

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	488	309	1	26	279
# contigs (>= 5000 bp)	26	3	0	1	1
# contigs (>= 10000 bp)	0	1	0	0	0
# contigs (>= 25000 bp)	0	0	0	0	0
# contigs (>= 50000 bp)	0	0	0	0	0
Total length (>= 1000 bp)	1131964	478467	1248	37520	424946
Total length (>= 5000 bp)	166626	27698	0	5062	8971
Total length (>= 10000 bp)	0	12581	0	0	0
Total length (>= 25000 bp)	0	0	0	0	0
Total length (>= 50000 bp)	0	0	0	0	0
# contigs	714	939	42	370	999
Largest contig	8972	12581	1248	5062	8971
Total length	1299279	927320	26588	259501	935147
Reference length	1422478	1422478	1422478	1422478	1422478
GC (%)	35.49	35.49	37.30	35.47	35.76
Reference GC (%)	35.48	35.48	35.48	35.48	35.48
N50	2237	1023	583	669	946
NG50	2072	726	-	-	704
N75	1441	749	542	577	718
NG75	1189	-	-	-	-
L50	176	295	18	144	323
LG50	205	580	-	-	622
L75	360	559	30	249	608
LG75	429	-	-	-	-
# misassemblies	0	7	0	0	4
# misassembled contigs	0	7	0	0	4
Misassembled contigs length	0	8080	0	0	5441
# local misassemblies	0	1	0	0	2
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 36 part	0 + 0 part	0 + 2 part	0 + 38 part
Unaligned length	0	26292	0	262	30764
Genome fraction (%)	90.713	63.015	1.868	18.246	63.252
Duplication ratio	1.007	1.005	1.001	0.999	1.005
# N's per 100 kbp	0.00	0.00	0.00	99.42	0.00
# mismatches per 100 kbp	0.00	285.70	0.00	331.35	766.44
# indels per 100 kbp	0.00	1.45	0.00	37.76	2.56
Largest alignment	8972	8948	1248	5062	8971
NA50	2237	981	583	669	906
NGA50	2072	687	-	-	667
NA75	1441	700	542	576	678
NGA75	1189	-	-	-	-
LA50	176	317	18	144	351
LGA50	205	617	-	-	663
LA75	360	594	30	249	649
LGA75	429	-	-	-	-

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

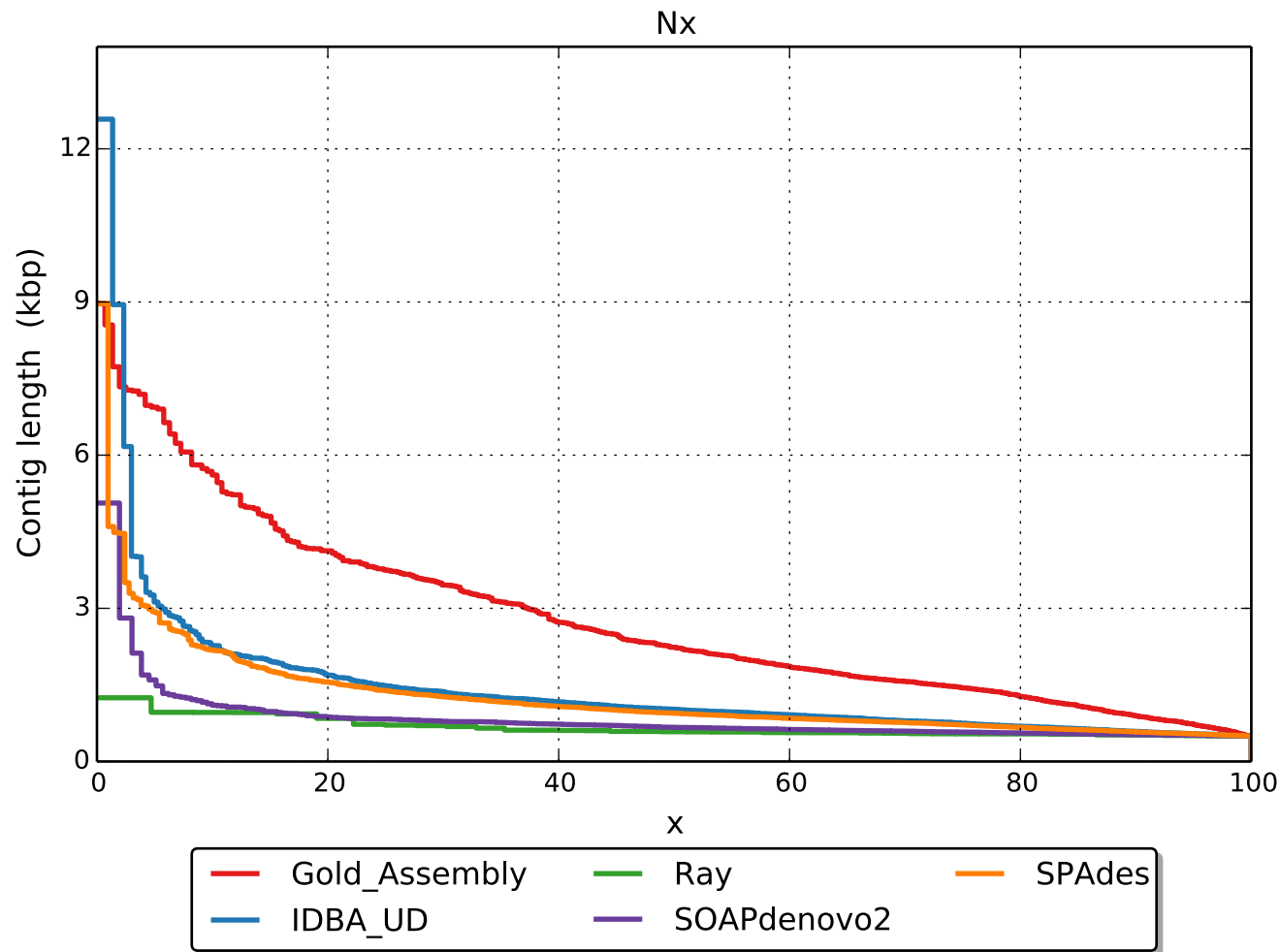
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	7	0	0	4
# relocations	0	7	0	0	4
# translocations	0	0	0	0	0
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	2	0	0	7
# misassembled contigs	0	7	0	0	4
Misassembled contigs length	0	8080	0	0	5441
# local misassemblies	0	1	0	0	2
# structural variations	0	0	0	0	0
# mismatches	0	2561	0	860	6896
# indels	0	13	0	98	23
# short indels	0	11	0	39	23
# long indels	0	2	0	59	0
Indels length	0	44	0	773	31

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).

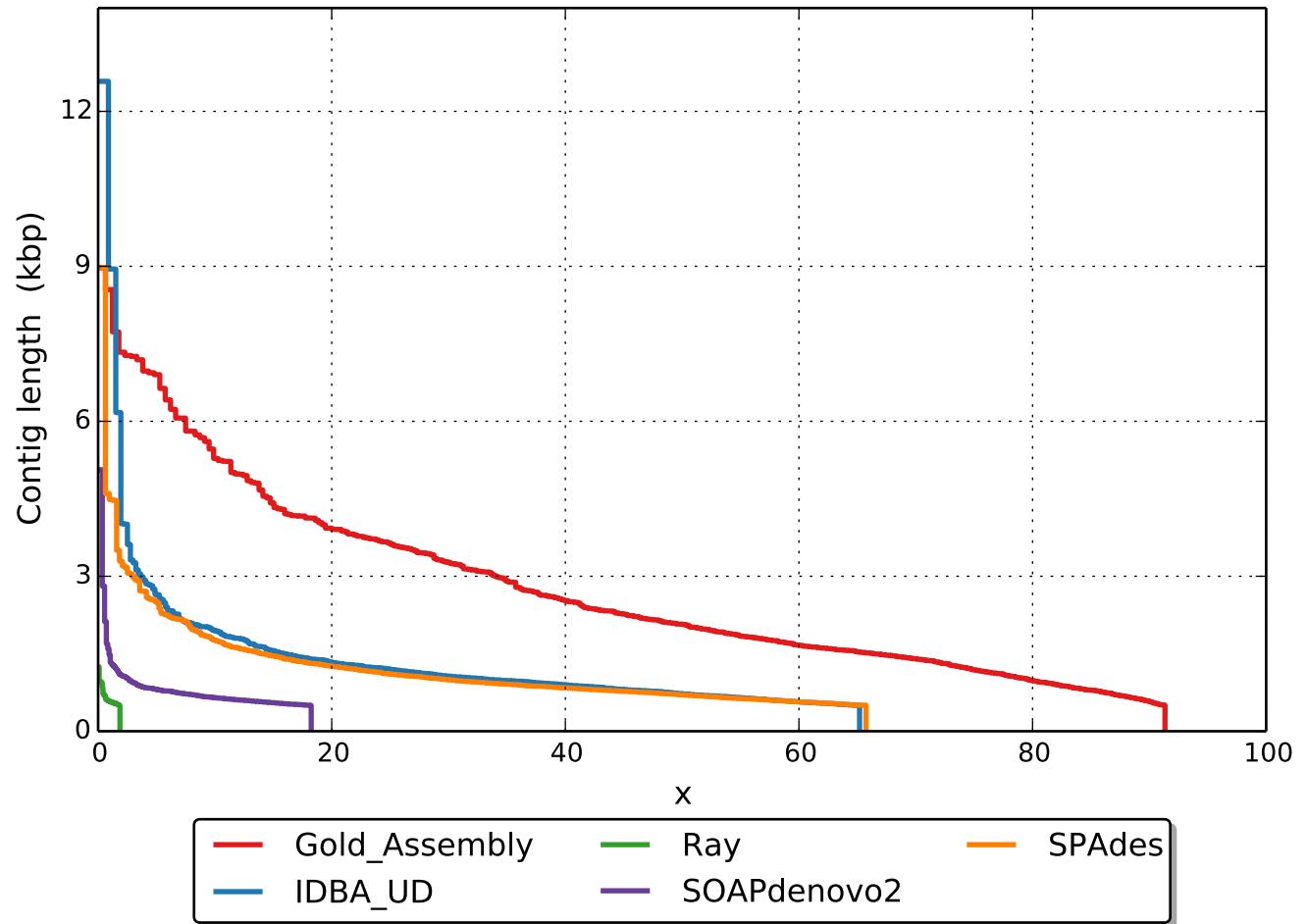
Unaligned report

	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	36	0	2	38
# with misassembly	0	0	0	0	0
# both parts are significant	0	2	0	0	7
Partially unaligned length	0	26292	0	262	30764
# N's	0	0	0	258	0

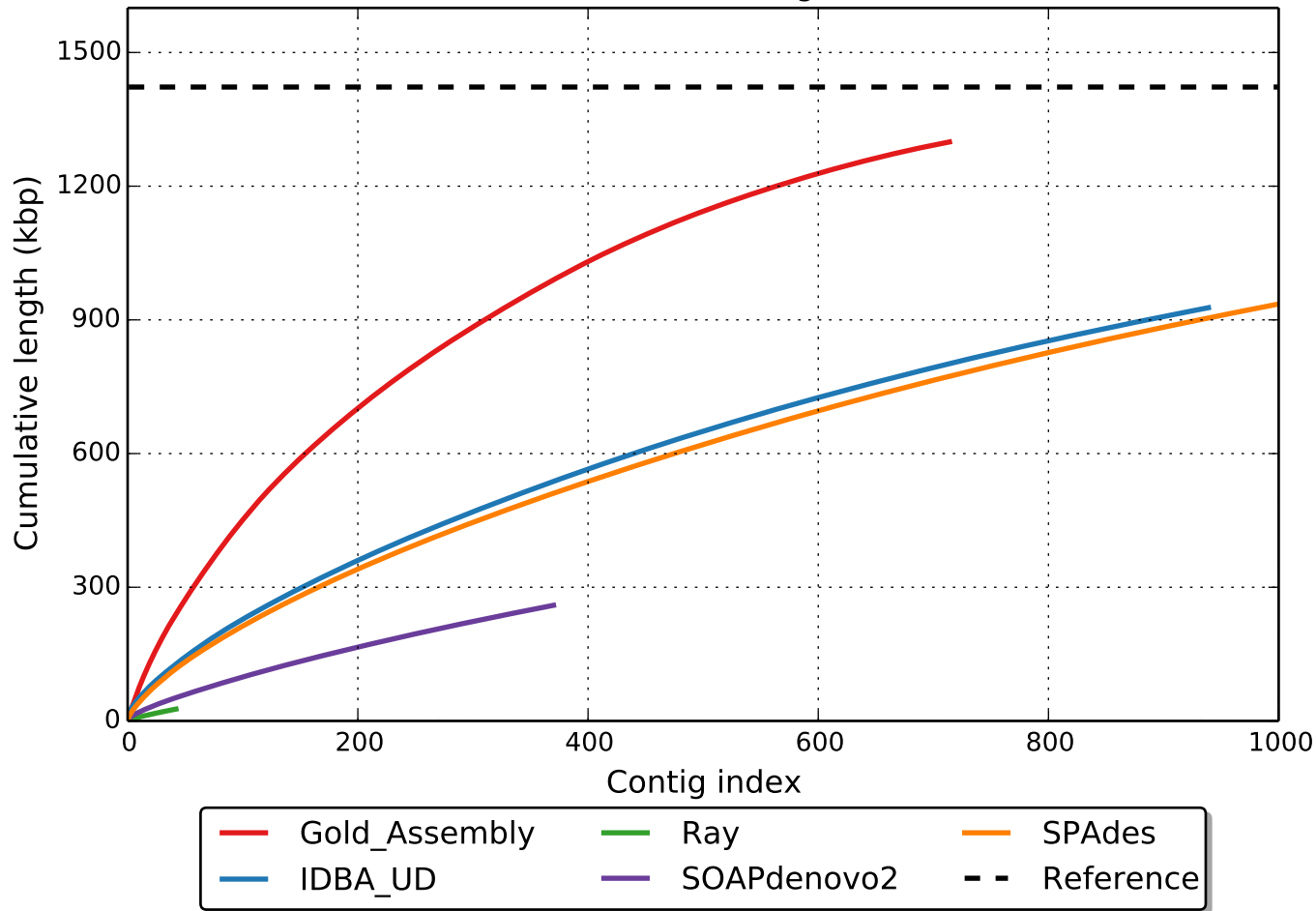
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



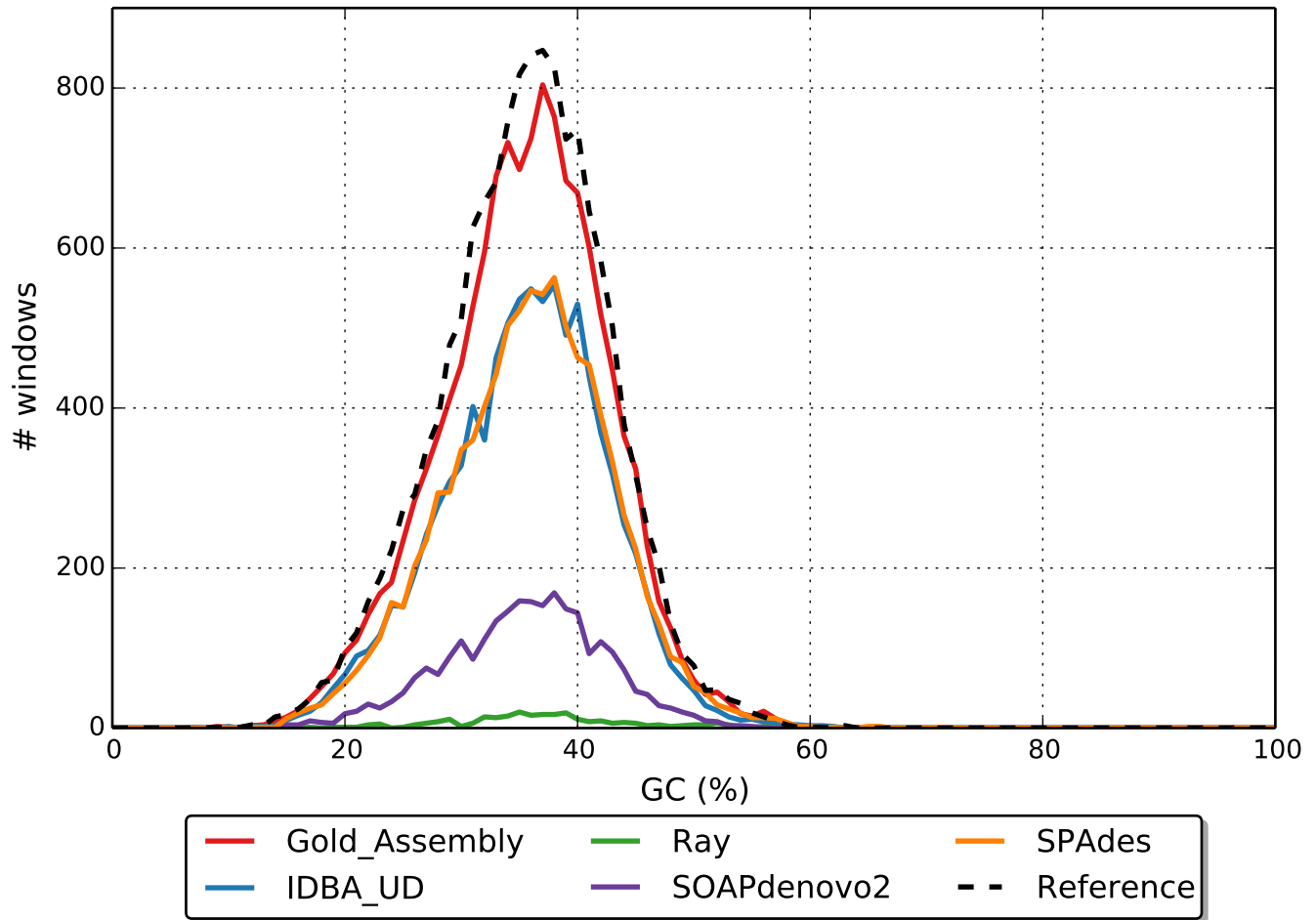
NGx

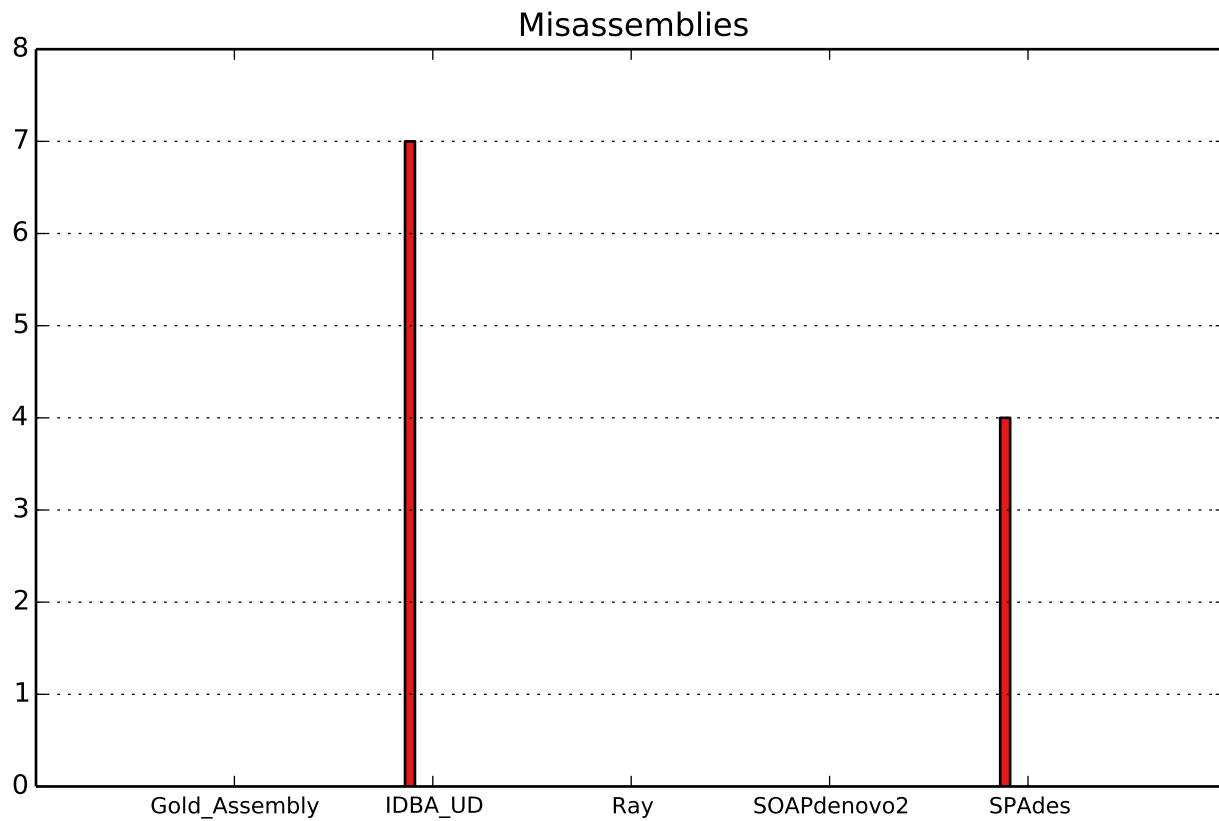


Cumulative length



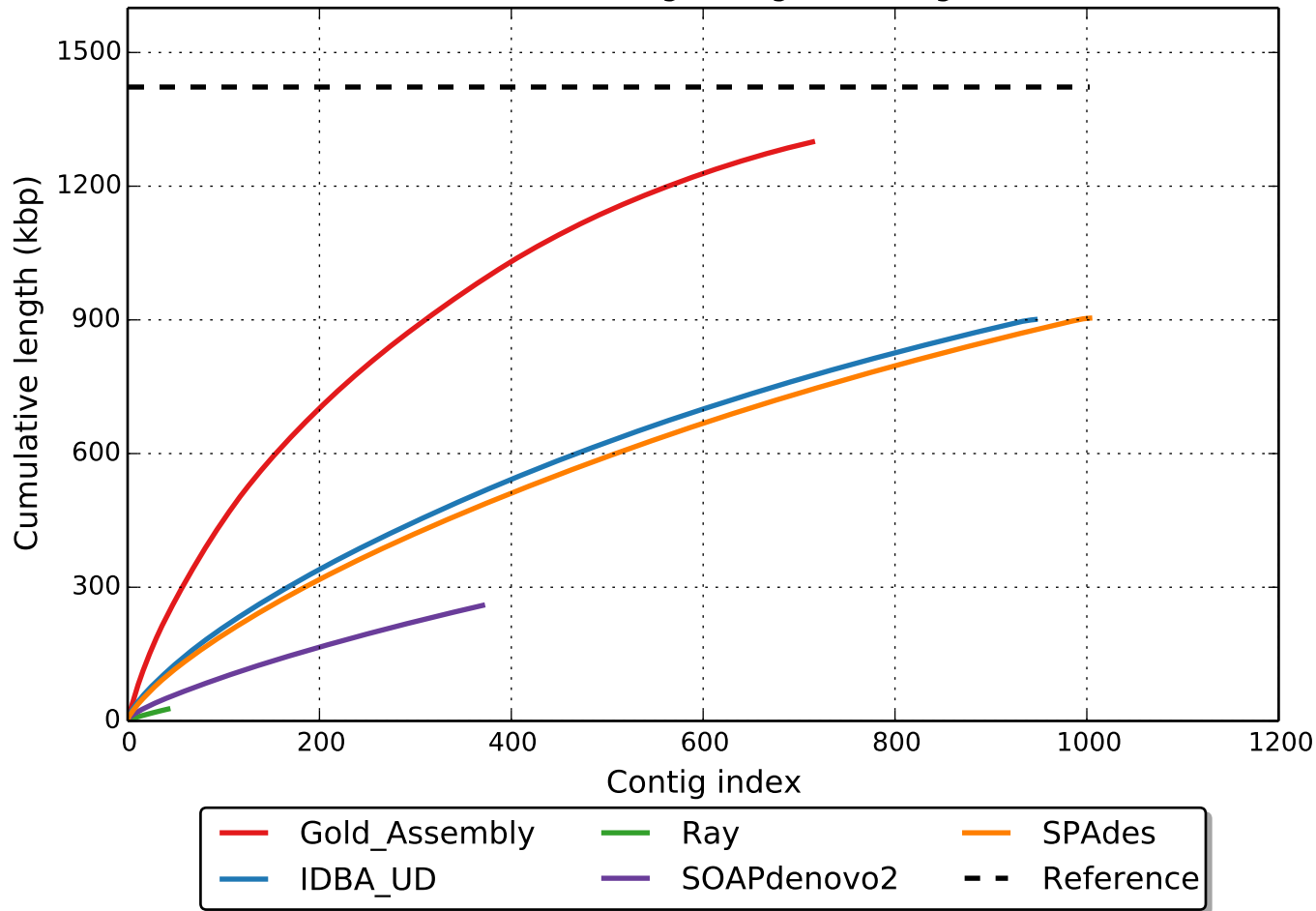
GC content



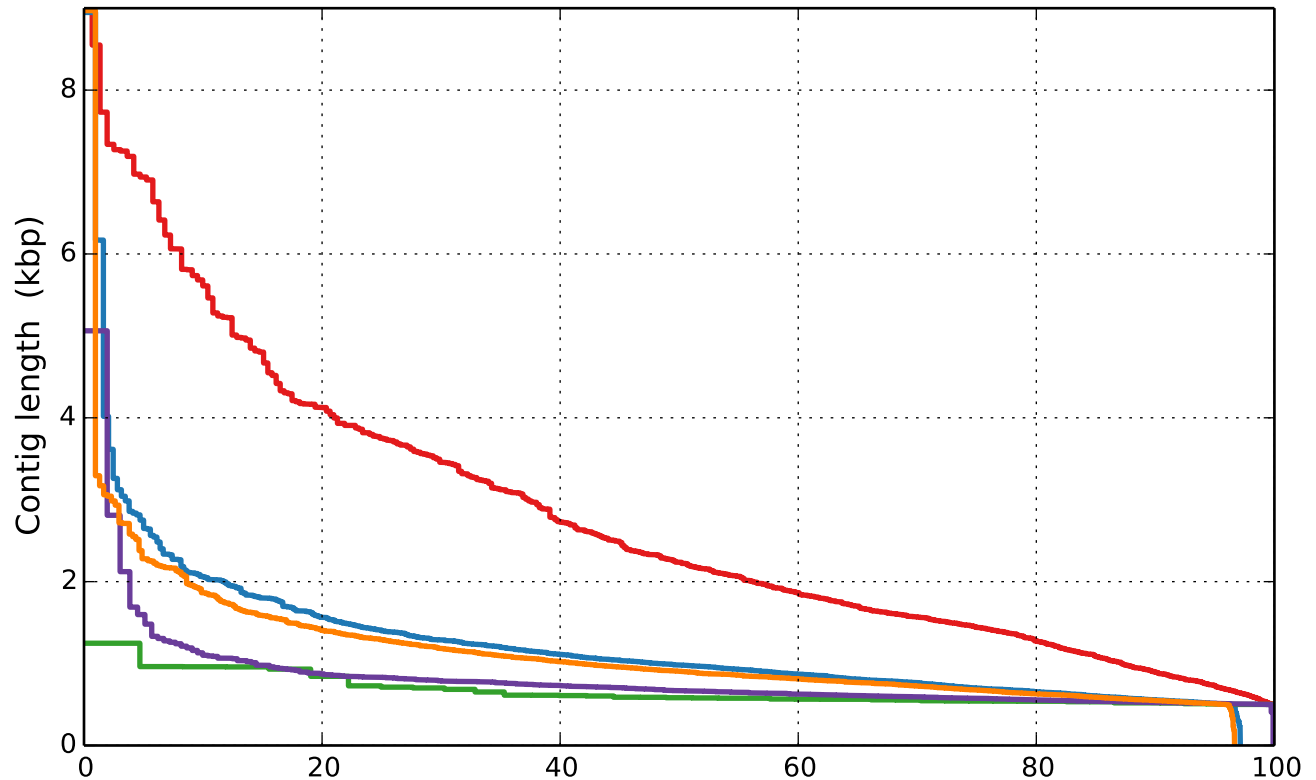


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

