

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	28	7	33	53
# contigs (>= 5000 bp)	13	4	2	10
# contigs (>= 10000 bp)	8	3	0	7
# contigs (>= 25000 bp)	2	1	0	5
# contigs (>= 50000 bp)	1	0	0	2
Total length (>= 1000 bp)	337251	85401	74306	422620
Total length (>= 5000 bp)	313065	77643	11764	358602
Total length (>= 10000 bp)	273476	71727	0	338108
Total length (>= 25000 bp)	161447	43716	0	308758
Total length (>= 50000 bp)	123909	0	0	194608
# contigs	206	9	68	308
Largest contig	123909	43716	6297	144537
Total length	453119	86890	98647	586204
Reference length	5116282	5116282	5116282	5116282
GC (%)	45.34	44.94	44.17	43.05
Reference GC (%)	43.17	43.17	43.17	43.17
N50	20269	43716	1833	34221
N75	948	13809	1053	871
L50	5	1	15	5
L75	31	3	33	72
# misassemblies	1	0	0	2
# misassembled contigs	1	0	0	2
Misassembled contigs length	37538	0	0	51405
# local misassemblies	0	0	12	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 18 part	0 + 3 part	0 + 6 part	0 + 32 part
Unaligned length	234543	20859	3101	298071
Genome fraction (%)	4.207	1.273	1.834	5.301
Duplication ratio	1.015	1.014	1.018	1.062
# N's per 100 kbp	23.39	0.00	1241.80	590.24
# mismatches per 100 kbp	488.24	752.39	375.12	692.47
# indels per 100 kbp	14.87	12.28	9.59	60.47
Largest alignment	30864	39321	6297	30864
NA50	-	14202	1801	-
NGA50	-	-	-	-
NA75	-	518	905	-
LA50	-	2	15	-
LA75	-	7	34	-

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	0	0	2
# relocations	1	0	0	1
# translocations	0	0	0	1
# inversions	0	0	0	0
# possibly misassembled contigs	3	1	0	5
# misassembled contigs	1	0	0	2
Misassembled contigs length	37538	0	0	51405
# local misassemblies	0	0	12	0
# structural variations	0	0	0	0
# mismatches	1051	490	352	1878
# indels	32	8	9	164
# short indels	27	8	9	117
# long indels	5	0	0	47
Indels length	130	11	13	812

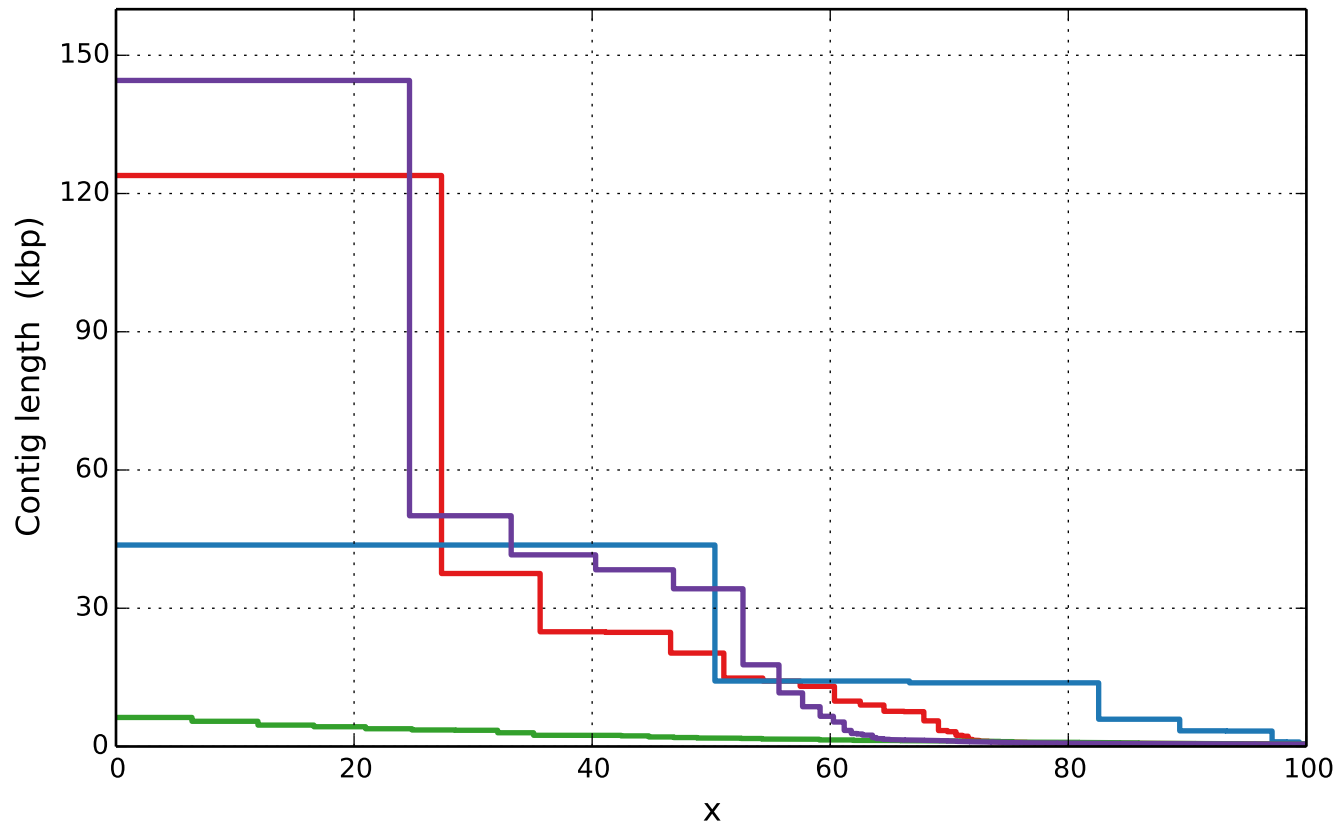
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	18	3	6	32
# with misassembly	1	0	1	3
# both parts are significant	2	1	0	4
Partially unaligned length	234543	20859	3101	298071
# N's	106	0	1225	3460

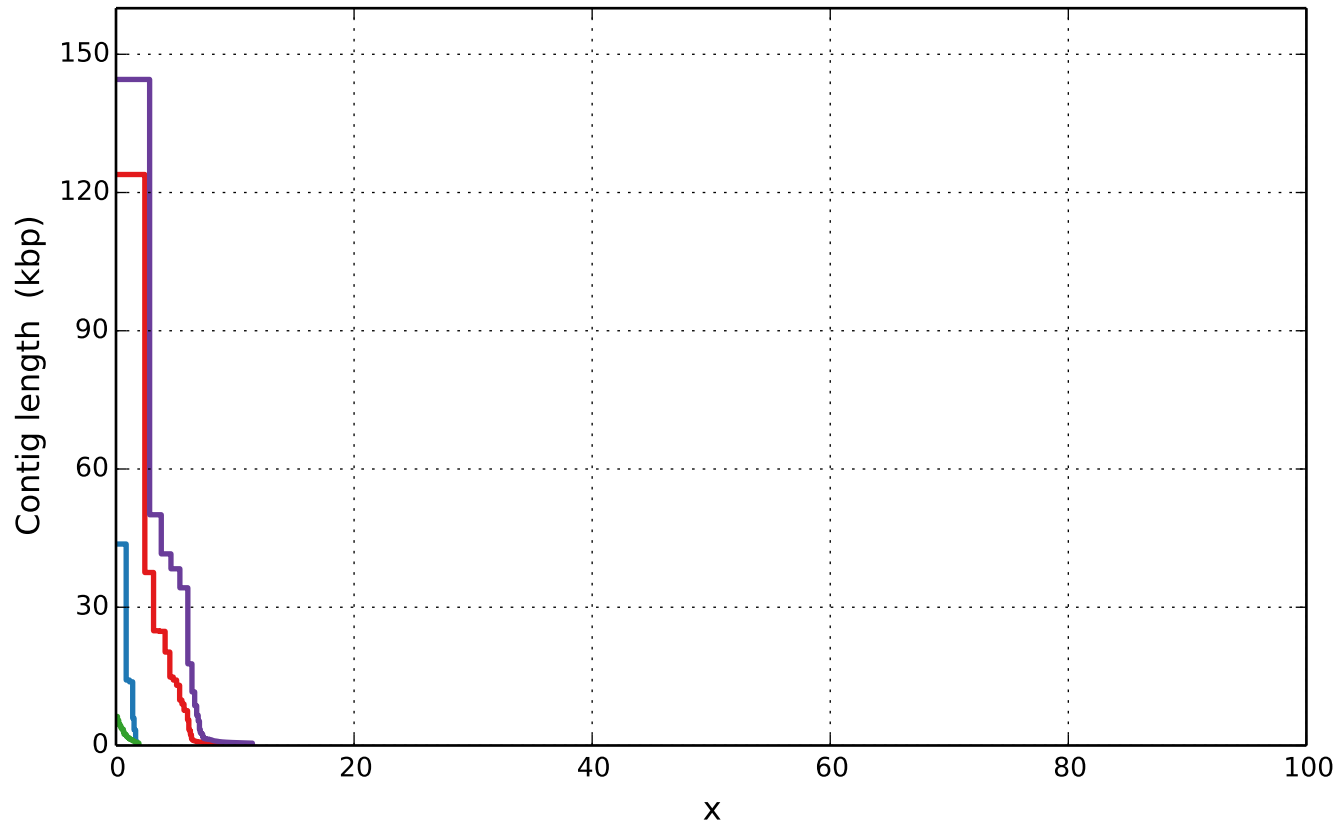
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

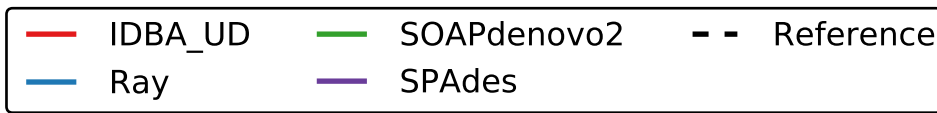
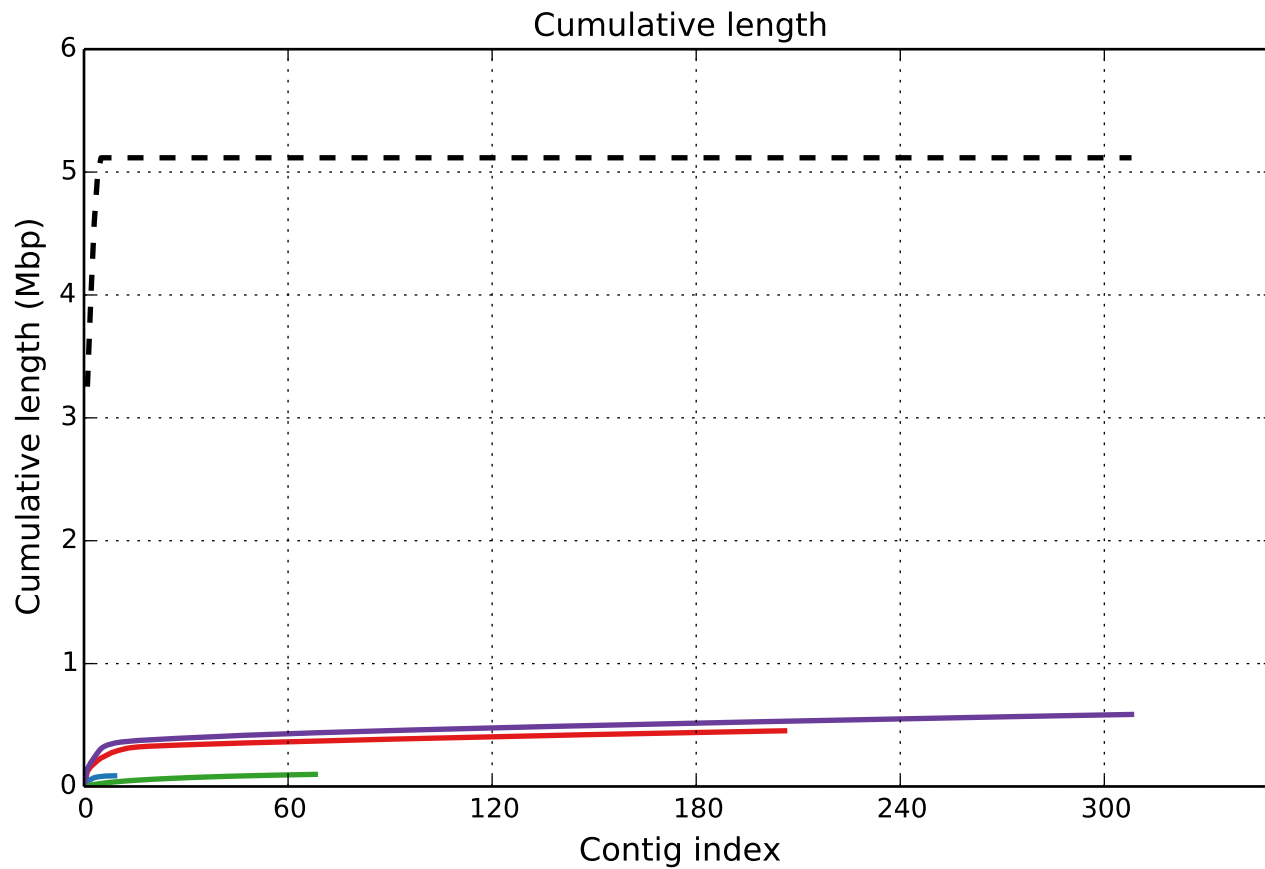
Nx



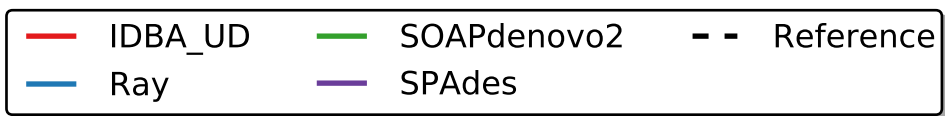
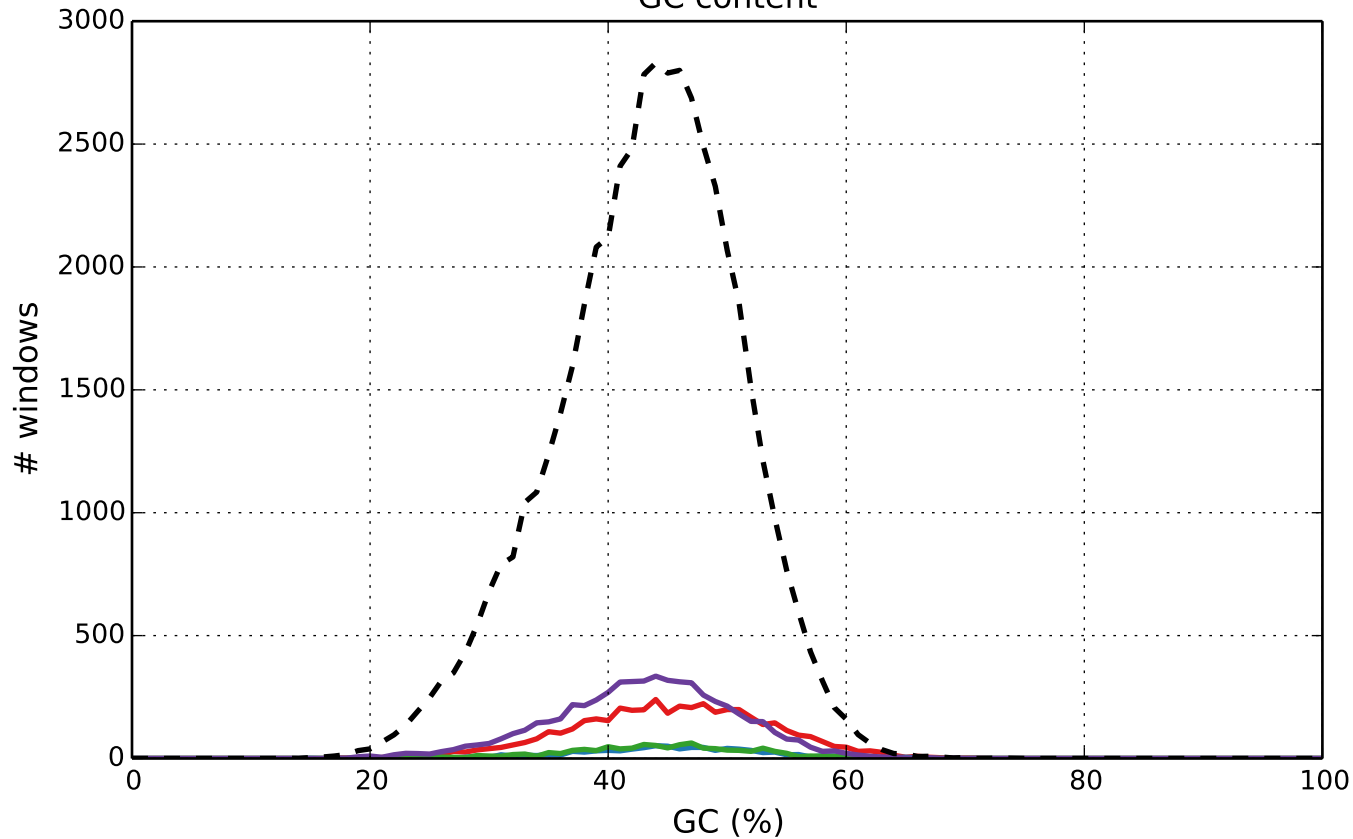
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray

NGx

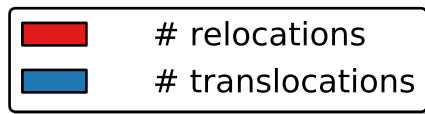
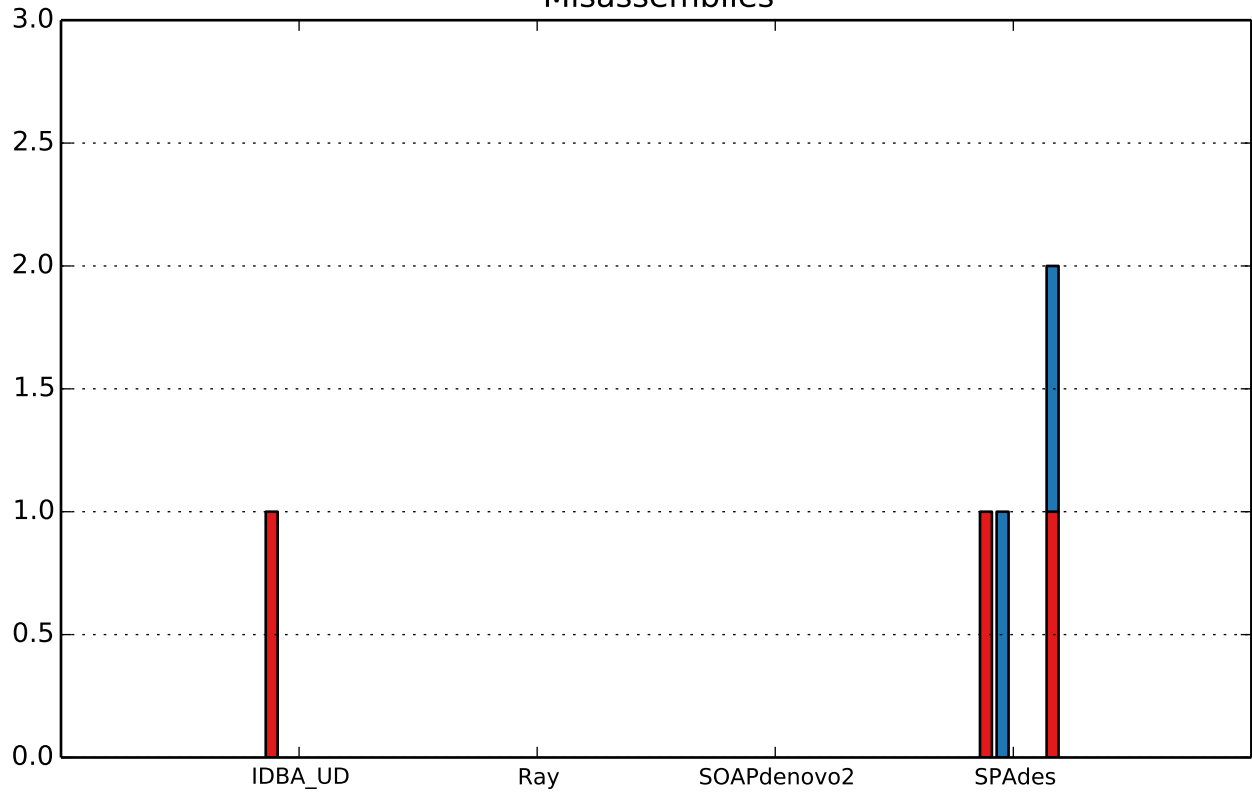


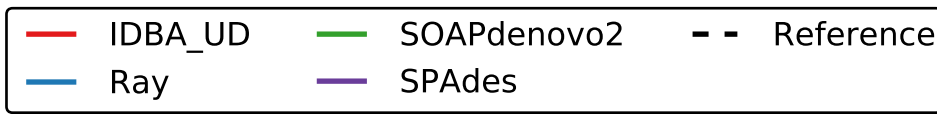
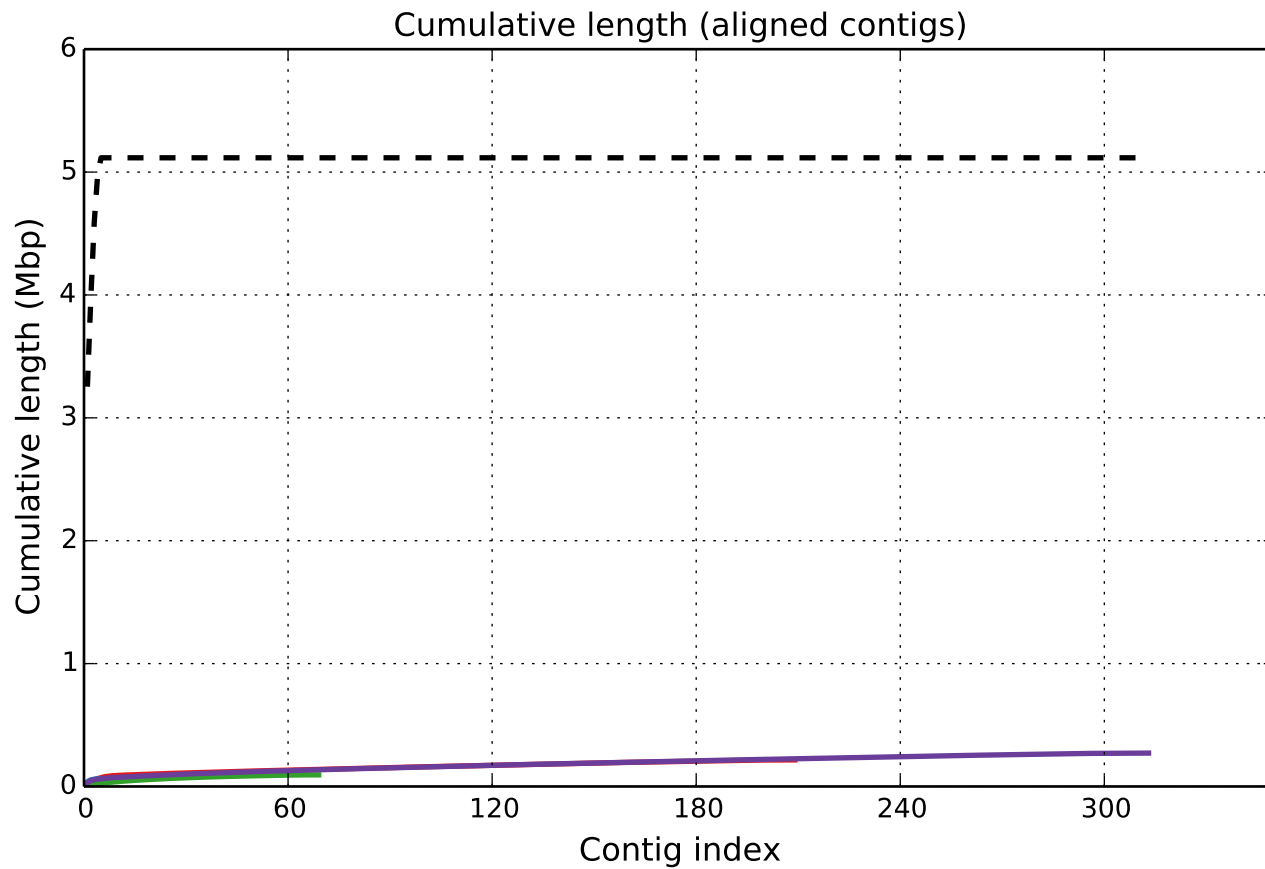


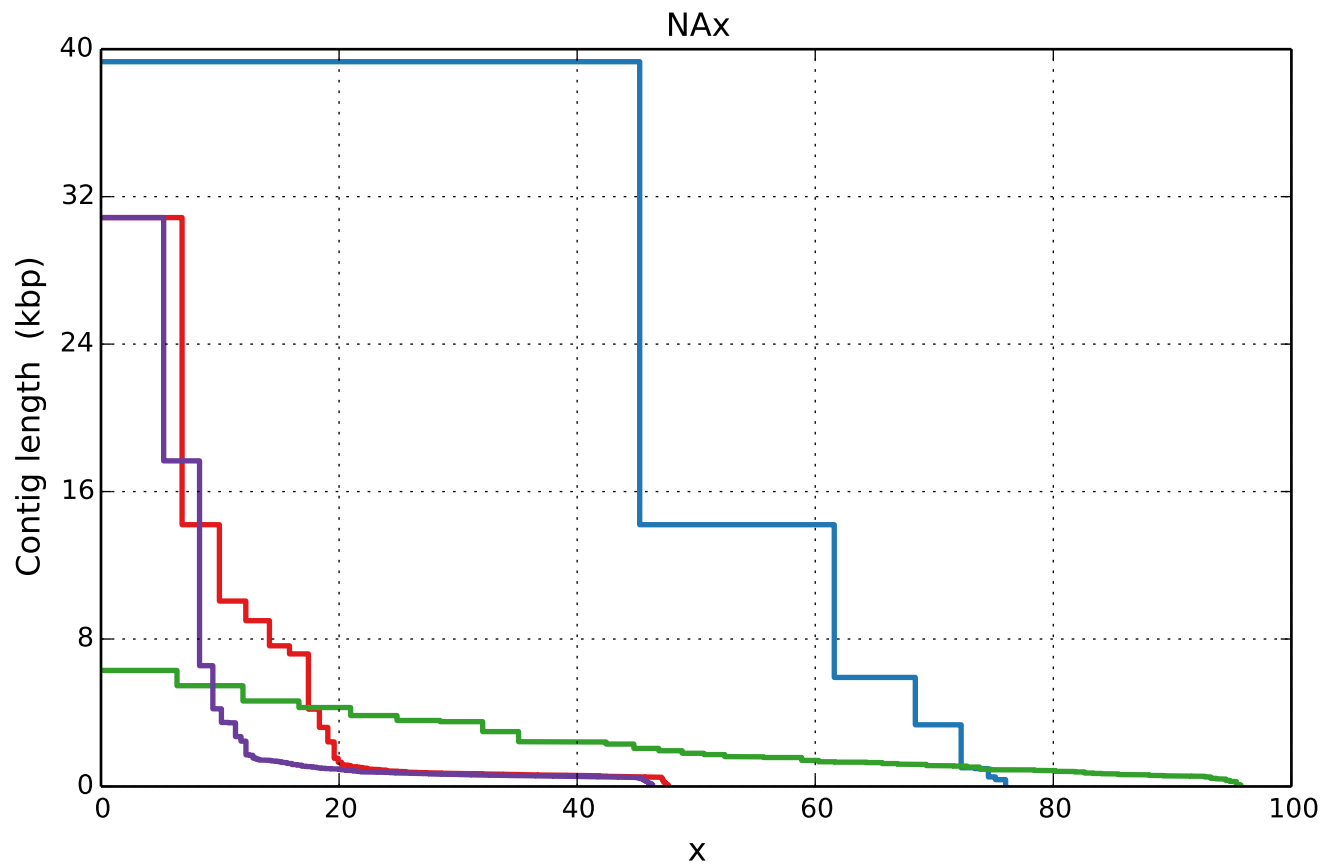
GC content



Misassemblies







IDBA_UD SOAPdenovo2 SPAdes
Ray

NGAx

