Report

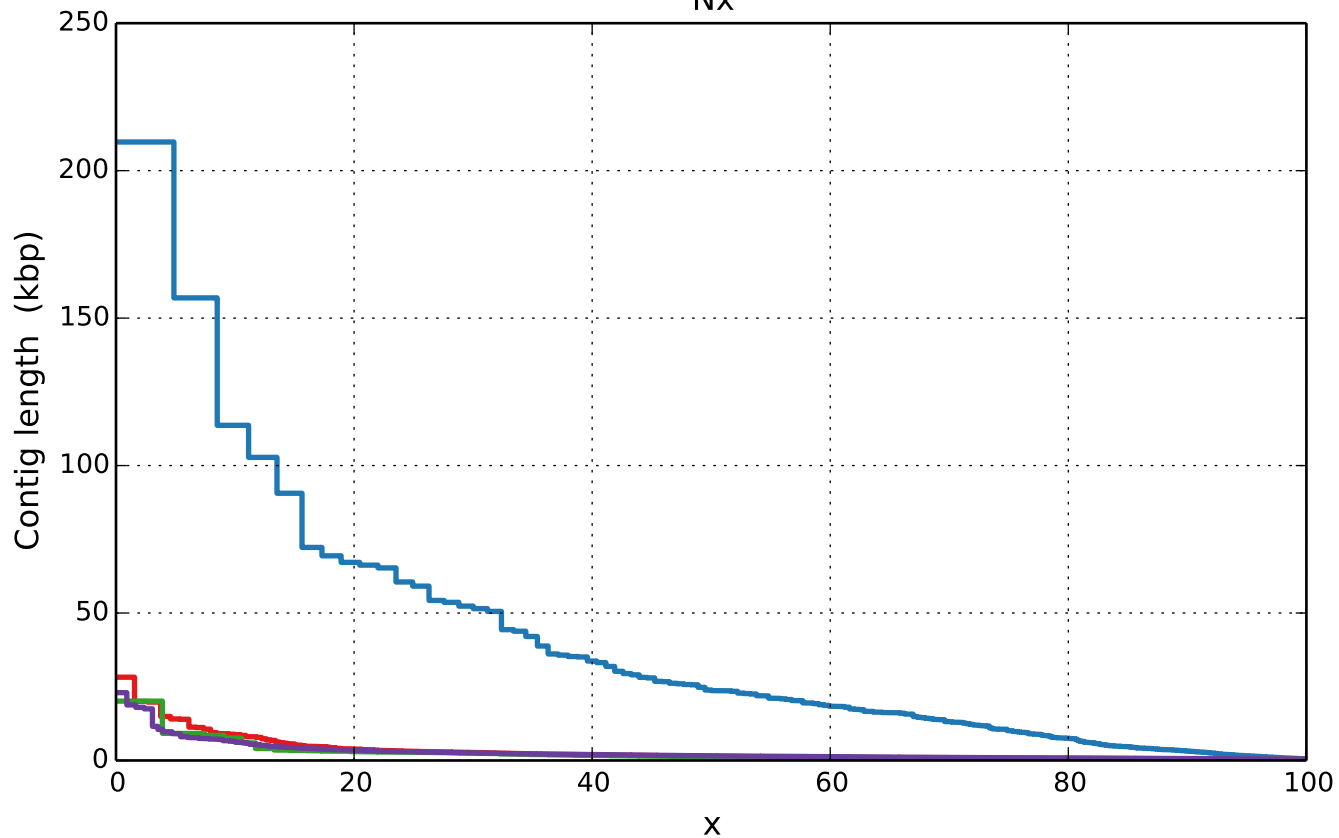|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	501	410	154	861
# contigs (>= 5000 bp)	29	157	6	38
# contigs (>= 10000 bp)	9	108	1	6
# contigs (>= 25000 bp)	1	39	0	0
# contigs (>= 50000 bp)	0	17	0	0
Total length (>= 1000 bp)	1152621	4207802	323333	1810264
Total length (>= 5000 bp)	287829	3603751	60548	321263
Total length (>= 10000 bp)	144134	3247125	20126	99447
Total length (>= 25000 bp)	28239	2107947	0	0
Total length (>= 50000 bp)	0	1395863	0	0
# contigs	1473	551	443	1879
Largest contig	28239	209717	20126	23001
Total length	1813472	4310925	516627	2527852
Reference length	1869505	1869505	1869505	1869505
GC (%)	38.85	40.21	38.35	39.52
Reference GC (%)	39.57	39.57	39.57	39.57
N50	1452	23892	1317	1576
NG50	1386	66233	-	2137
N75	778	10136	755	933
NG75	745	44352	-	1411
L50	295	41	98	425
LG50	315	9	-	246
L75	738	107	229	950
LG75	793	18	-	518
# misassemblies	7	29	0	18
# misassembled contigs	6	23	0	17
Misassembled contigs length	7675	314617	0	30955
# local misassemblies	46	61	11	30
# structural variations	2	7	0	9
# unaligned contigs	0 + 552 part	0 + 298 part	0 + 325 part	0 + 509 part
Unaligned length	871186	2733335	342183	737944
Genome fraction (%)	40.579	60.183	8.951	54.963
Duplication ratio	1.242	1.402	1.042	1.742
# N's per 100 kbp	0.99	454.36	9563.57	61.63
# mismatches per 100 kbp	2742.19	3477.90	2414.90	3053.83
# indels per 100 kbp	89.64	99.54	75.30	89.05
Largest alignment	7823	38107	7648	8040
NA50	156	-	-	779
NGA50	75	4936	-	1079
NGA75	-	523	-	677
LA50	1241	-	-	865
LGA50	1490	77	-	503
LGA75	-	387	-	1056

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	7	29	0	18
# relocations	4	17	0	4
# translocations	3	12	0	14
# inversions	0	0	0	0
# possibly misassembled contigs	56	146	8	109
# misassembled contigs	6	23	0	17
Misassembled contigs length	7675	314617	0	30955
# local misassemblies	46	61	11	30
# structural variations	2	7	0	9
# mismatches	20803	39131	4041	31379
# indels	680	1120	126	915
# short indels	601	1063	116	883
# long indels	79	57	10	32
Indels length	2781	2098	512	1470

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	552	298	325	509
# with misassembly	23	65	32	23
# both parts are significant	52	118	7	100
Partially unaligned length	871186	2733335	342183	737944
# N's	18	19587	49408	1558

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

- IDBA_UD
- Ray
- SOAPdenovo2
- SPAdes
- Reference
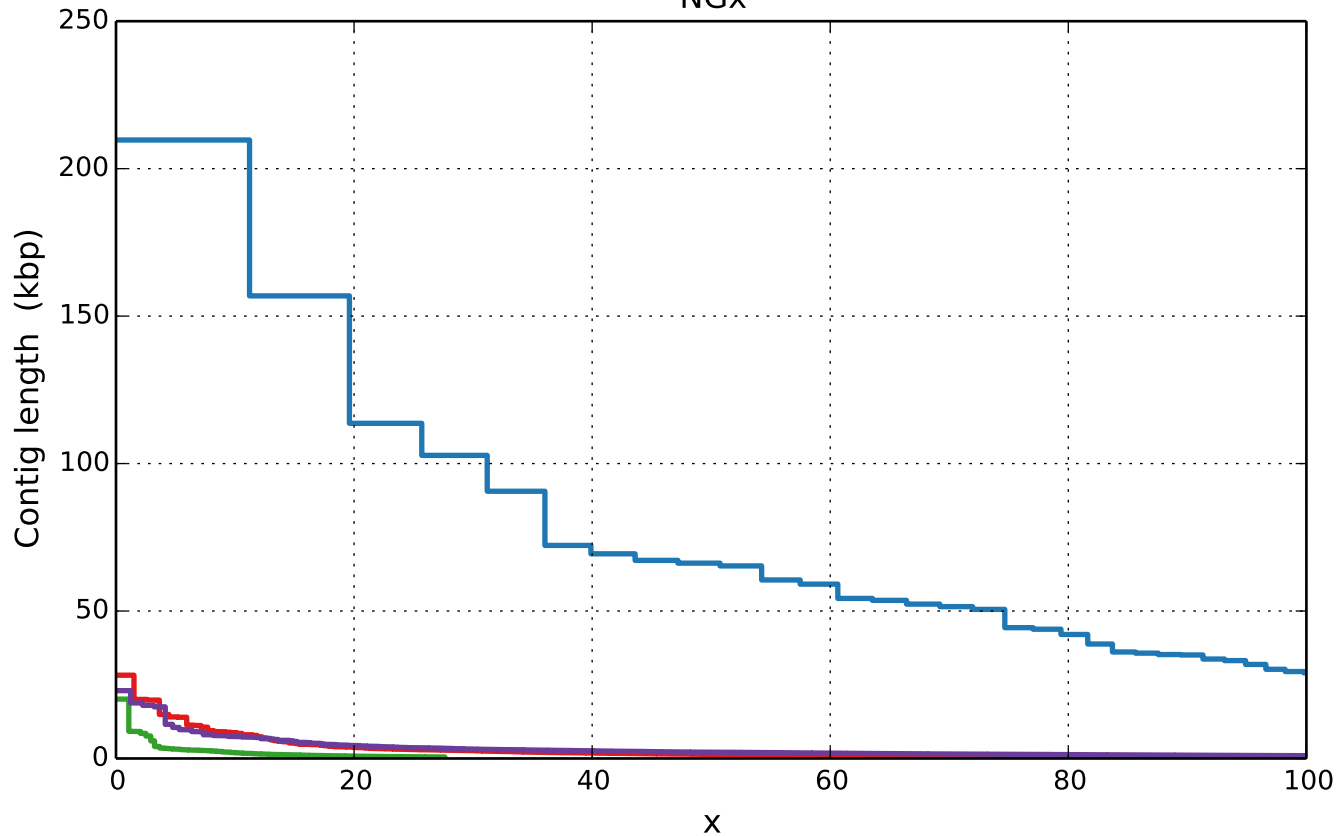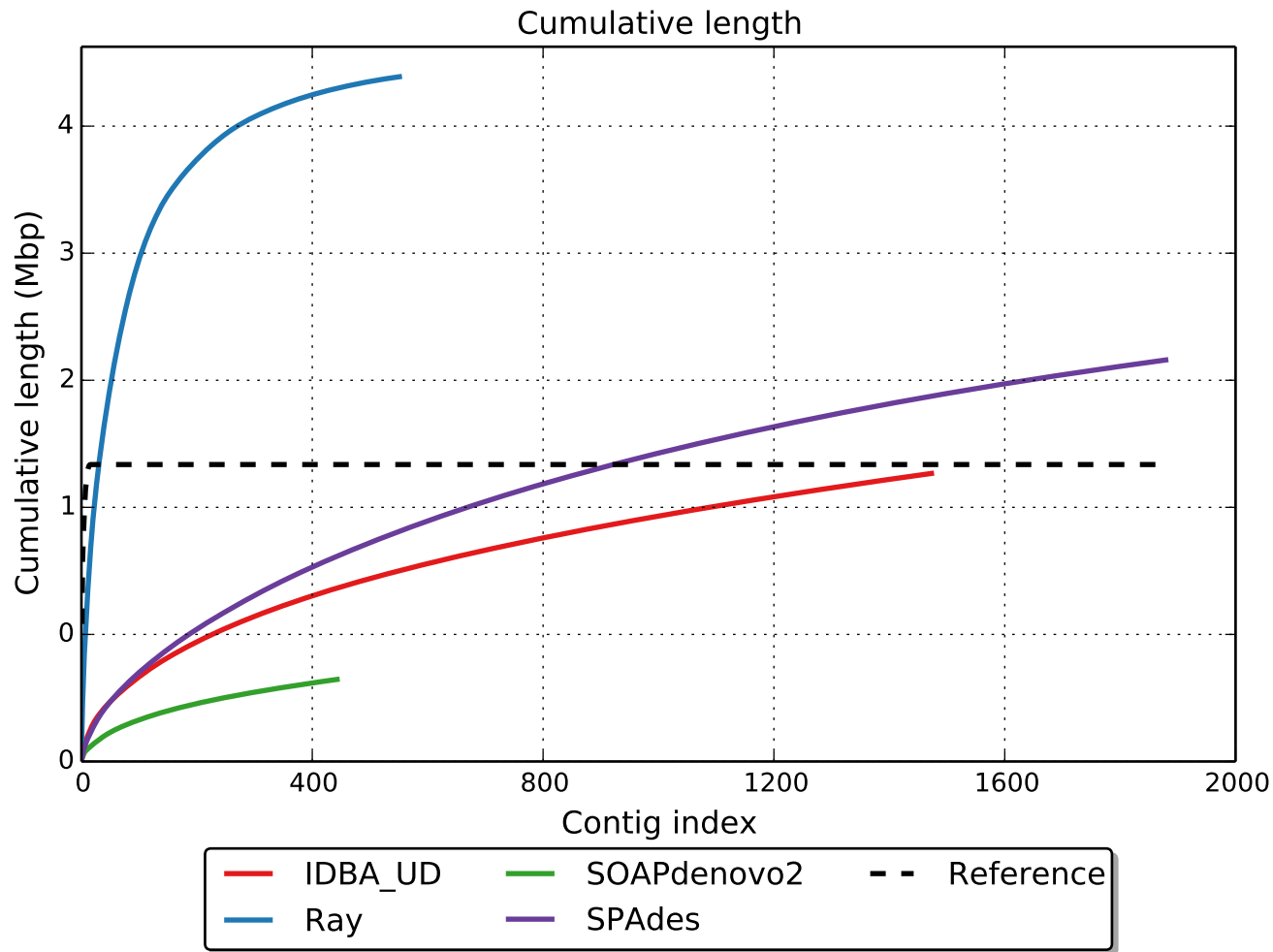
GC content
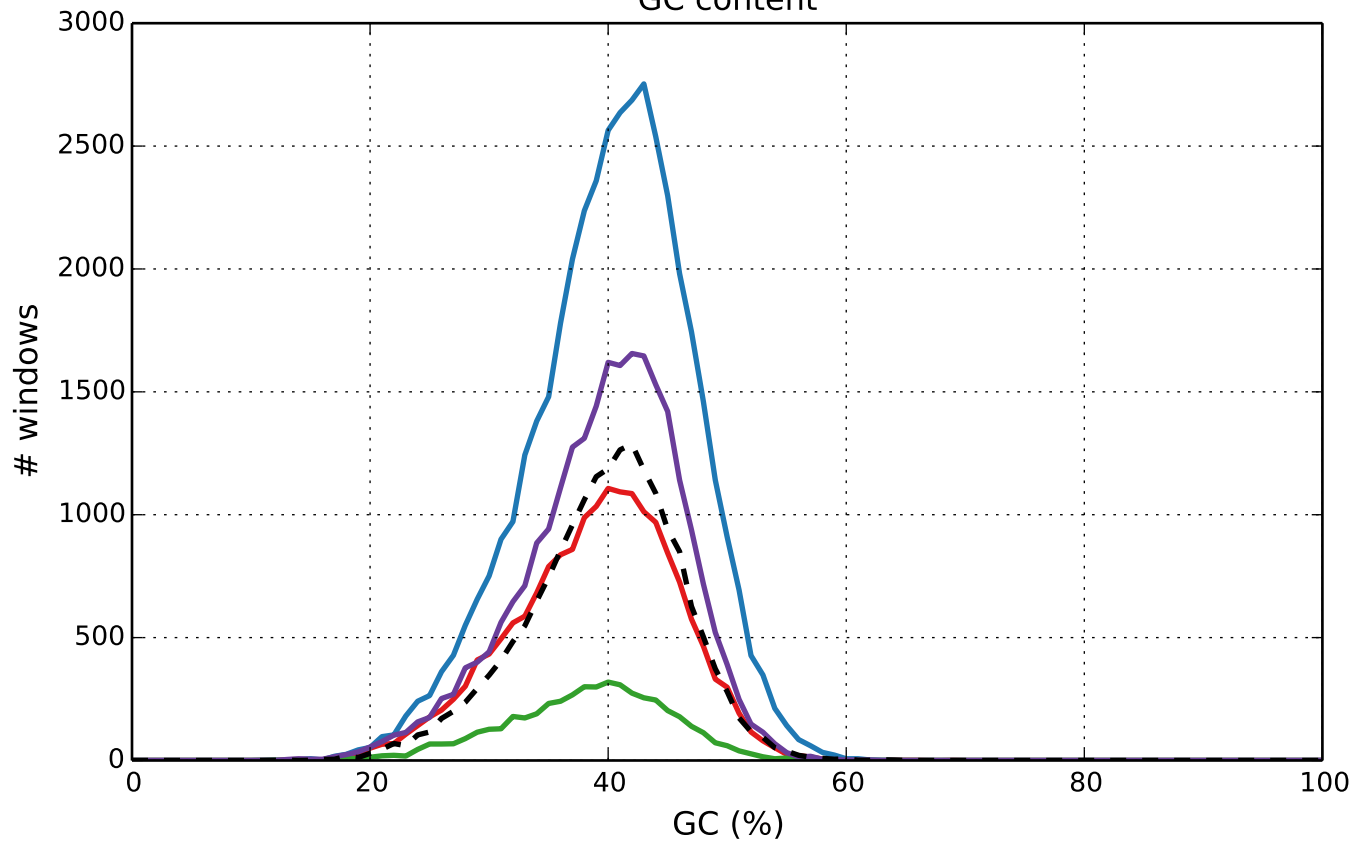
Misassemblies
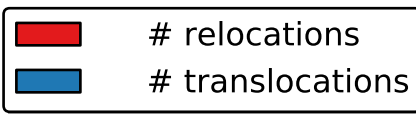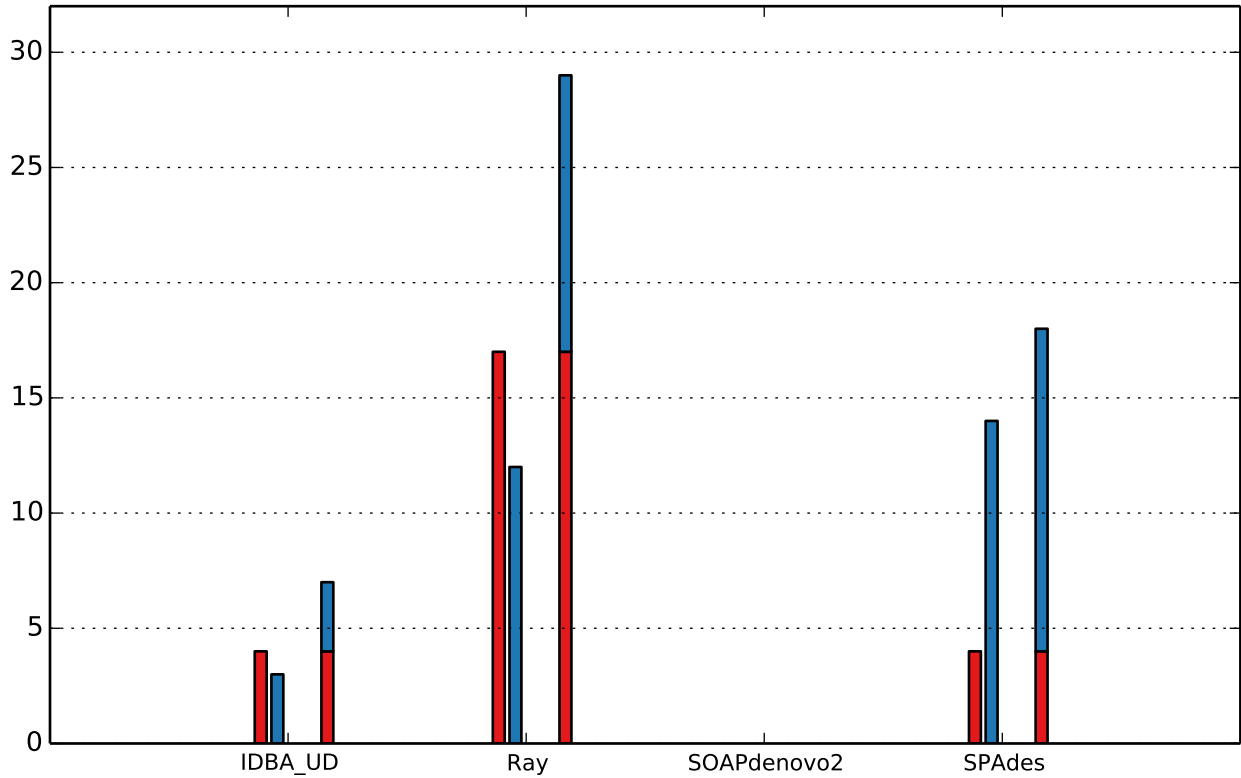
Cumulative length (aligned contigs)

Genome fraction, %