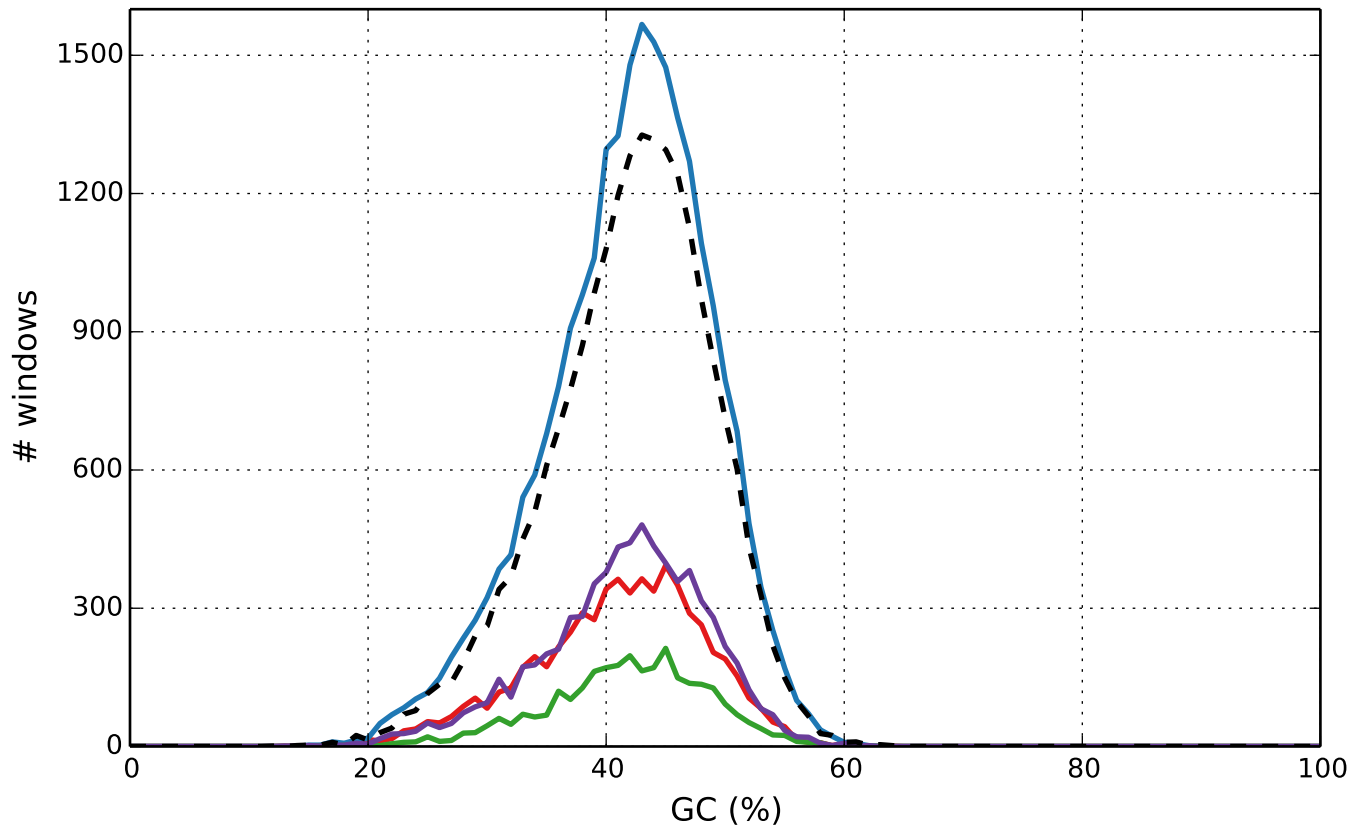
Misassemblies
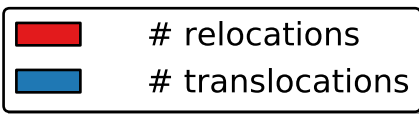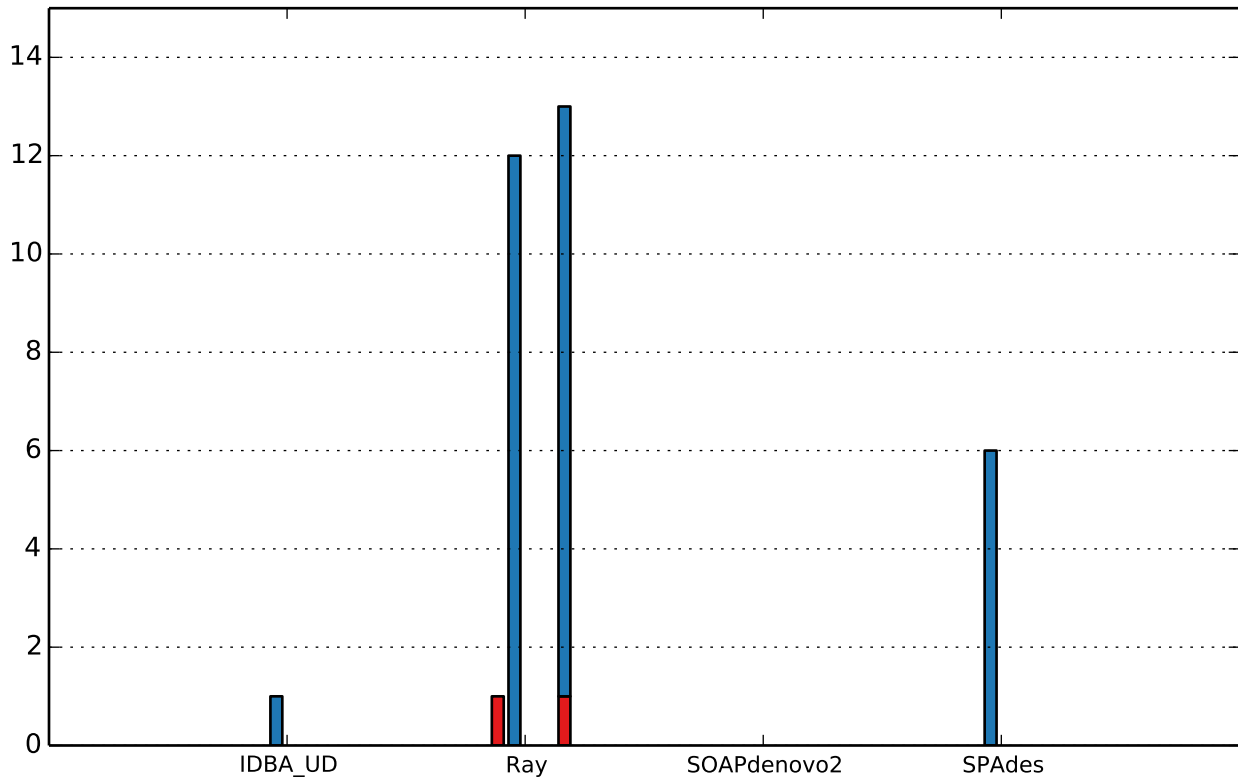
Cumulative length (aligned contigs)

Genome fraction, %

- IDBA_UD
- Ray
- SOAPdenovo2
- SPAdes