

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	97	19	33	232
# contigs (>= 5000 bp)	15	4	2	15
# contigs (>= 10000 bp)	9	3	0	8
# contigs (>= 25000 bp)	3	1	0	2
# contigs (>= 50000 bp)	2	0	0	1
Total length (>= 1000 bp)	411759	88705	72331	604198
Total length (>= 5000 bp)	278093	63856	13468	263228
Total length (>= 10000 bp)	238288	58409	0	214998
Total length (>= 25000 bp)	149954	25646	0	120082
Total length (>= 50000 bp)	114756	0	0	85875
# contigs	528	42	124	904
Largest contig	57618	25646	7495	85875
Total length	704255	103824	132361	1059048
Reference length	5180144	5180144	5180144	5180144
GC (%)	43.02	44.45	44.01	44.08
Reference GC (%)	45.08	45.08	45.08	45.08
N50	1422	15539	1067	1187
N75	721	1580	684	721
L50	47	3	28	164
L75	239	11	67	458
# misassemblies	10	0	0	11
# misassembled contigs	10	0	0	11
Misassembled contigs length	22587	0	0	14936
# local misassemblies	1	7	103	10
# structural variations	2	0	0	0
# unaligned contigs	0 + 103 part	0 + 1 part	0 + 13 part	0 + 216 part
Unaligned length	194722	574	4027	277592
Genome fraction (%)	9.762	1.939	2.333	14.550
Duplication ratio	1.008	1.028	1.062	1.037
# N's per 100 kbp	245.51	1501.58	5069.47	2930.93
# mismatches per 100 kbp	1053.00	1310.22	580.93	1122.06
# indels per 100 kbp	43.11	65.71	12.41	81.07
Largest alignment	53084	25497	7493	53115
NA50	670	14965	1055	638
NGA50	-	-	-	-
NA75	-	1417	562	-
LA50	239	3	28	436
LA75	-	12	72	-

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

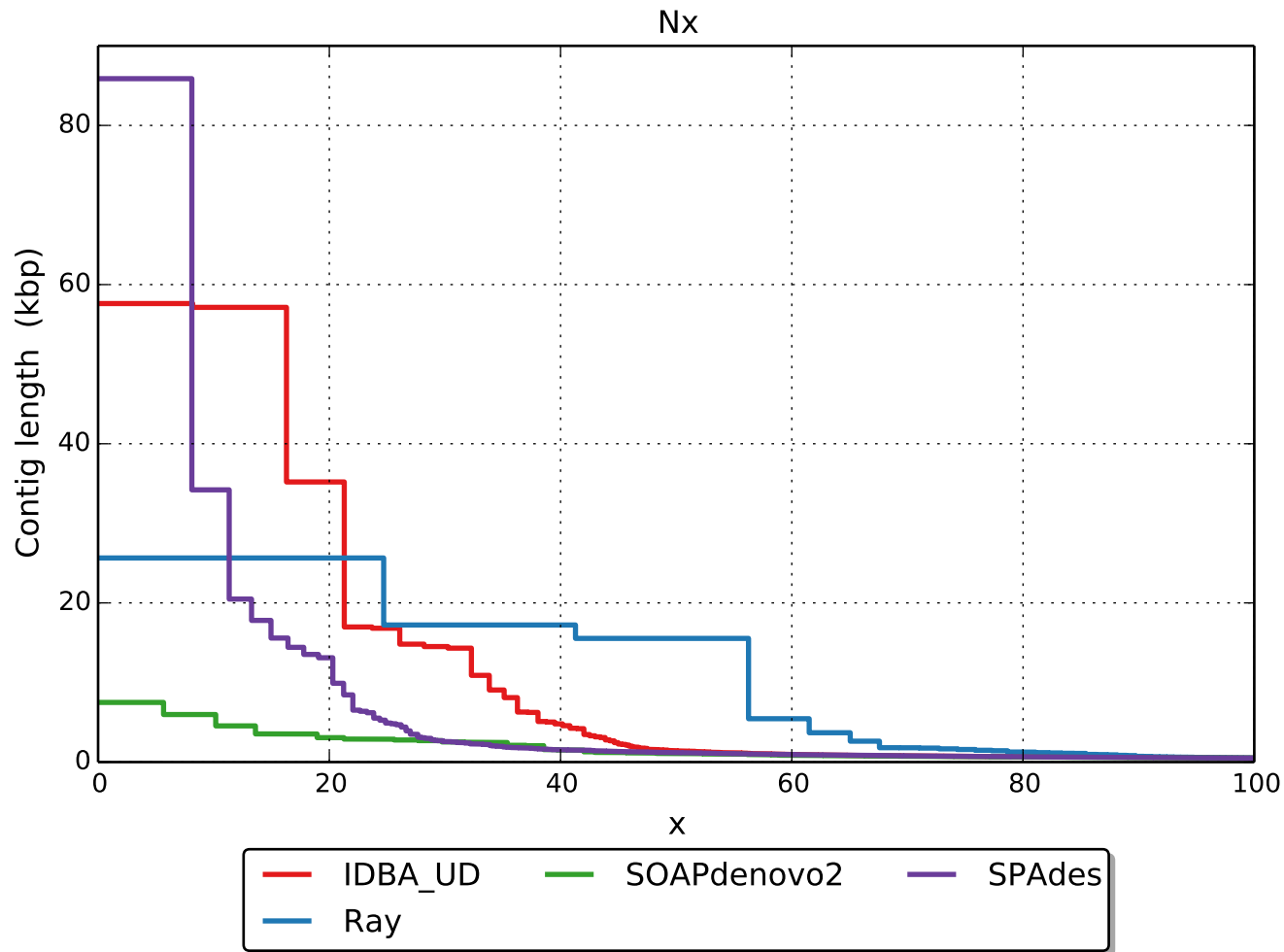
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	10	0	0	11
# relocations	2	0	0	3
# translocations	6	0	0	8
# inversions	2	0	0	0
# possibly misassembled contigs	14	1	0	36
# misassembled contigs	10	0	0	11
Misassembled contigs length	22587	0	0	14936
# local misassemblies	1	7	103	10
# structural variations	2	0	0	0
# mismatches	5325	1316	702	8457
# indels	218	66	15	611
# short indels	192	63	14	432
# long indels	26	3	1	179
Indels length	659	172	28	3089

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).

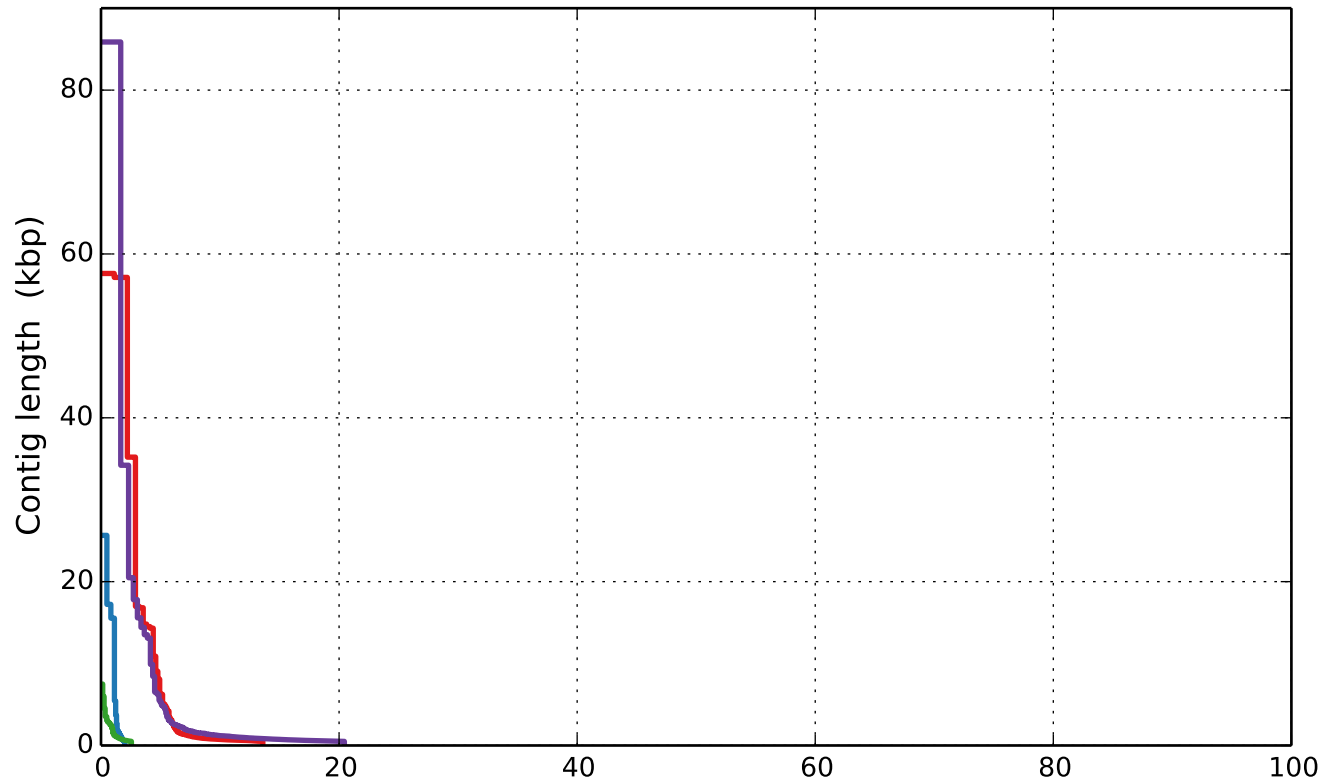
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	103	1	13	216
# with misassembly	3	0	6	7
# both parts are significant	12	1	0	32
Partially unaligned length	194722	574	4027	277592
# N's	1729	1559	6710	31040

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).

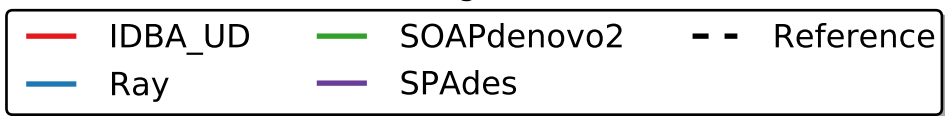
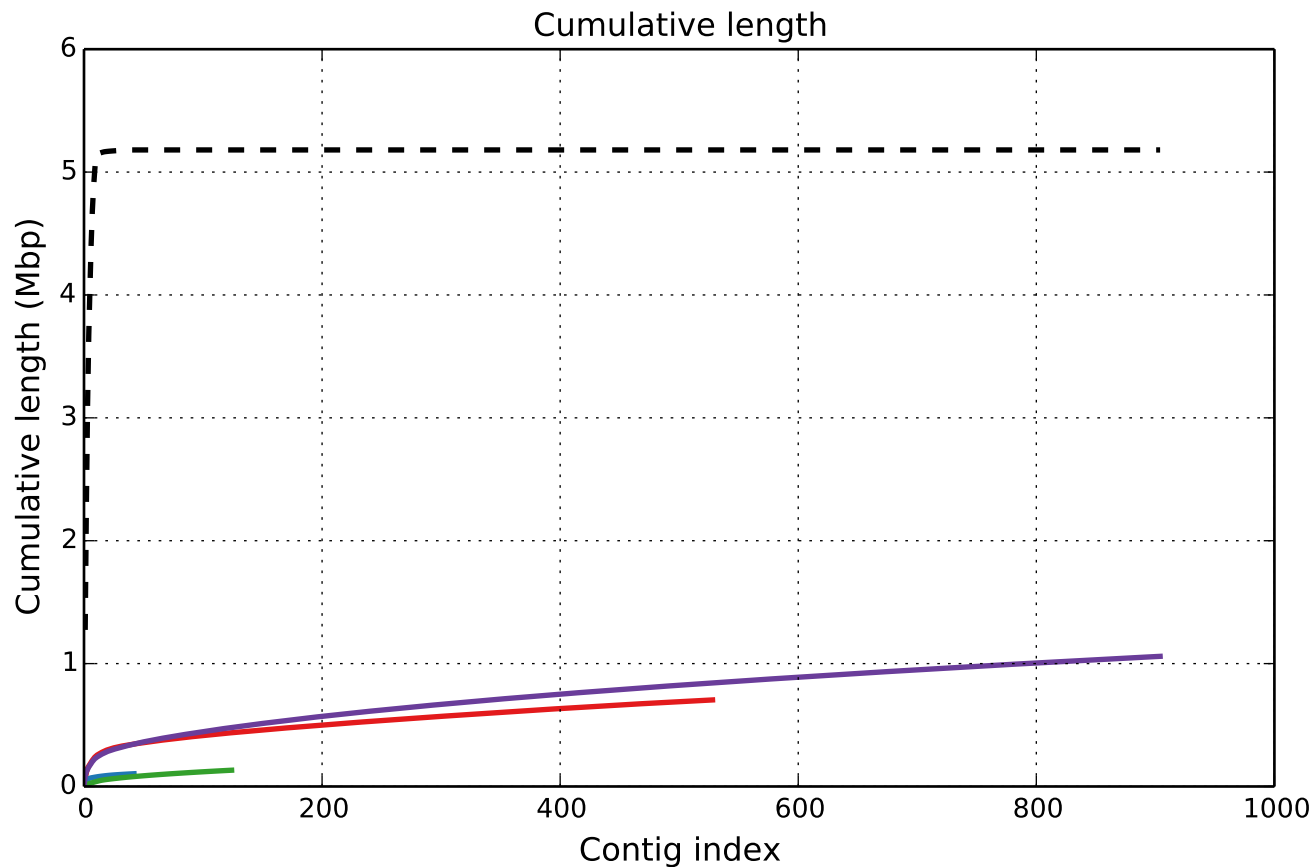


NGx

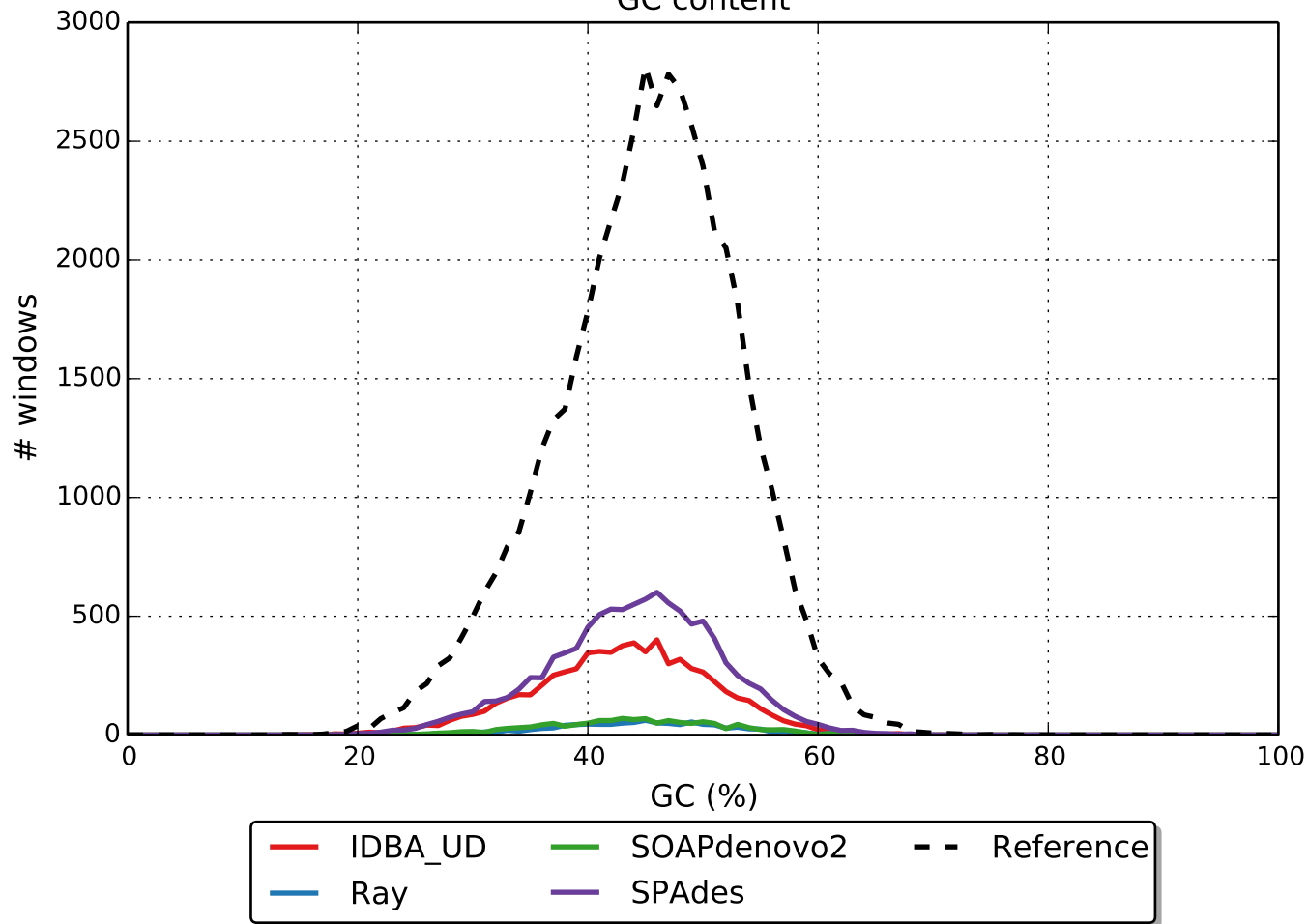


x

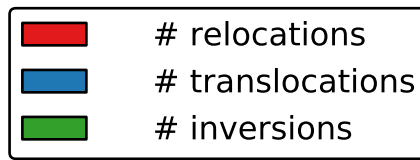
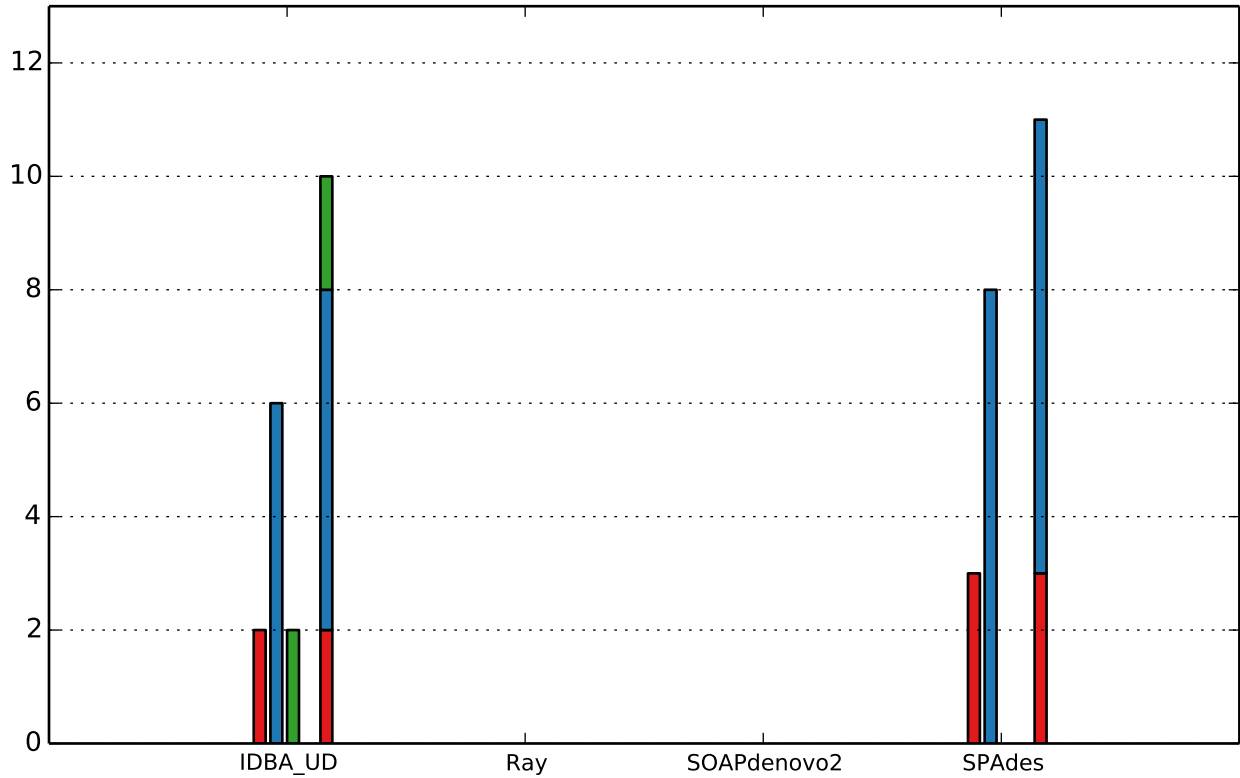


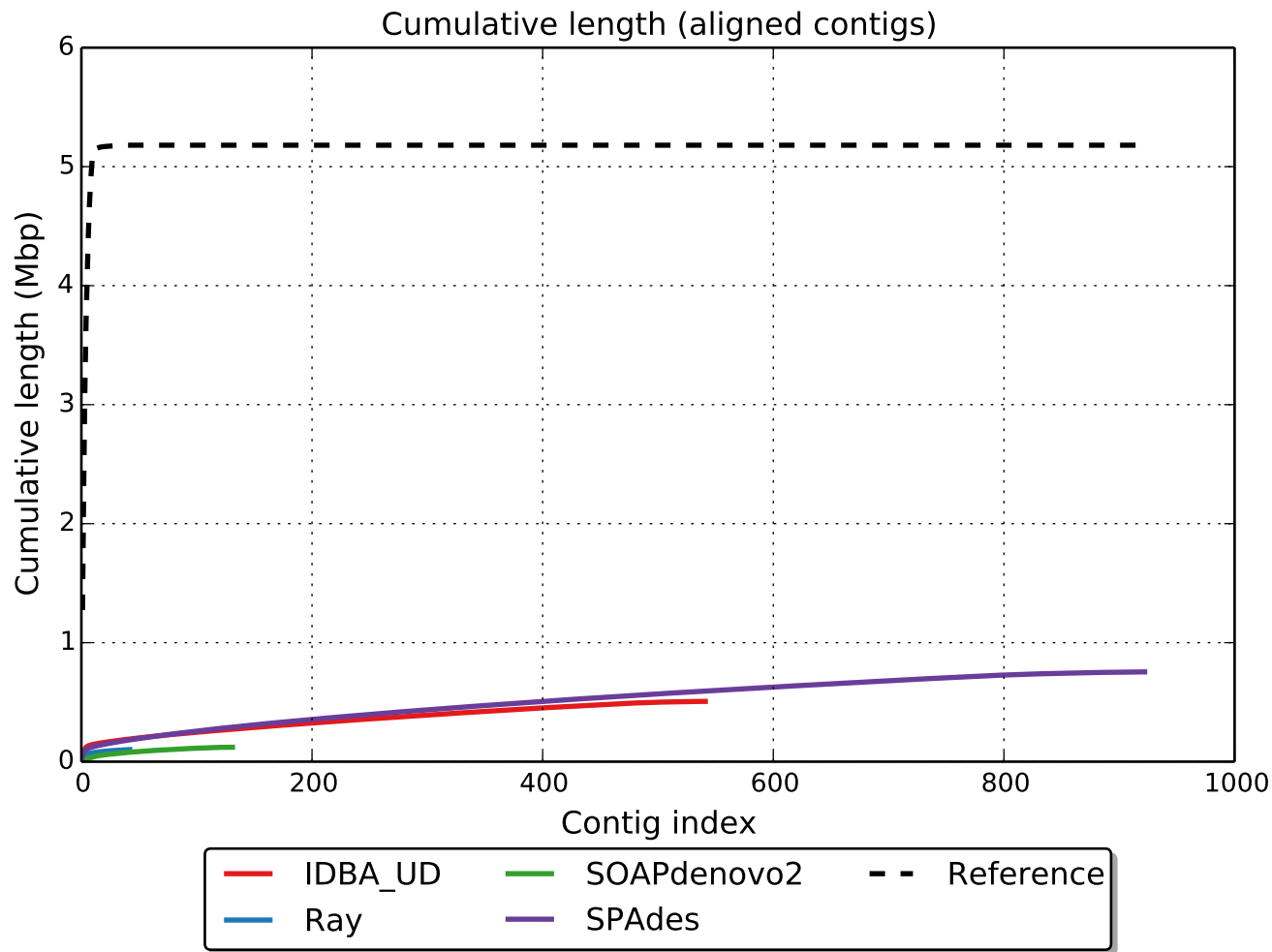


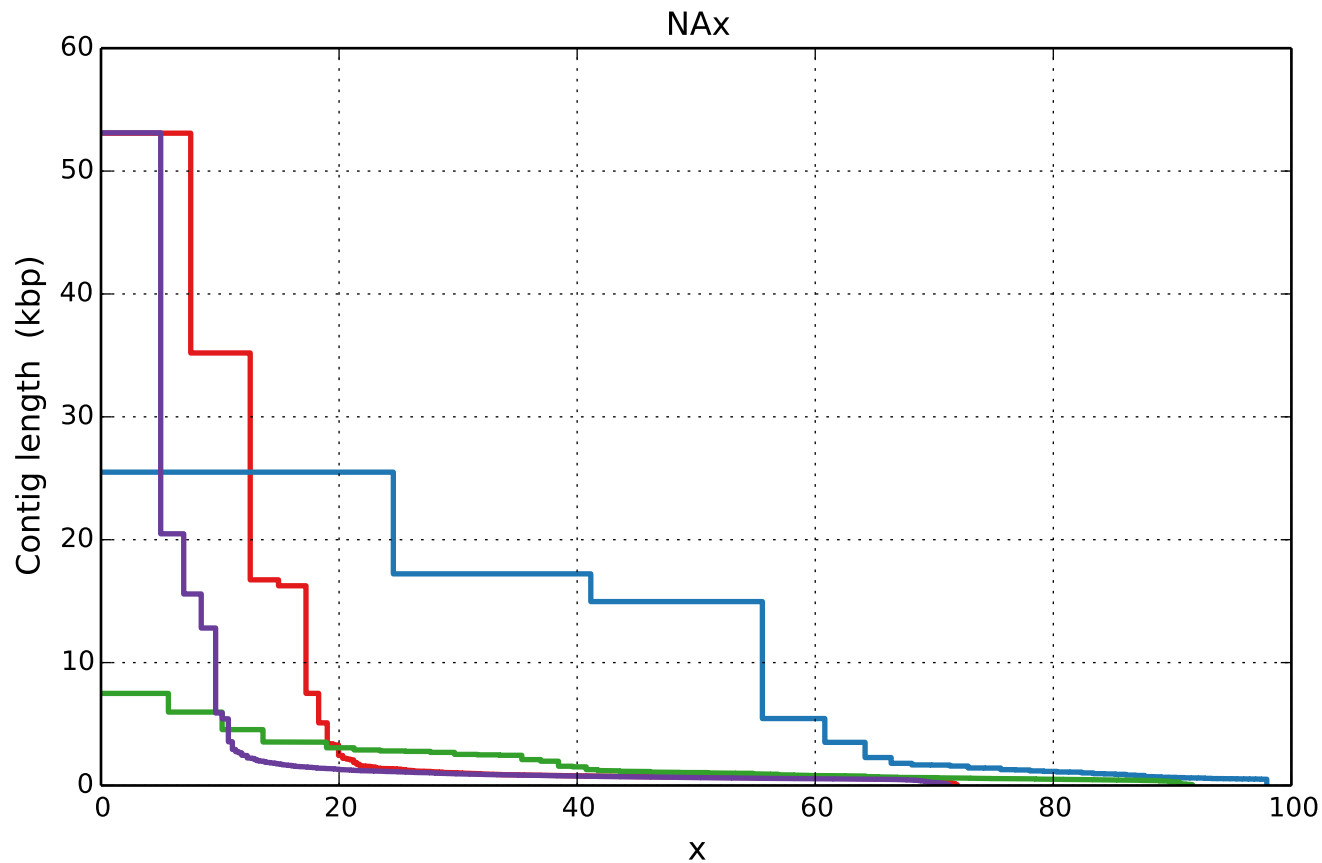
GC content



Misassemblies







IDBA_UD SOAPdenovo2 SPAdes
Ray

