

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	58	13	23	58
# contigs (>= 5000 bp)	8	4	0	12
# contigs (>= 10000 bp)	4	4	0	6
# contigs (>= 25000 bp)	1	1	0	3
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 1000 bp)	227170	109525	35256	293106
Total length (>= 5000 bp)	133507	93740	0	186123
Total length (>= 10000 bp)	105940	93740	0	140733
Total length (>= 25000 bp)	52119	43716	0	96687
Total length (>= 50000 bp)	52119	0	0	0
# contigs	102	23	89	117
Largest contig	52119	43716	3539	41203
Total length	259646	116902	80015	333237
Reference length	5124109	5124109	5124109	5124109
GC (%)	42.83	45.08	43.48	43.05
Reference GC (%)	42.50	42.50	42.50	42.50
N50	5498	19388	918	7087
N75	1606	13412	674	2248
L50	8	2	28	10
L75	32	4	55	30
# misassemblies	1	0	0	0
# misassembled contigs	1	0	0	0
Misassembled contigs length	1762	0	0	0
# local misassemblies	2	2	41	2
# structural variations	0	0	0	0
# unaligned contigs	0 + 42 part	0 + 6 part	0 + 29 part	0 + 72 part
Unaligned length	122703	27411	21066	203170
Genome fraction (%)	2.644	1.403	1.089	2.507
Duplication ratio	1.011	1.245	1.056	1.013
# N's per 100 kbp	469.49	218.13	6903.71	1308.68
# mismatches per 100 kbp	1800.99	2738.01	1985.59	2106.69
# indels per 100 kbp	42.07	87.65	28.67	68.51
Largest alignment	19869	29006	3539	19690
NA50	529	3137	583	-
NGA50	-	-	-	-
LA50	74	4	40	-

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

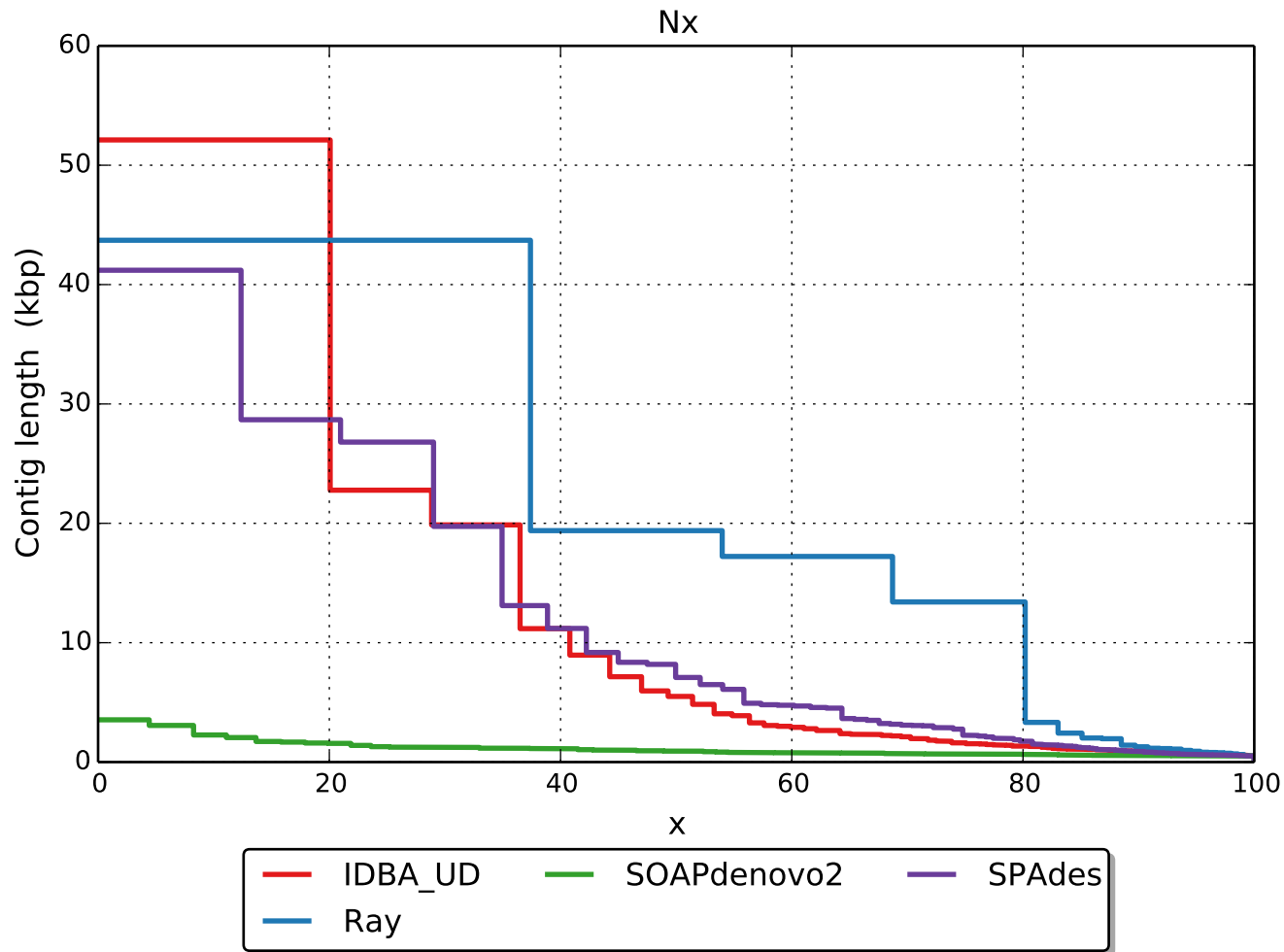
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	1	0	0	0
# relocations	1	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	6	3	0	13
# misassembled contigs	1	0	0	0
Misassembled contigs length	1762	0	0	0
# local misassemblies	2	2	41	2
# structural variations	0	0	0	0
# mismatches	2440	1968	1108	2706
# indels	57	63	16	88
# short indels	50	62	15	77
# long indels	7	1	1	11
Indels length	133	160	31	304

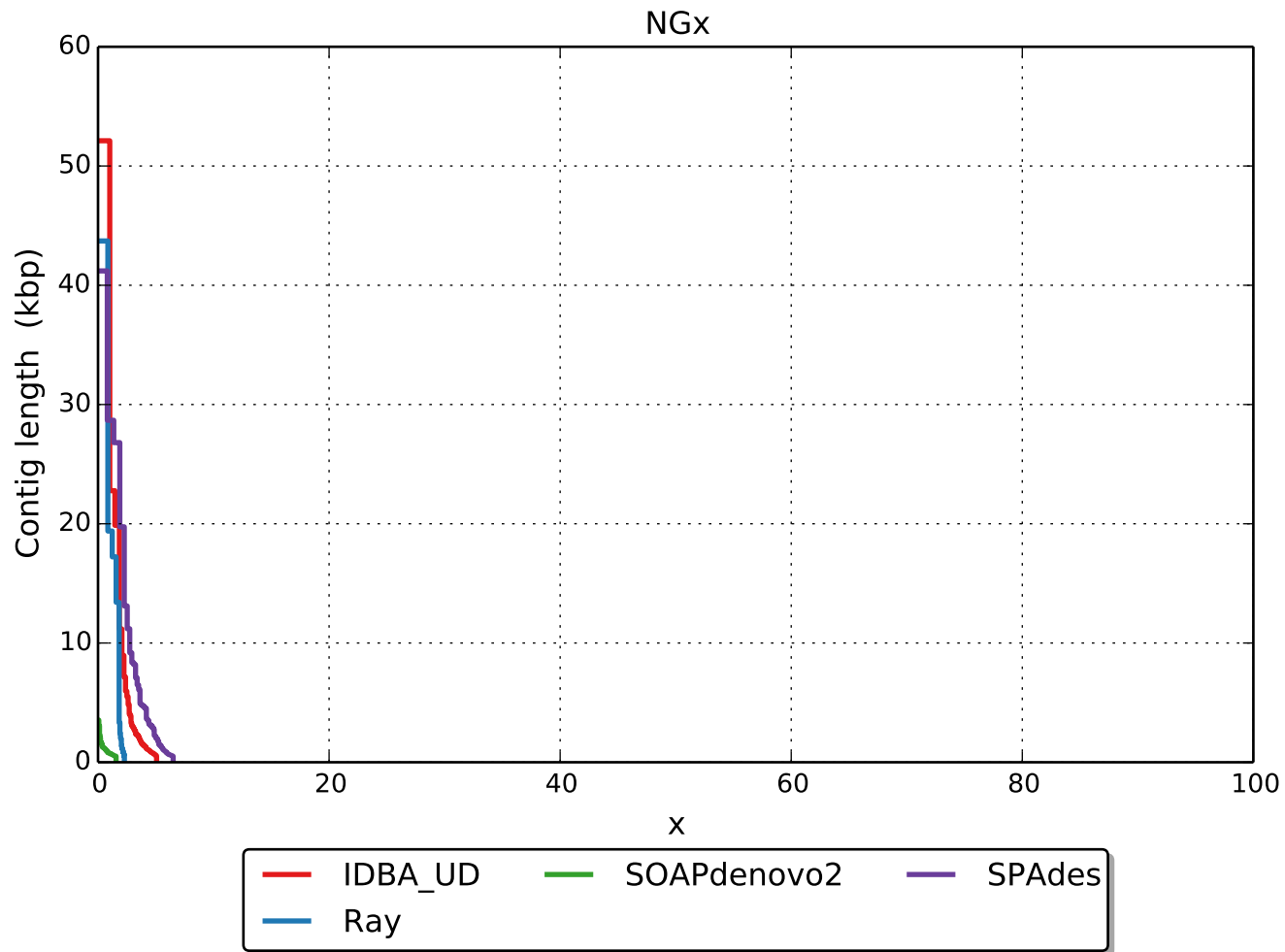
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

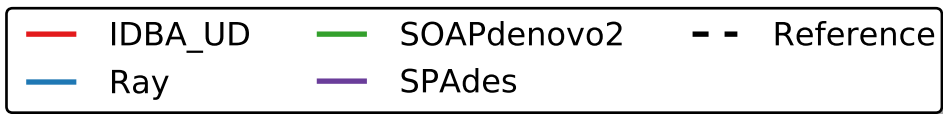
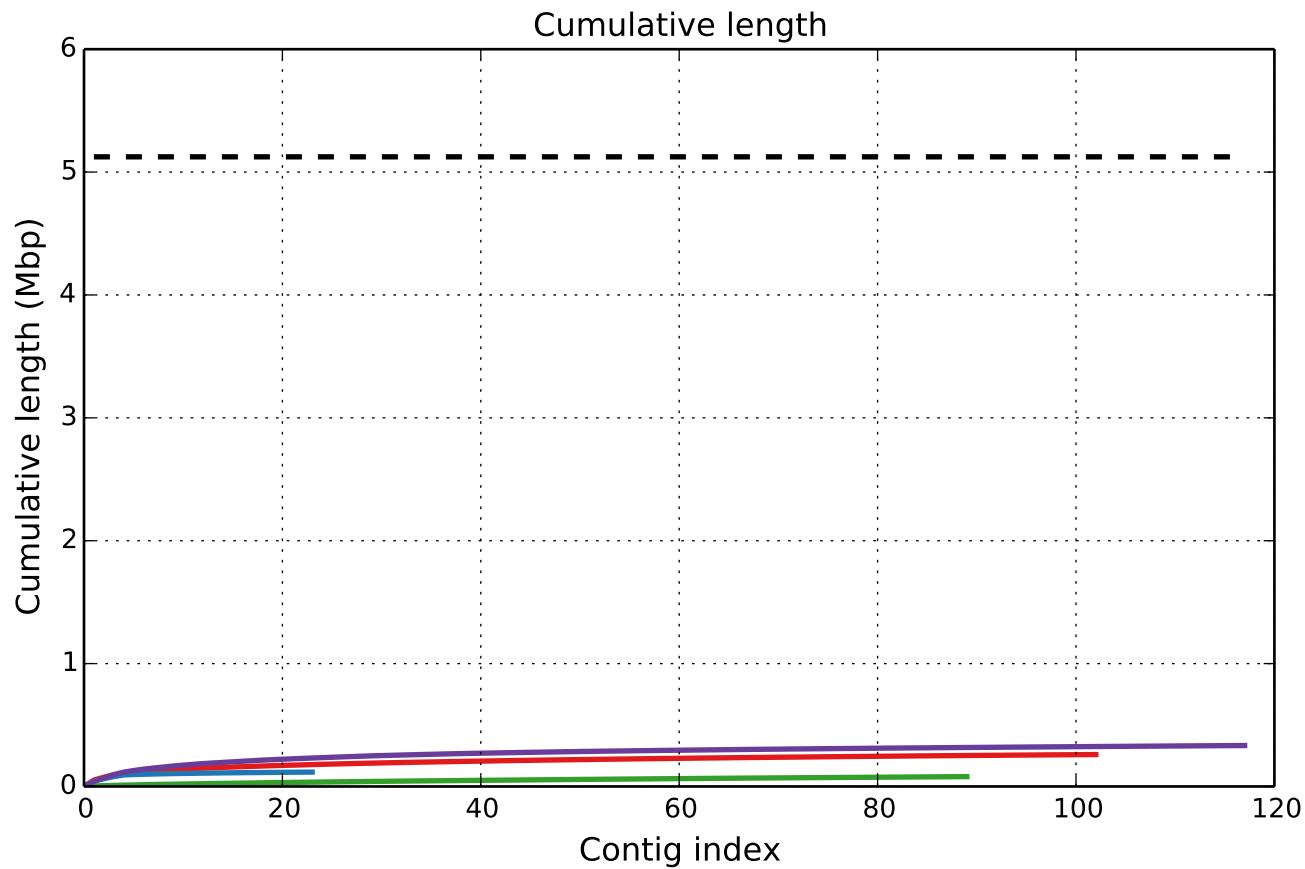
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	42	6	29	72
# with misassembly	3	1	5	3
# both parts are significant	6	2	0	13
Partially unaligned length	122703	27411	21066	203170
# N's	1219	255	5524	4361

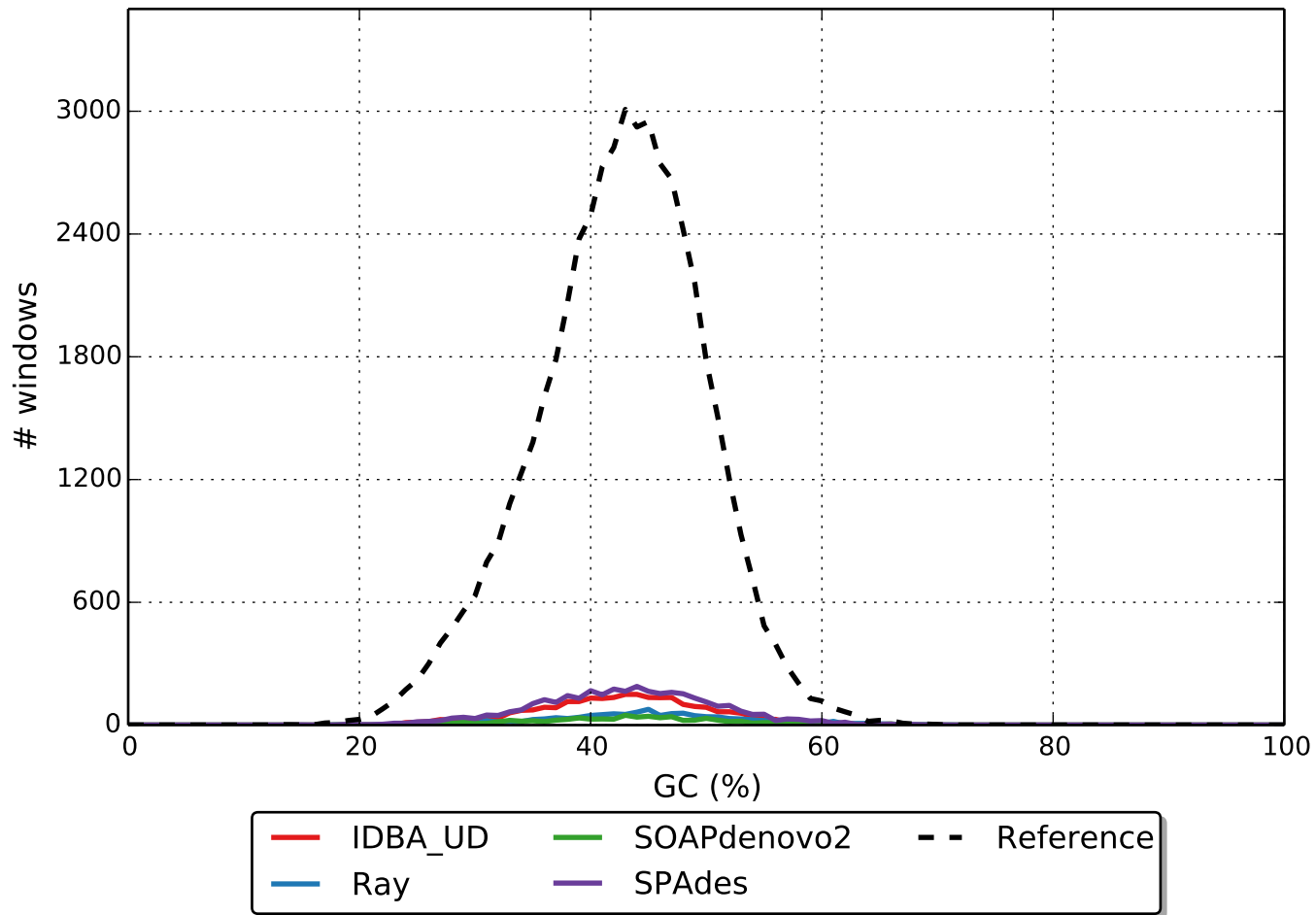
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

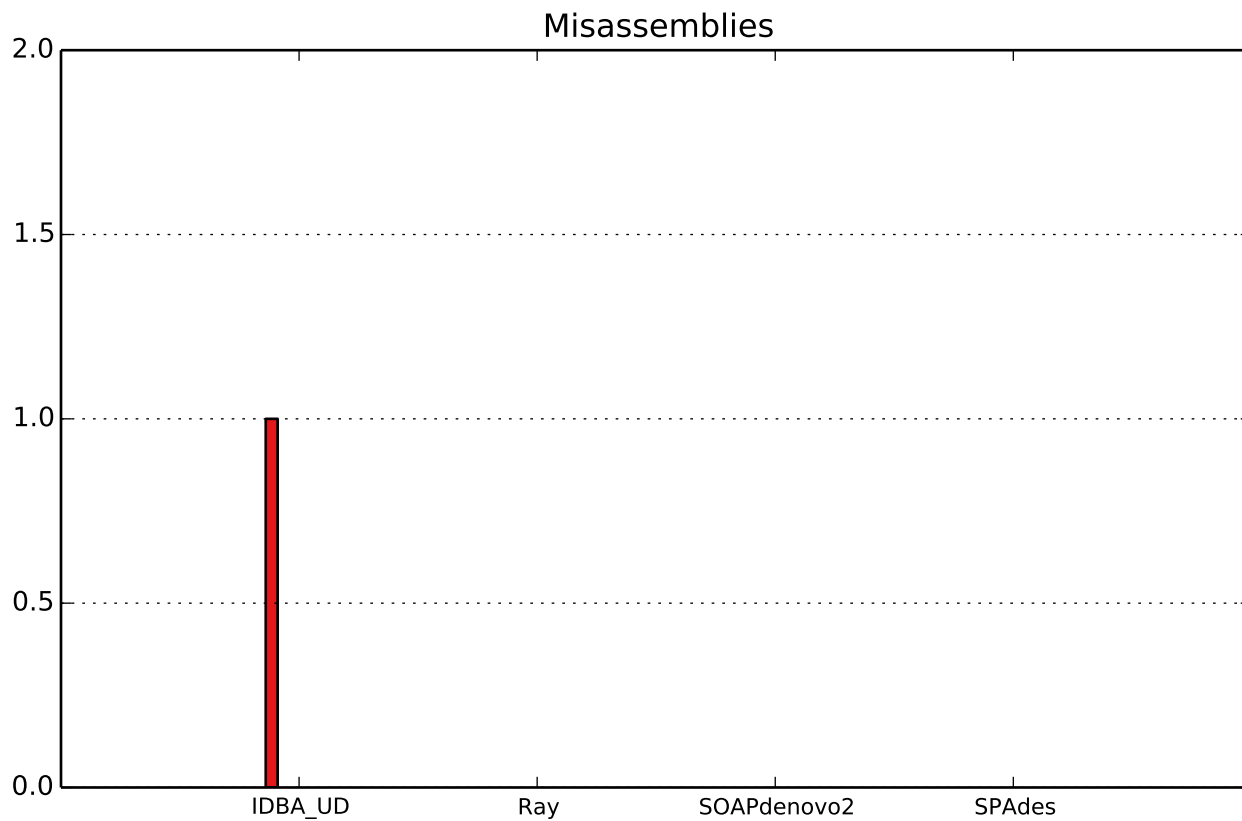




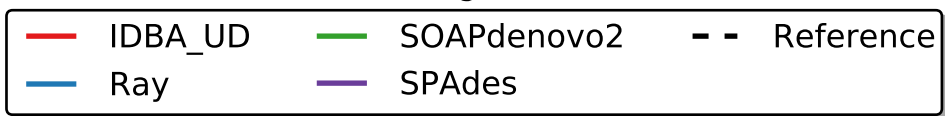
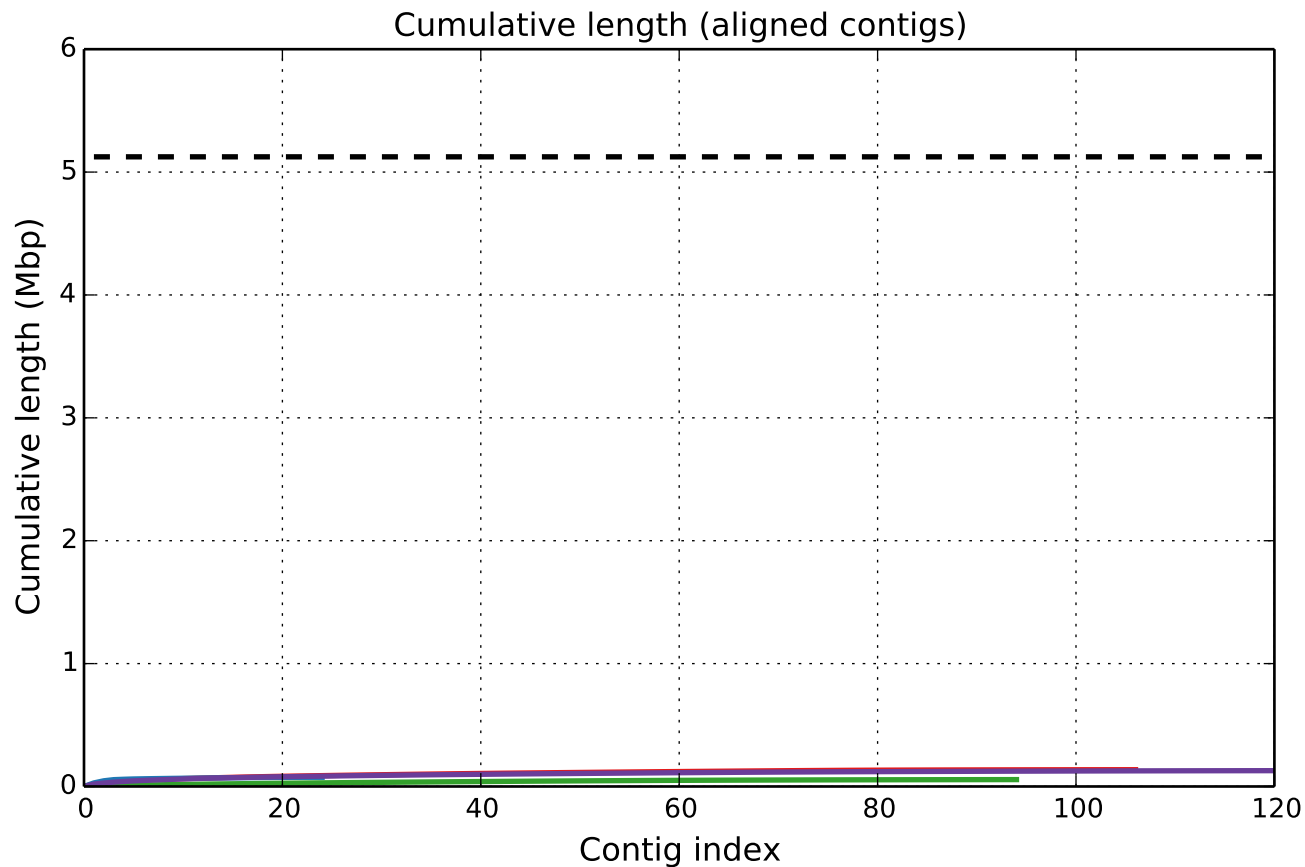


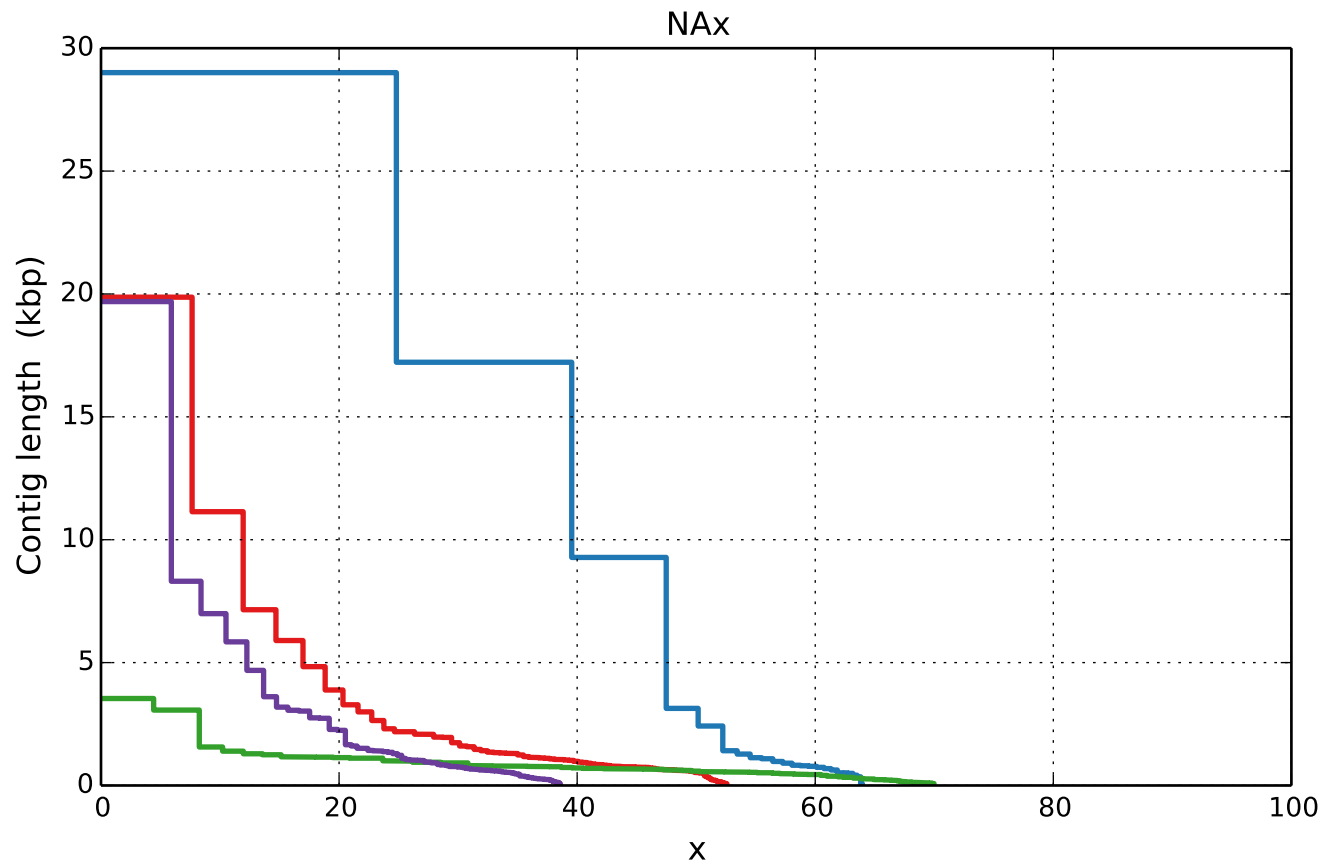
GC content





 # relocations





IDBA_UD SOAPdenovo2 SPAdes
Ray

