

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	22	12	25	12
# contigs (>= 5000 bp)	7	4	2	7
# contigs (>= 10000 bp)	4	3	0	4
# contigs (>= 25000 bp)	2	0	0	1
# contigs (>= 50000 bp)	1	0	0	1
Total length (>= 1000 bp)	185966	68297	57714	230903
Total length (>= 5000 bp)	157298	56833	14779	222504
Total length (>= 10000 bp)	138293	51386	0	200069
Total length (>= 25000 bp)	93046	0	0	144537
Total length (>= 50000 bp)	65305	0	0	144537
# contigs	32	19	59	18
Largest contig	65305	20485	9328	144537
Total length	193206	73261	81242	235177
Reference length	4421924	4421924	4421924	4421924
GC (%)	46.54	48.28	50.53	43.52
Reference GC (%)	44.31	44.31	44.31	44.31
N50	24894	19388	1545	144537
N75	7179	5447	872	21074
L50	3	2	12	1
L75	5	4	29	3
# misassemblies	1	1	0	0
# misassembled contigs	1	1	0	0
Misassembled contigs length	24894	11513	0	0
# local misassemblies	2	3	12	1
# structural variations	0	0	0	0
# unaligned contigs	0 + 7 part	0 + 2 part	0 + 5 part	0 + 10 part
Unaligned length	80644	21948	3584	185062
Genome fraction (%)	2.287	1.069	1.694	1.113
Duplication ratio	1.113	1.085	1.037	1.018
# N's per 100 kbp	82.30	734.36	1427.83	200.27
# mismatches per 100 kbp	1758.95	1142.18	1328.12	2114.82
# indels per 100 kbp	45.48	42.30	25.36	54.85
Largest alignment	19452	11139	8452	20187
NA50	837	1483	1345	-
NGA50	-	-	-	-
NA75	-	-	739	-
LA50	26	10	13	-
LA75	-	-	33	-

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	1	0	0
# relocations	1	0	0	0
# translocations	0	1	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	4	3	3	6
# misassembled contigs	1	1	0	0
Misassembled contigs length	24894	11513	0	0
# local misassemblies	2	3	12	1
# structural variations	0	0	0	0
# mismatches	1779	540	995	1041
# indels	46	20	19	27
# short indels	40	19	18	26
# long indels	6	1	1	1
Indels length	134	35	32	52

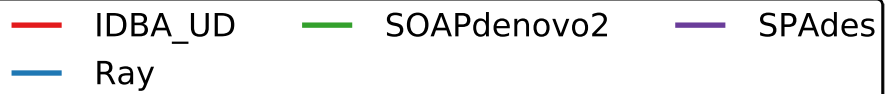
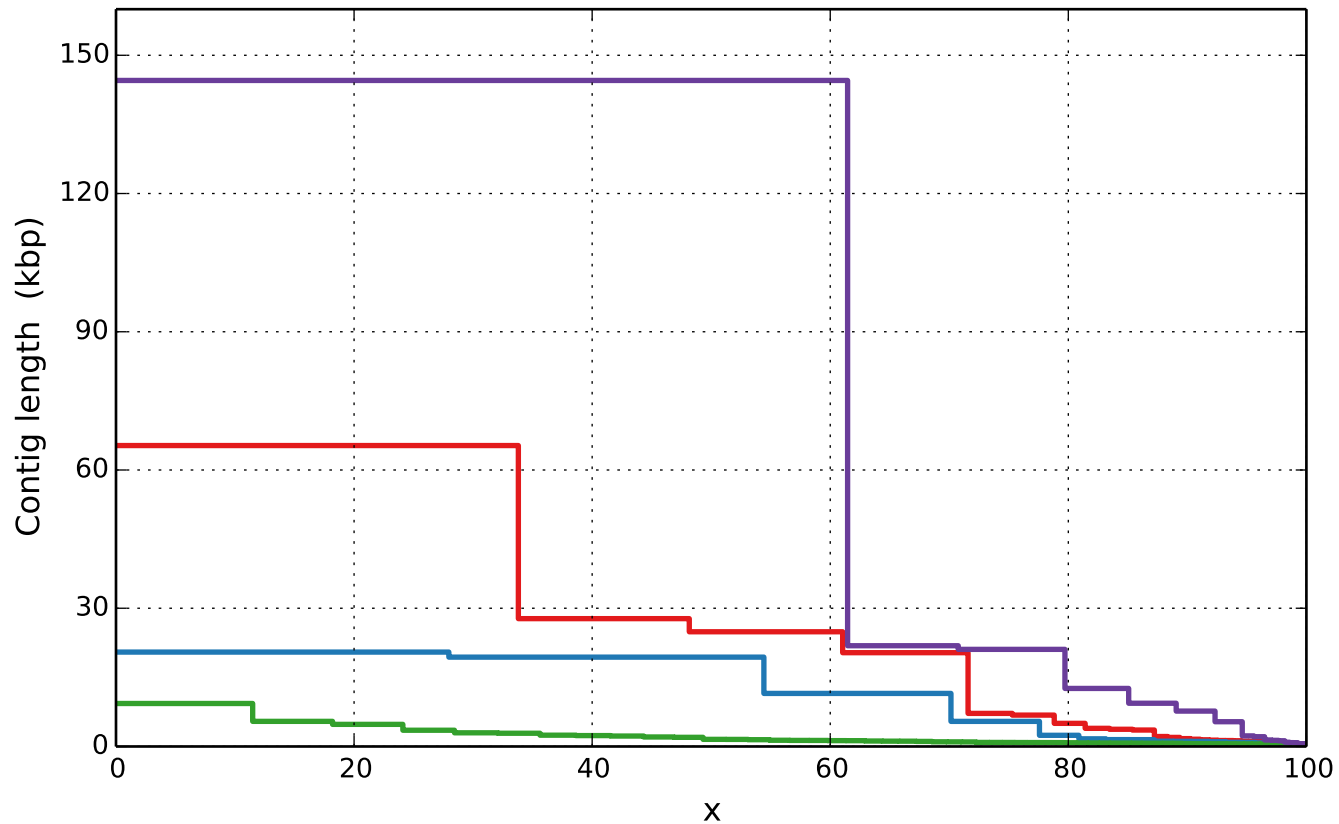
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

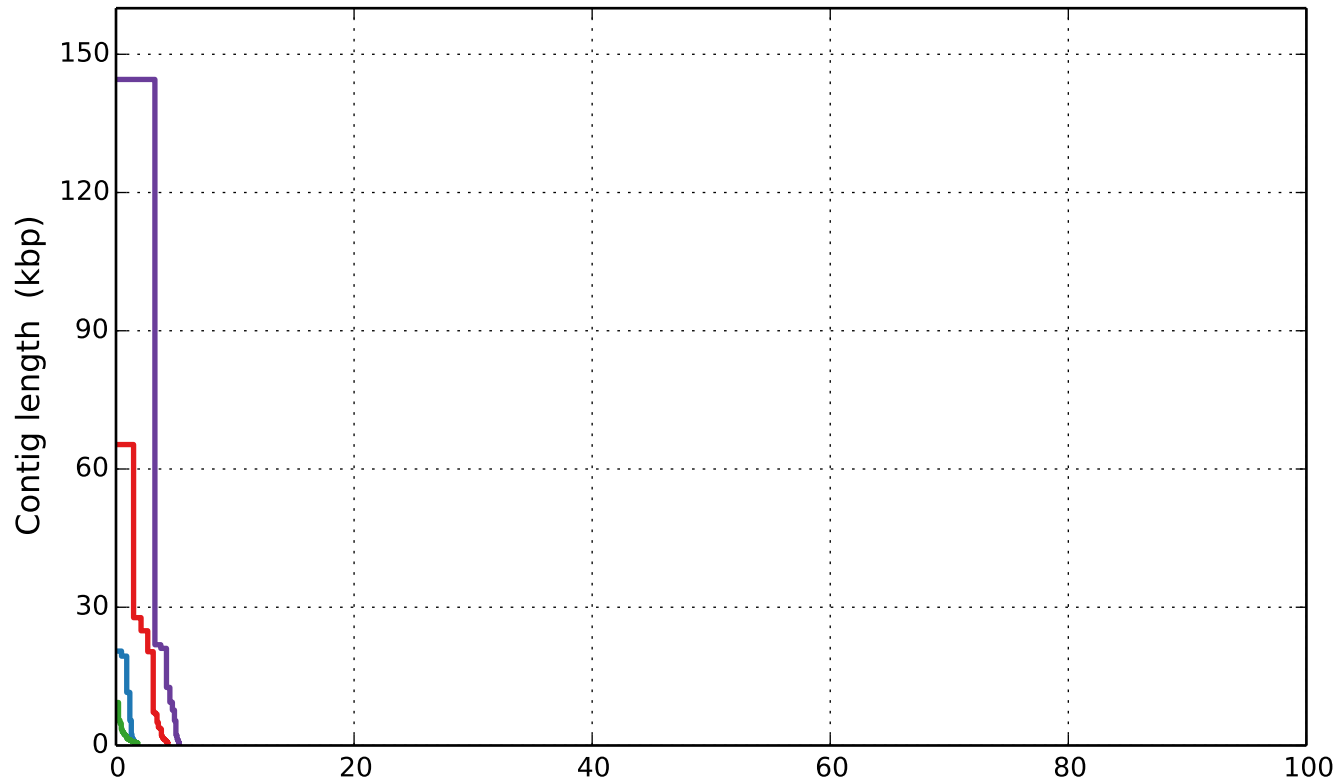
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	7	2	5	10
# with misassembly	1	1	1	1
# both parts are significant	2	2	1	5
Partially unaligned length	80644	21948	3584	185062
# N's	159	538	1160	471

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

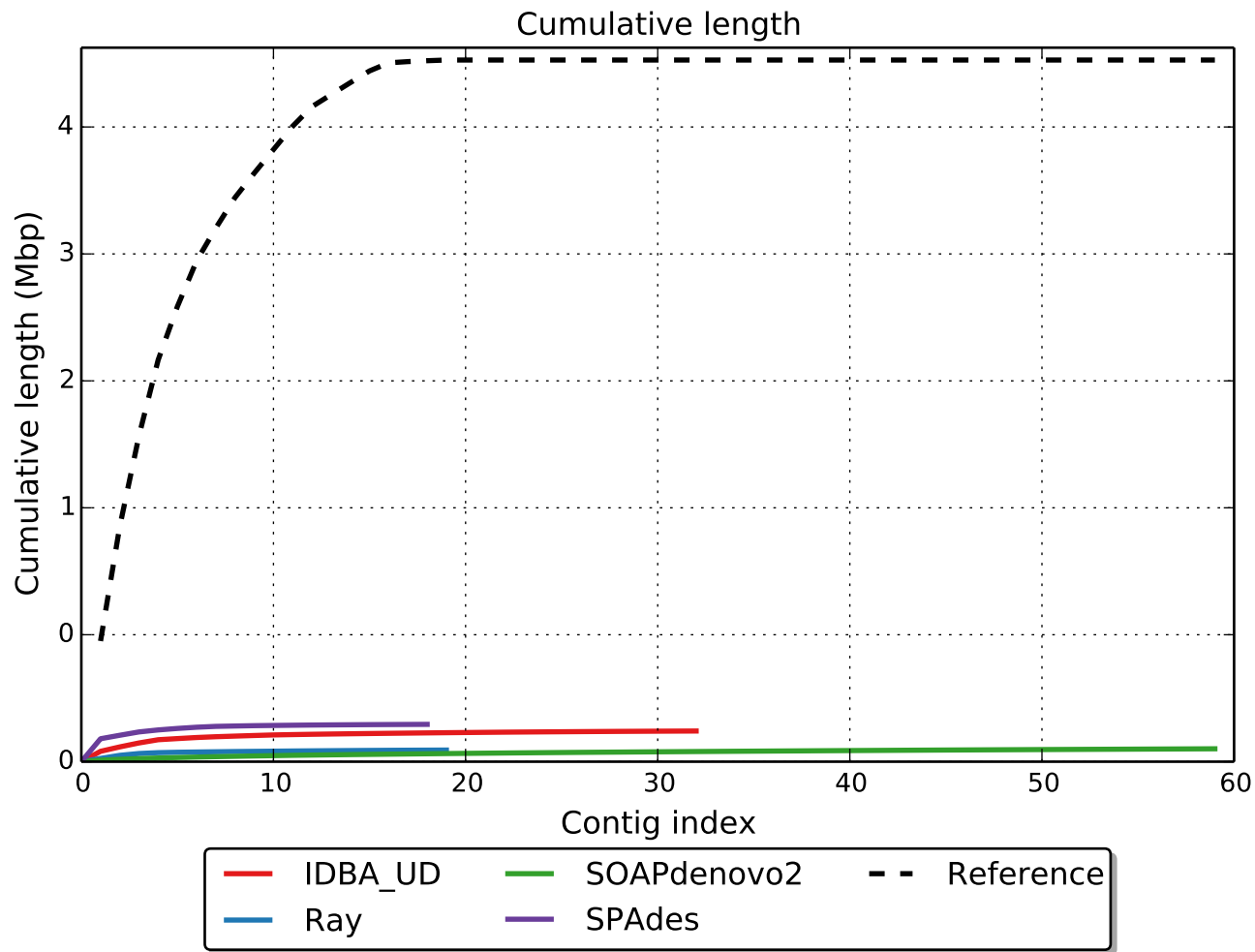


NGx

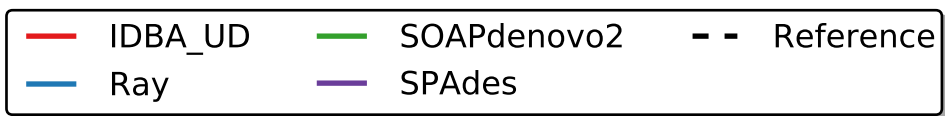
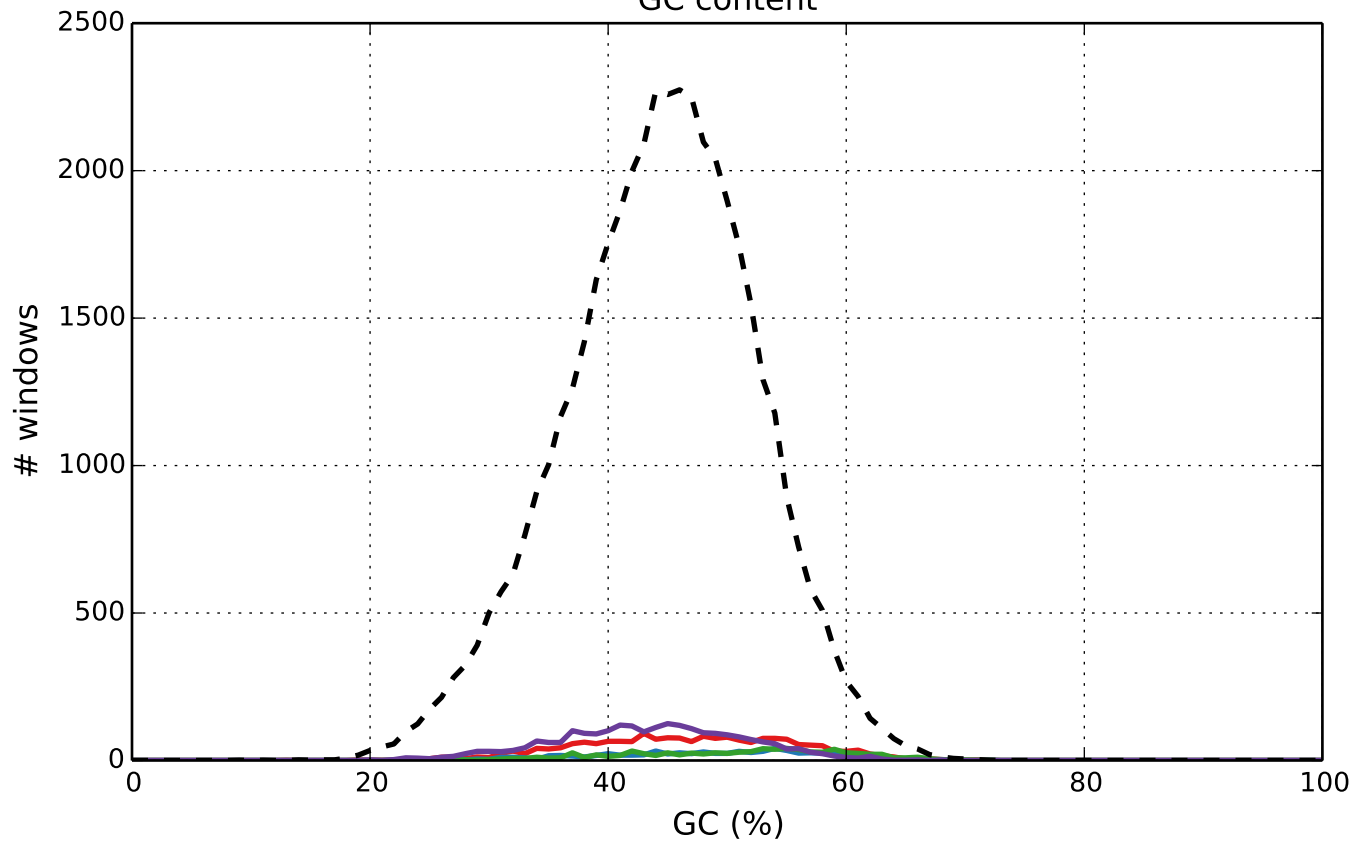


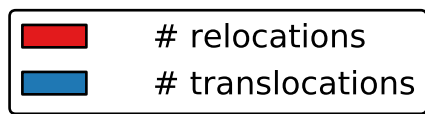
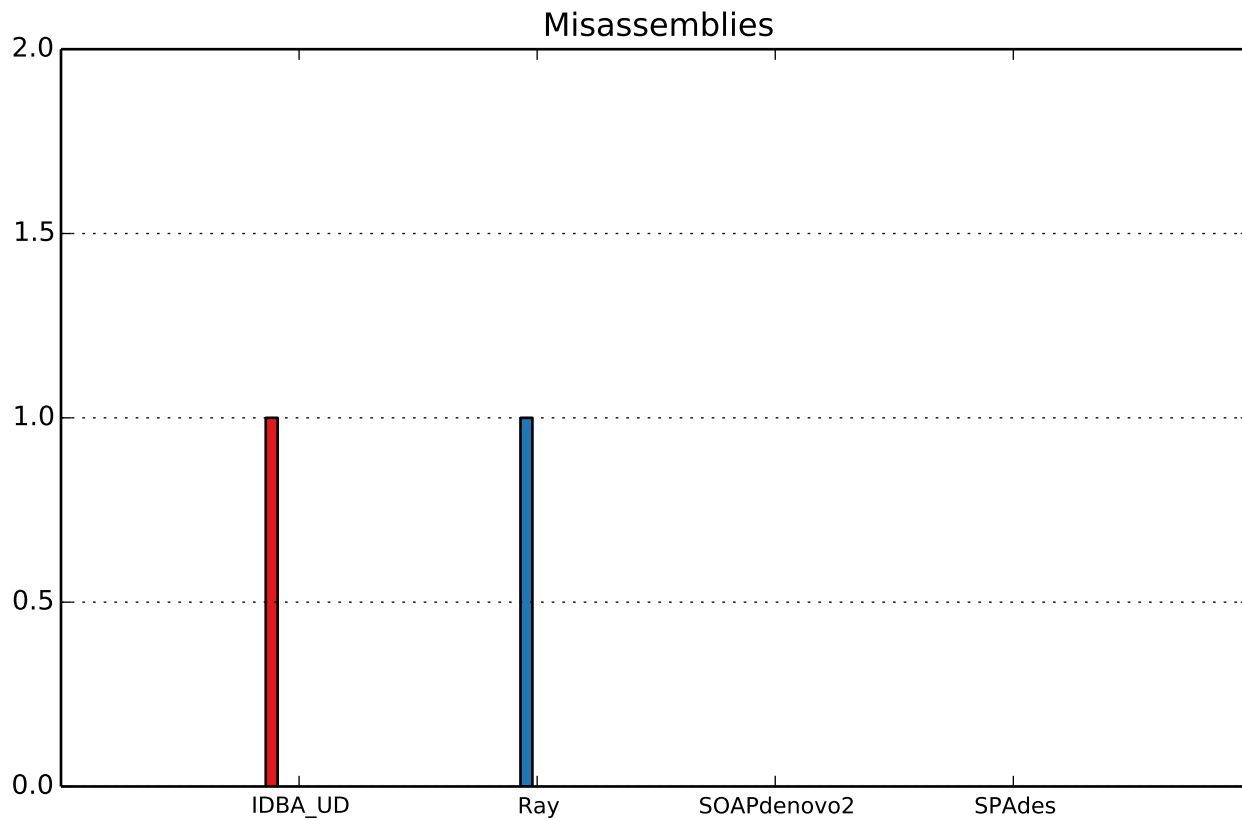
x

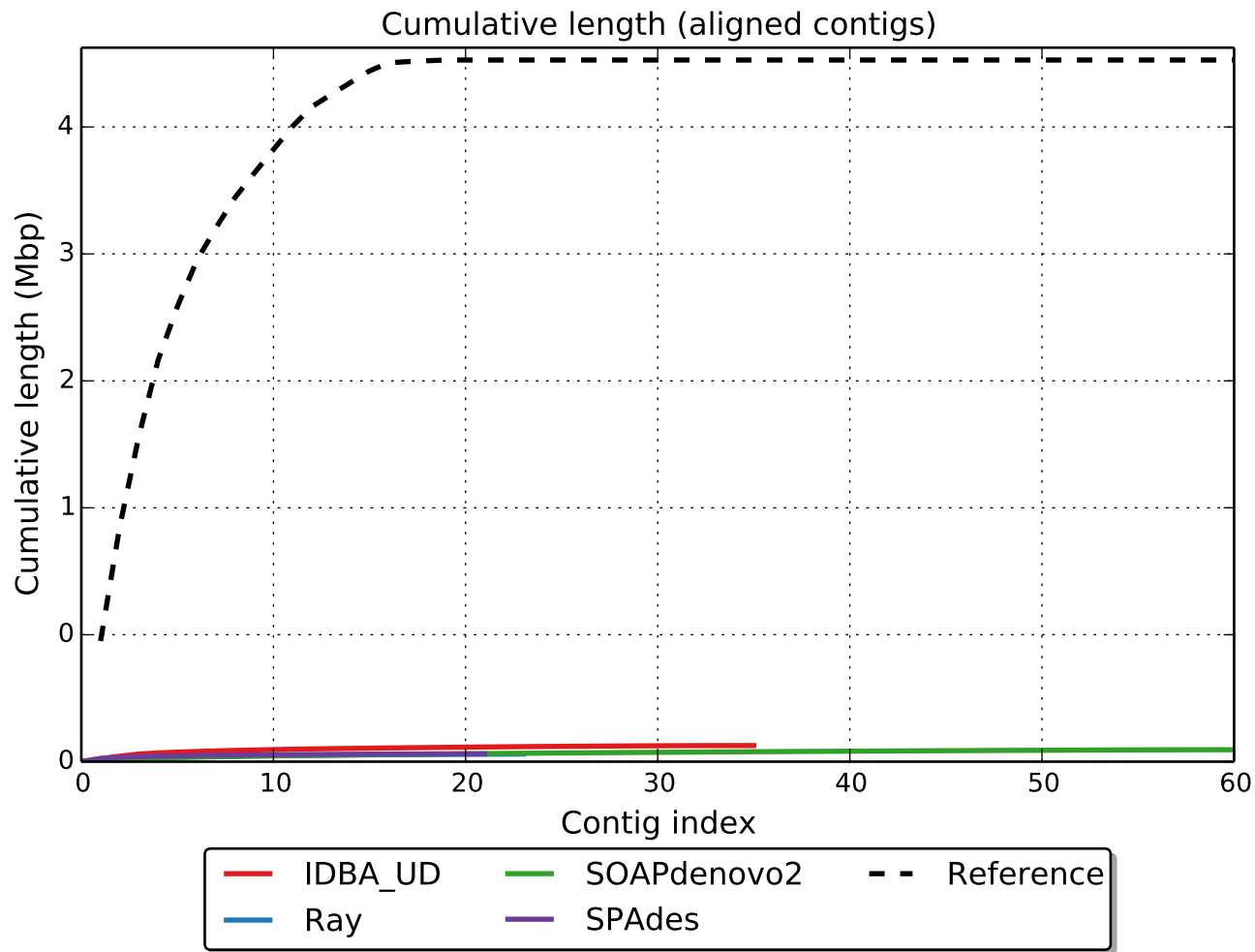


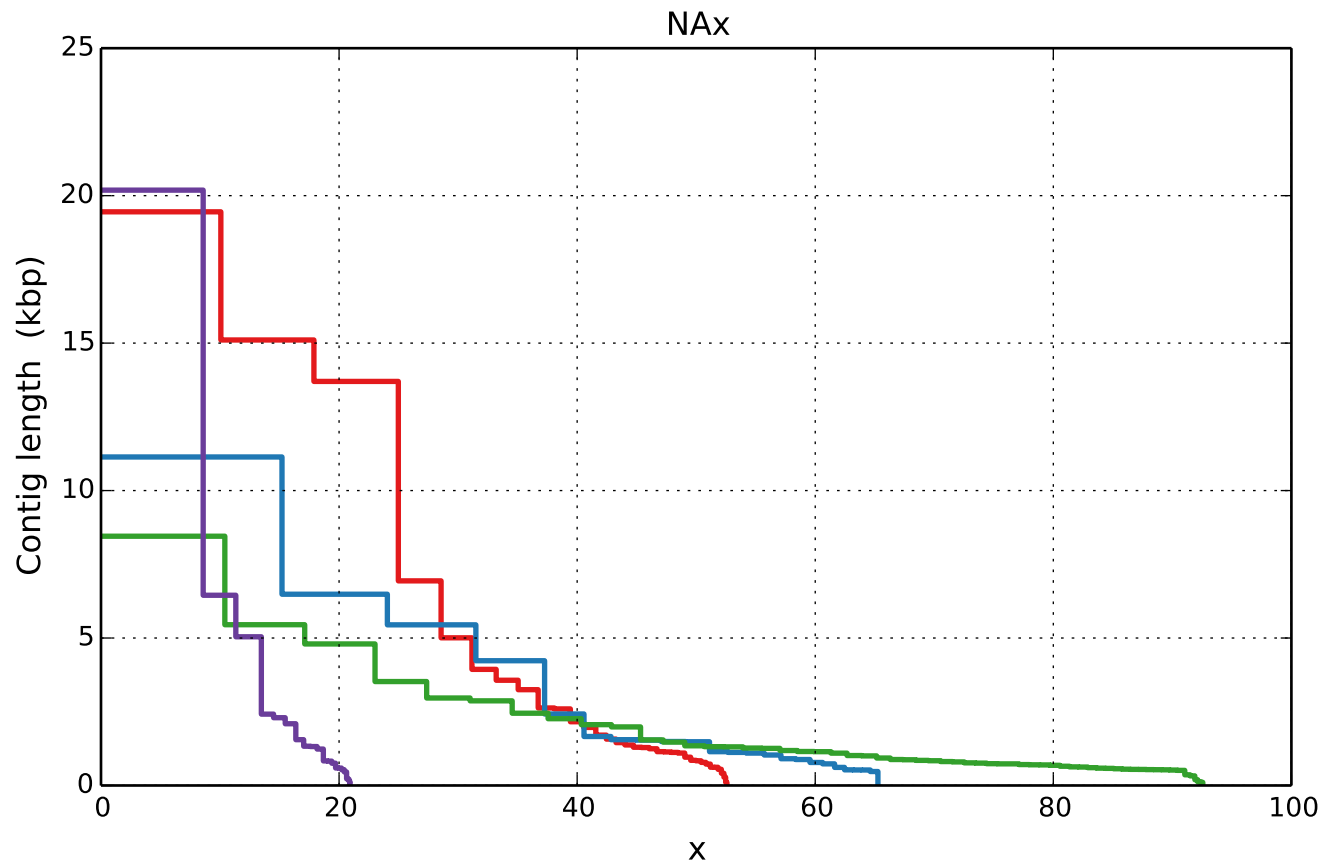


GC content









IDBA_UD	SOAPdenovo2	SPAdes
Ray		

