

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	816	157	0	0	179
# contigs (>= 5000 bp)	0	18	0	0	29
# contigs (>= 10000 bp)	0	2	0	0	12
# contigs (>= 25000 bp)	0	1	0	0	3
# contigs (>= 50000 bp)	0	0	0	0	1
Total length (>= 1000 bp)	1173763	420763	0	0	644504
Total length (>= 5000 bp)	0	167433	0	0	391690
Total length (>= 10000 bp)	0	48270	0	0	272949
Total length (>= 25000 bp)	0	36310	0	0	114702
Total length (>= 50000 bp)	0	0	0	0	50890
# contigs	2381	888	4	81	1210
Largest contig	3526	36310	524	816	50890
Total length	2282565	893367	2063	46590	1306286
Reference length	3653464	3653464	3653464	3653464	3653464
GC (%)	65.12	64.65	68.06	64.04	65.54
Reference GC (%)	65.15	65.15	65.15	65.15	65.15
N50	1018	914	519	564	977
NG50	691	-	-	-	-
N75	743	635	515	523	630
L50	784	185	2	37	188
LG50	1603	-	-	-	-
L75	1443	487	3	59	627
# misassemblies	0	27	0	0	27
# misassembled contigs	0	26	0	0	27
Misassembled contigs length	0	19592	0	0	19514
# local misassemblies	0	0	0	0	0
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 253 part	0 + 0 part	0 + 0 part	0 + 373 part
Unaligned length	0	365254	0	0	594189
Genome fraction (%)	62.477	14.396	0.056	1.277	19.431
Duplication ratio	1.000	1.004	1.000	0.998	1.003
# N's per 100 kbp	0.00	0.00	0.00	49.37	69.59
# mismatches per 100 kbp	0.00	454.21	0.00	475.68	1122.39
# indels per 100 kbp	0.00	7.03	0.00	34.28	12.11
Largest alignment	3526	1909	524	816	1758
NA50	1018	510	519	564	403
NGA50	691	-	-	-	-
NA75	743	-	515	523	-
LA50	784	659	2	37	1017
LGA50	1603	-	-	-	-
LA75	1443	-	3	59	-

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

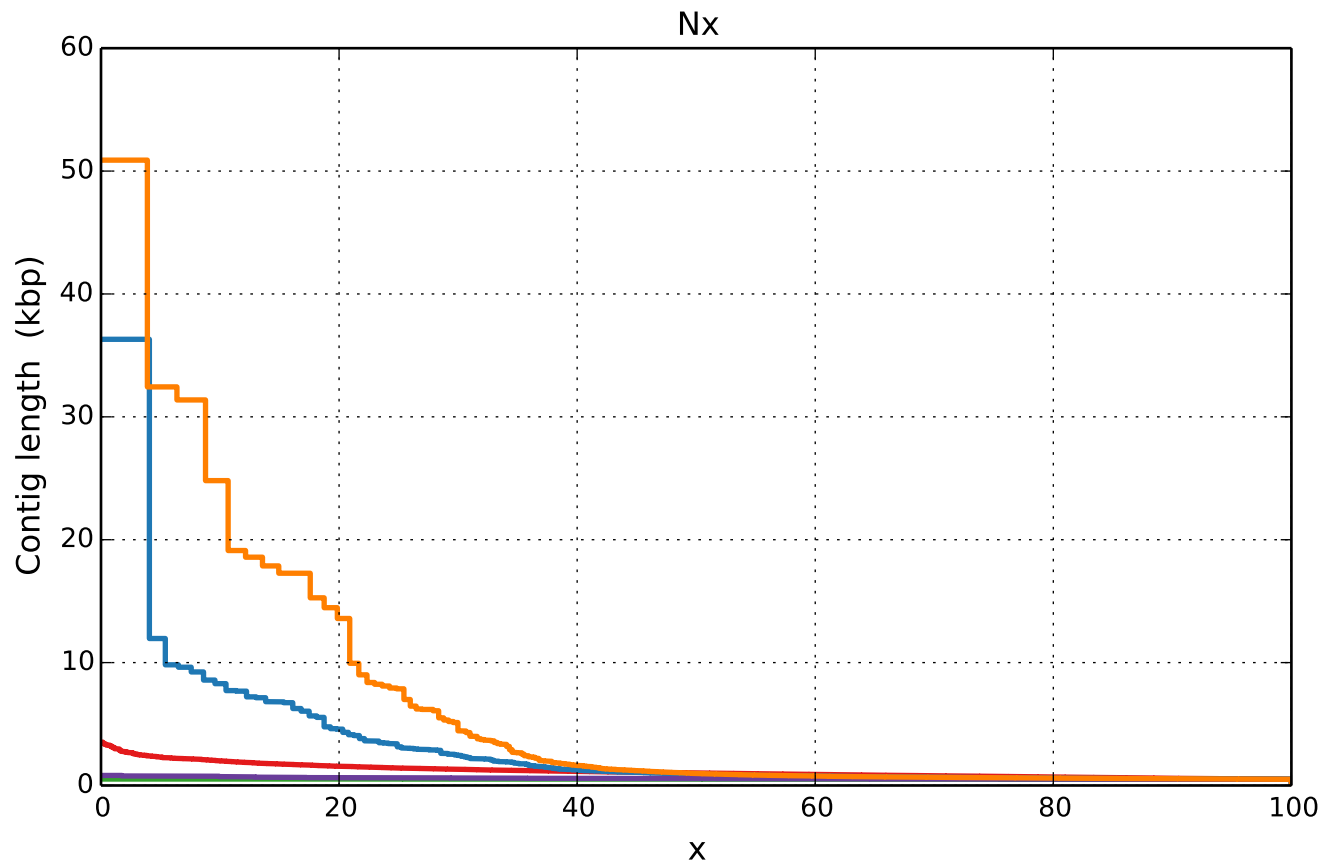
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	27	0	0	27
# relocations	0	3	0	0	5
# translocations	0	24	0	0	22
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	27	0	0	19
# misassembled contigs	0	26	0	0	27
Misassembled contigs length	0	19592	0	0	19514
# local misassemblies	0	0	0	0	0
# structural variations	0	0	0	0	0
# mismatches	0	2389	0	222	7968
# indels	0	37	0	16	86
# short indels	0	36	0	3	86
# long indels	0	1	0	13	0
Indels length	0	124	0	150	88

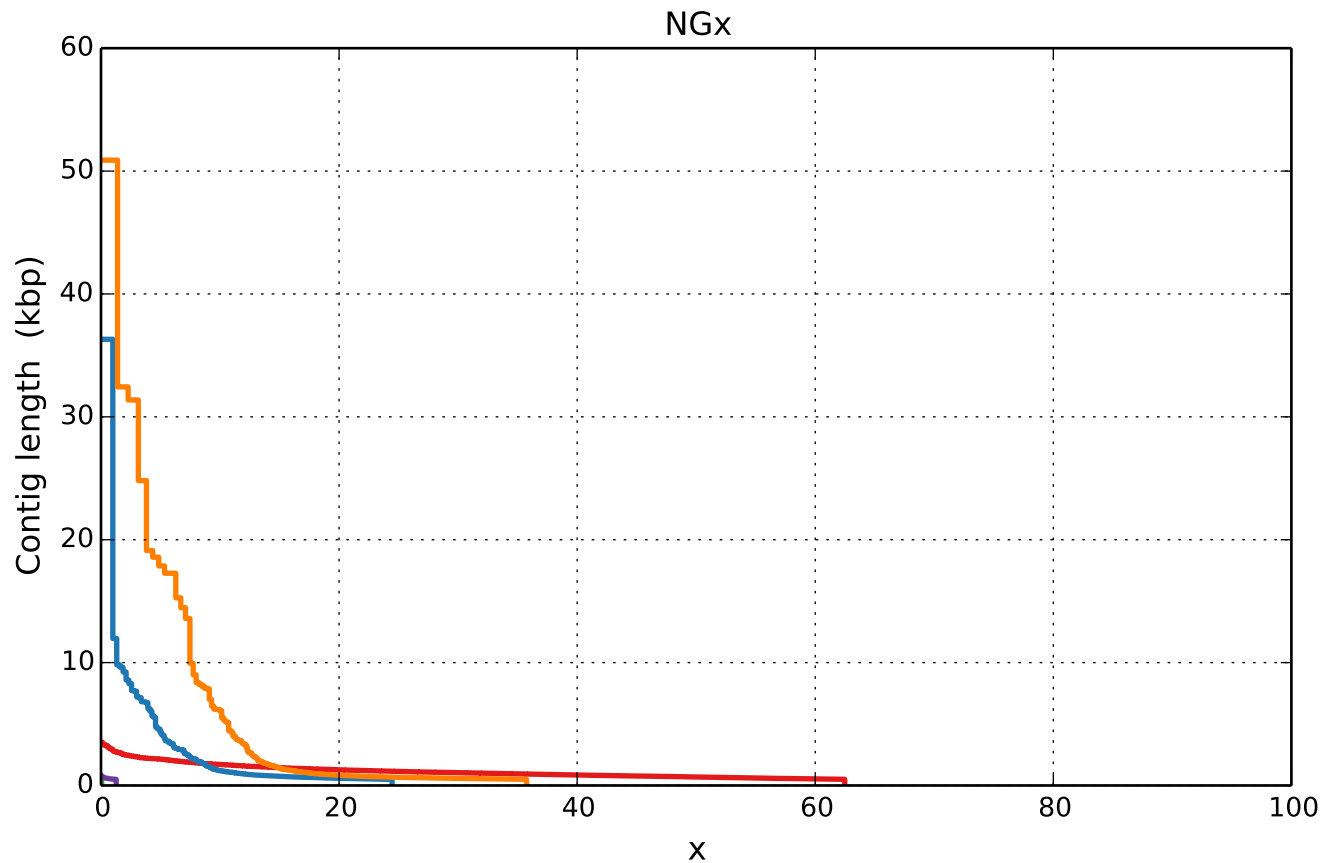
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

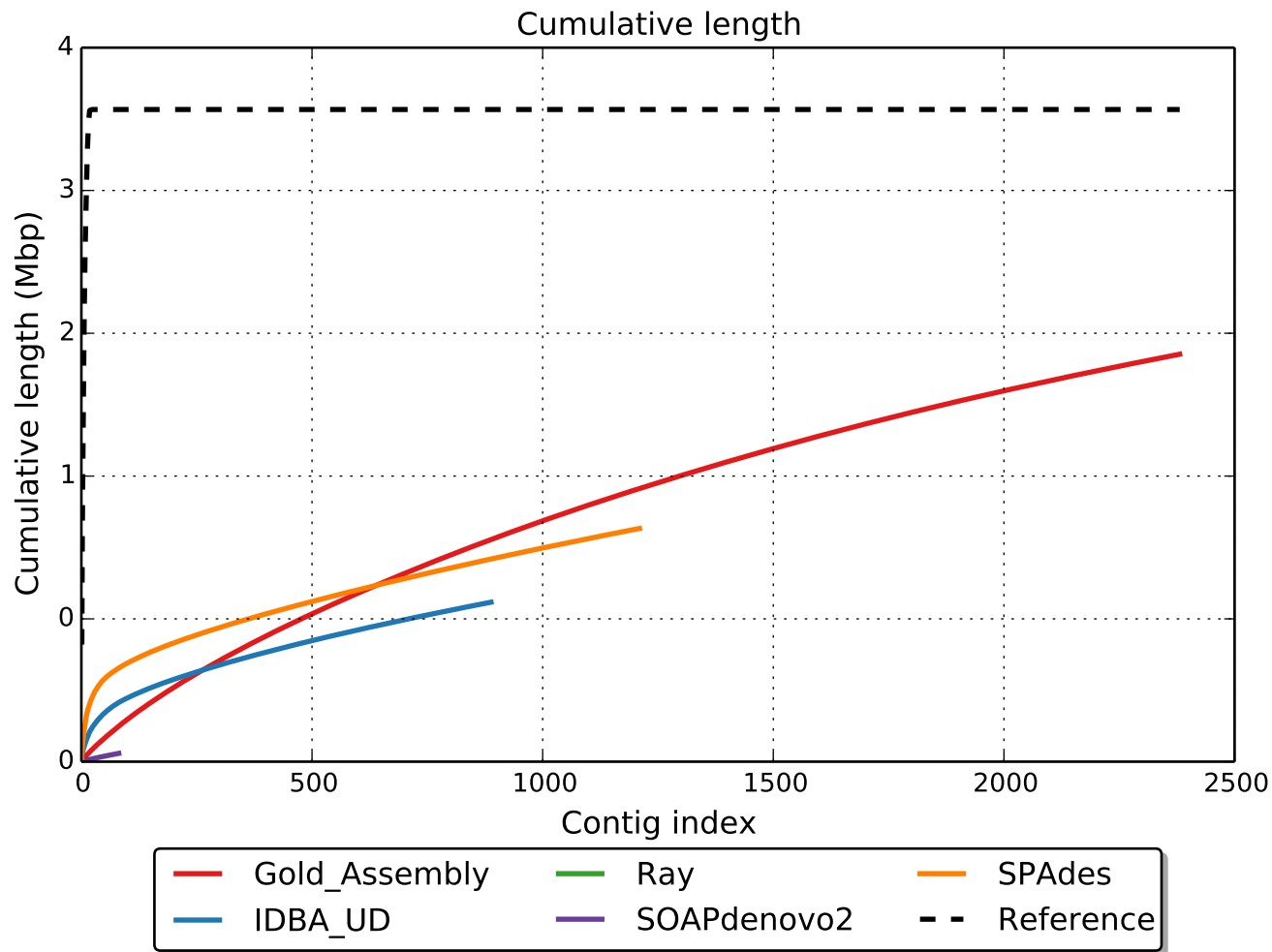
Unaligned report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	253	0	0	373
# with misassembly	0	1	0	0	4
# both parts are significant	0	27	0	0	19
Partially unaligned length	0	365254	0	0	594189
# N's	0	0	0	23	909

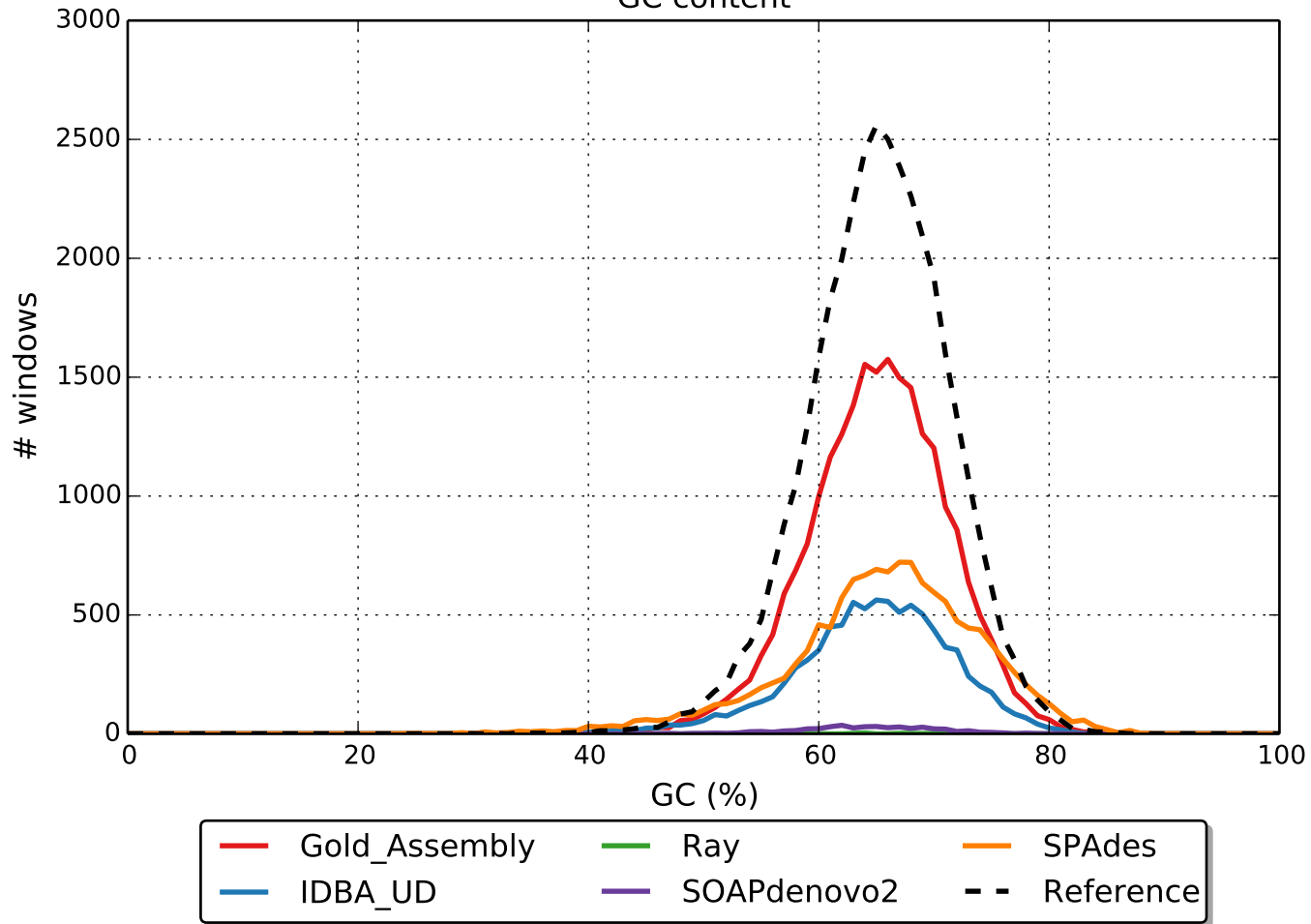
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

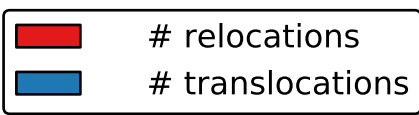
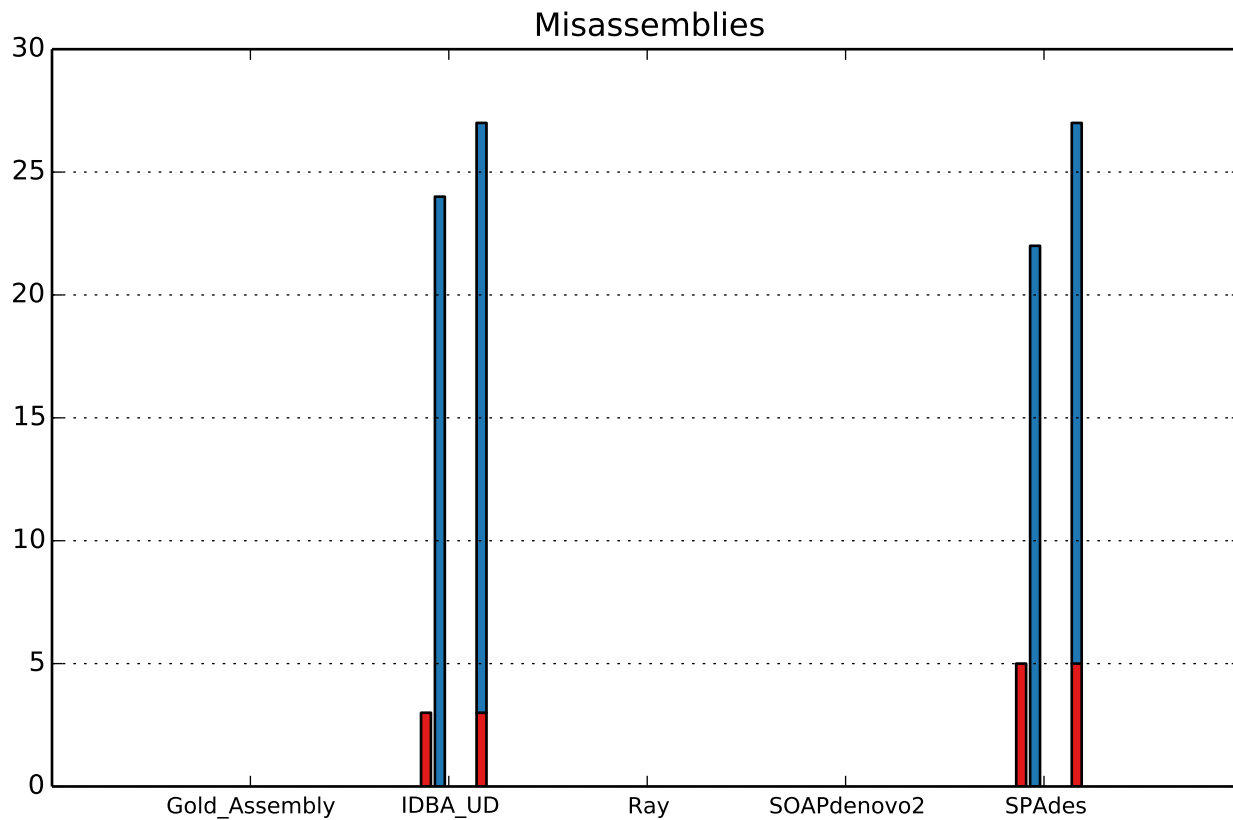


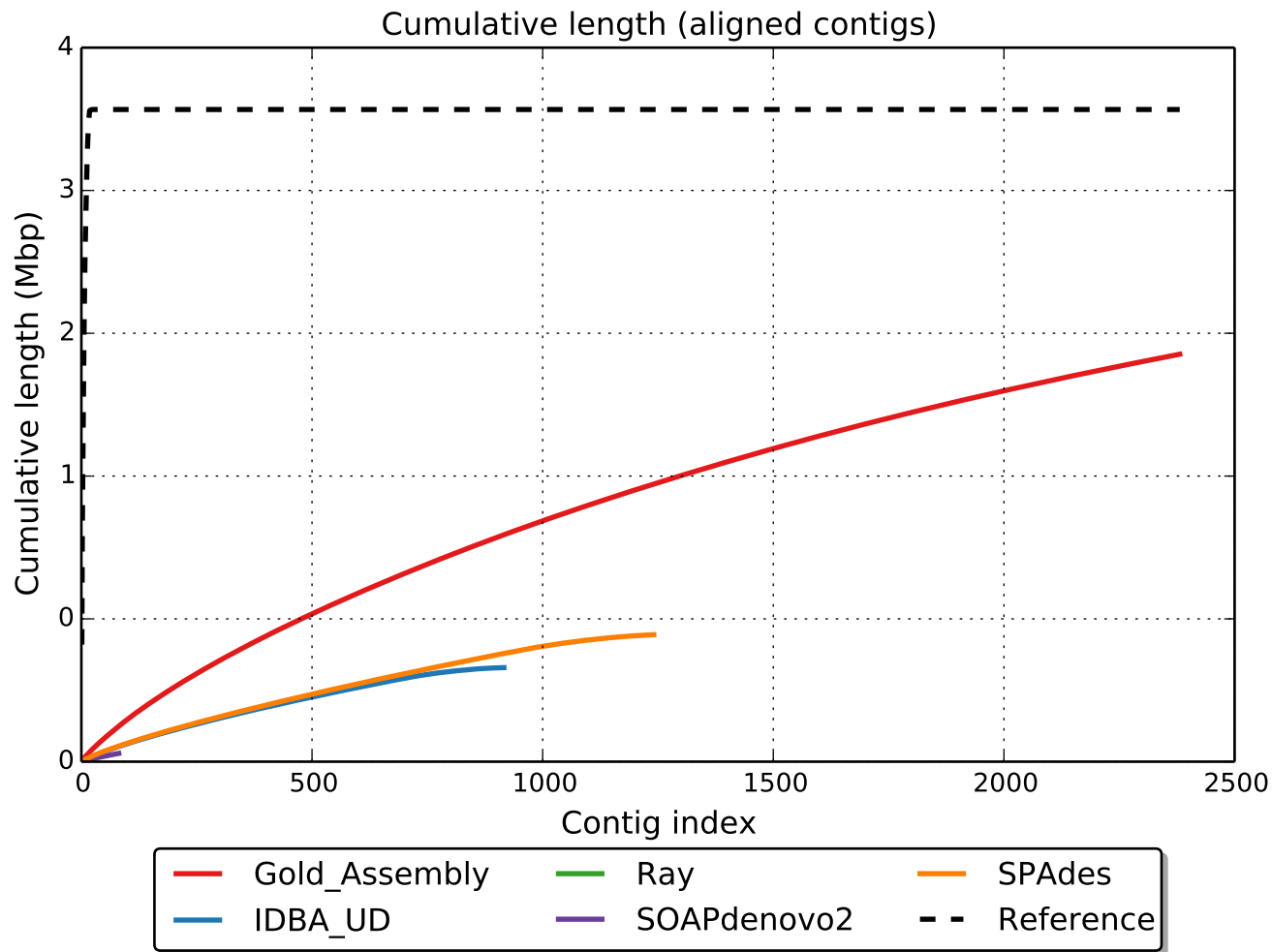


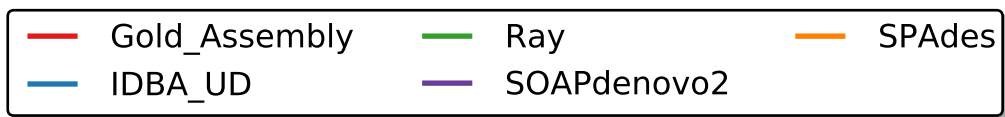
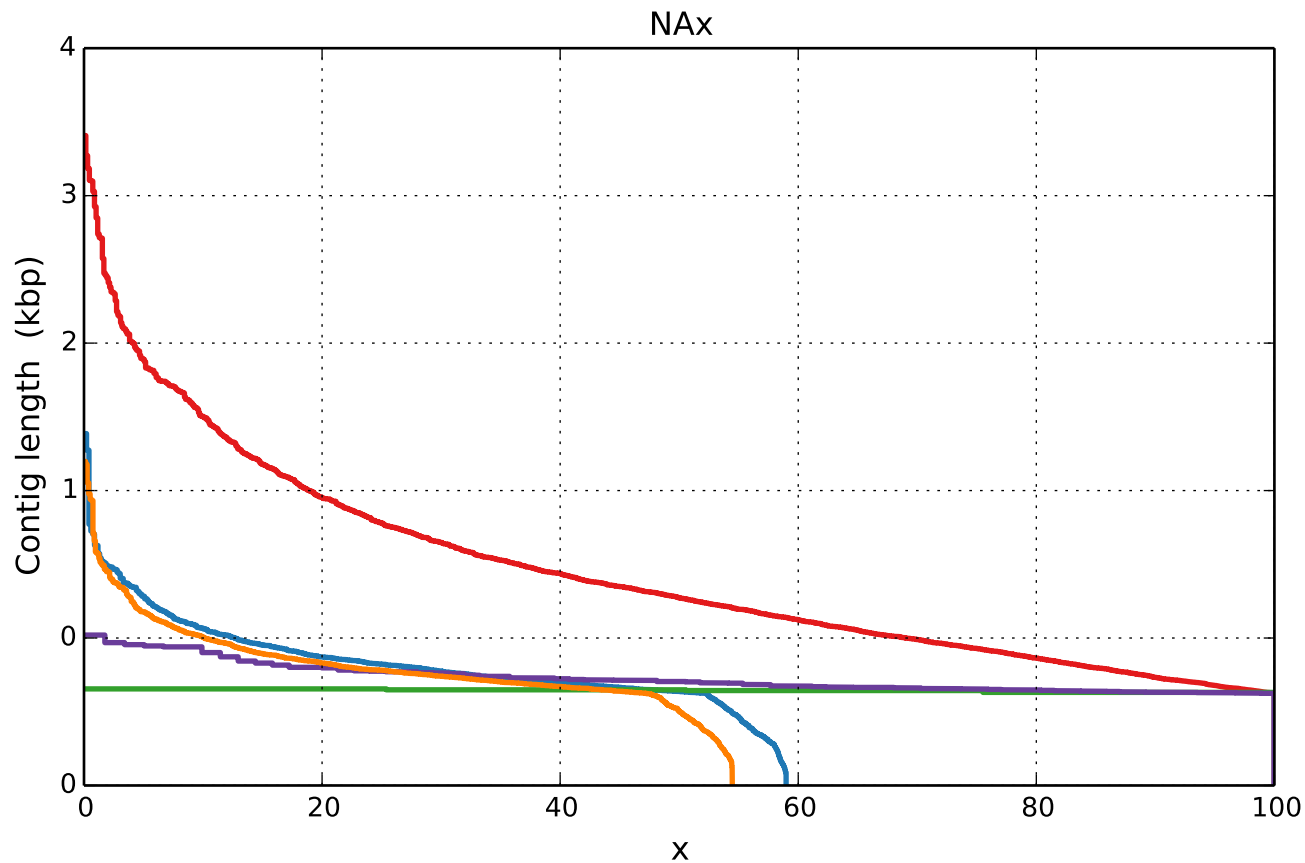


GC content









NGAx

