Report

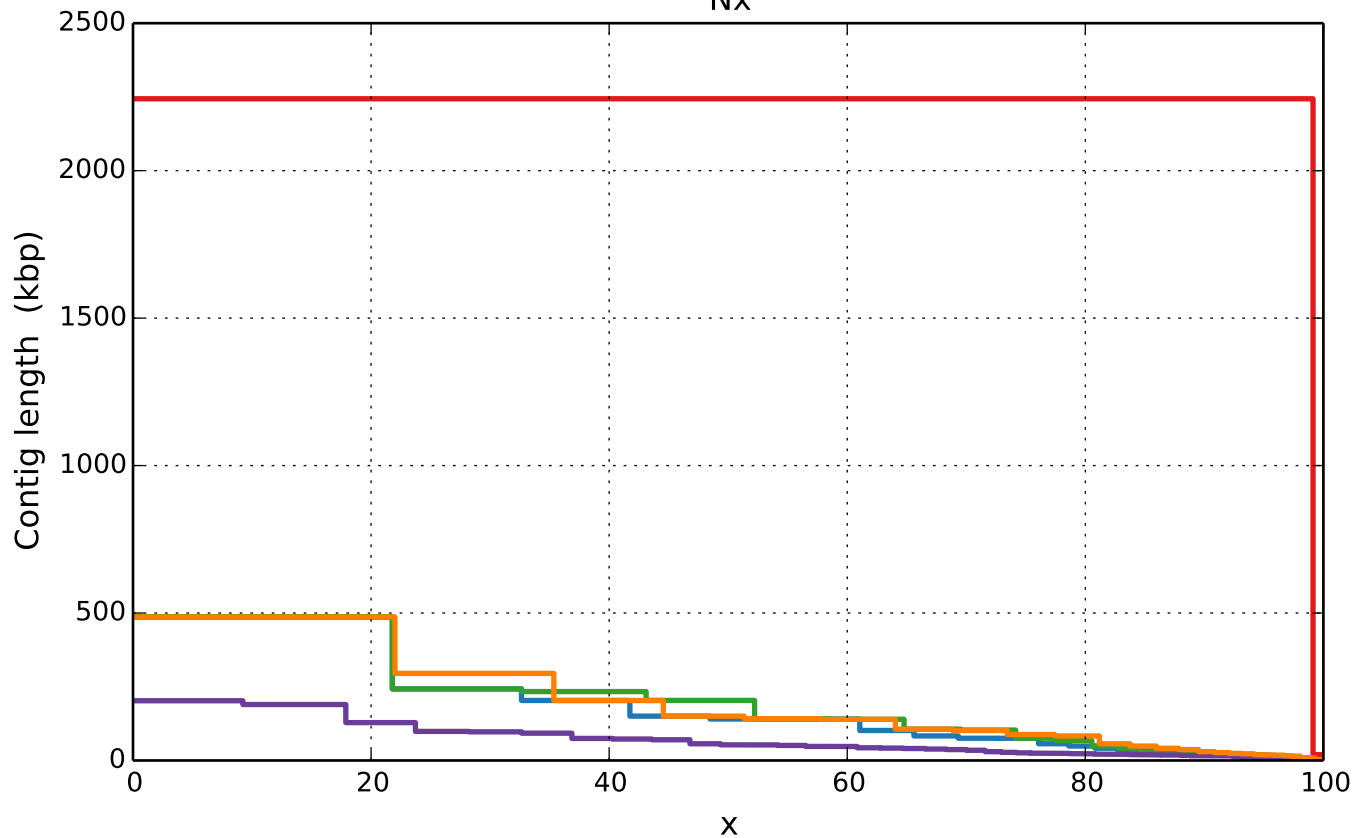|	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	2	42	37	68	35
# contigs (>= 5000 bp)	2	32	29	57	26
# contigs (>= 10000 bp)	2	27	26	48	23
# contigs (>= 25000 bp)	1	19	16	24	16
# contigs (>= 50000 bp)	1	11	10	13	11
Total length (>= 1000 bp)	2263465	2230402	2234789	2189114	2210494
Total length (>= 5000 bp)	2263465	2212461	2214065	2159308	2196126
Total length (>= 10000 bp)	2263465	2169078	2189665	2085081	2169351
Total length (>= 25000 bp)	2243761	2022994	2010780	1654095	2036420
Total length (>= 50000 bp)	2243761	1756760	1800167	1239876	1852362
# contigs	2	48	37	75	37
Largest contig	2243761	486791	486984	202548	486704
Total length	2263465	2234730	2234789	2194210	2211846
Reference length	2243772	2243772	2243772	2243772	2243772
GC (%)	68.58	68.62	68.62	68.72	68.66
Reference GC (%)	68.61	68.61	68.61	68.61	68.61
N50	2243761	140699	203675	53016	150321
NG50	2243761	140699	203675	53016	150321
N75	2243761	75307	75473	25906	88127
NG75	2243761	75307	75473	24450	88127
L50	1	5	4	11	4
LG50	1	5	4	11	4
L75	1	10	9	24	9
LG75	1	10	9	26	9
# misassemblies	0	0	0	0	1
# misassembled contigs	0	0	0	0	1
Misassembled contigs length	0	0	0	0	88127
# local misassemblies	0	0	1	0	0
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 1 part	0 + 2 part	0 + 2 part	0 + 0 part	0 + 0 part
Unaligned length	18691	18691	18655	0	0
Genome fraction (%)	100.000	98.698	98.694	97.760	98.557
Duplication ratio	1.000	1.001	1.001	1.000	1.000
# N's per 100 kbp	0.00	0.00	5.91	1.69	0.00
# mismatches per 100 kbp	0.00	0.36	0.23	0.82	2.26
# indels per 100 kbp	0.00	0.00	0.00	1.05	0.14
Largest alignment	2243761	486791	486984	202541	486704
NA50	2243761	140699	203675	53016	150321
NGA50	2243761	140699	203675	53016	150321
NA75	2243761	75307	75473	25906	83194
NGA75	2243761	75307	75473	24450	83194
LA50	1	5	4	11	4
LGA50	1	5	4	11	4
LA75	1	10	9	24	9
LGA75	1	10	9	26	9

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	0	0	0	1
# relocations	0	0	0	0	1
# translocations	0	0	0	0	0
# inversions	0	0	0	0	0
# possibly misassembled contigs	1	0	0	0	0
# misassembled contigs	0	0	0	0	1
Misassembled contigs length	0	0	0	0	88127
# local misassemblies	0	0	1	0	0
# structural variations	0	0	0	0	0
# mismatches	0	8	5	18	50
# indels	0	0	0	23	3
# short indels	0	0	0	4	3
# long indels	0	0	0	19	0
Indels length	0	0	0	778	5

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).
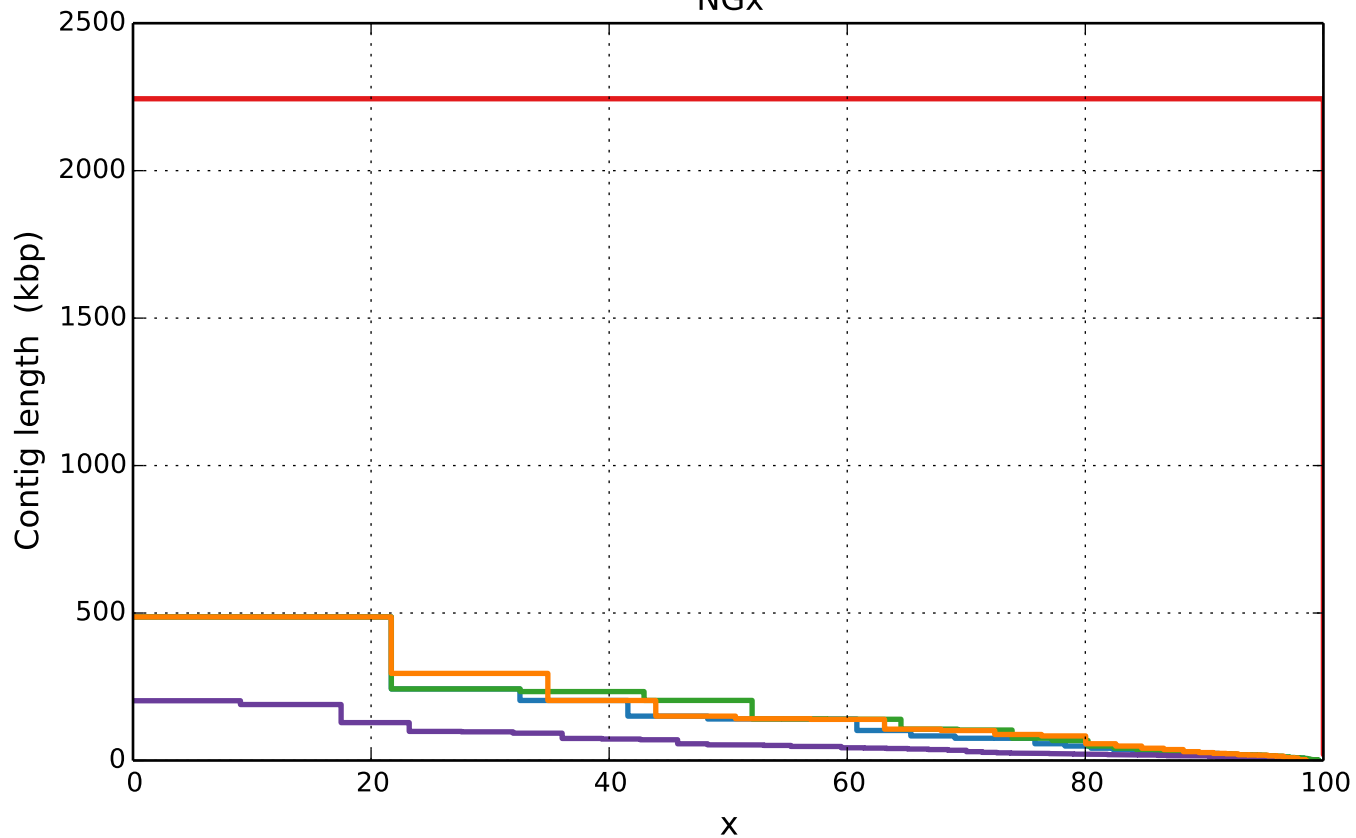
Unaligned report

	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	1	2	2	0	0
# with misassembly	0	0	0	0	0
# both parts are significant	1	0	0	0	0
Partially unaligned length	18691	18691	18655	0	0
# N's	0	0	132	37	0

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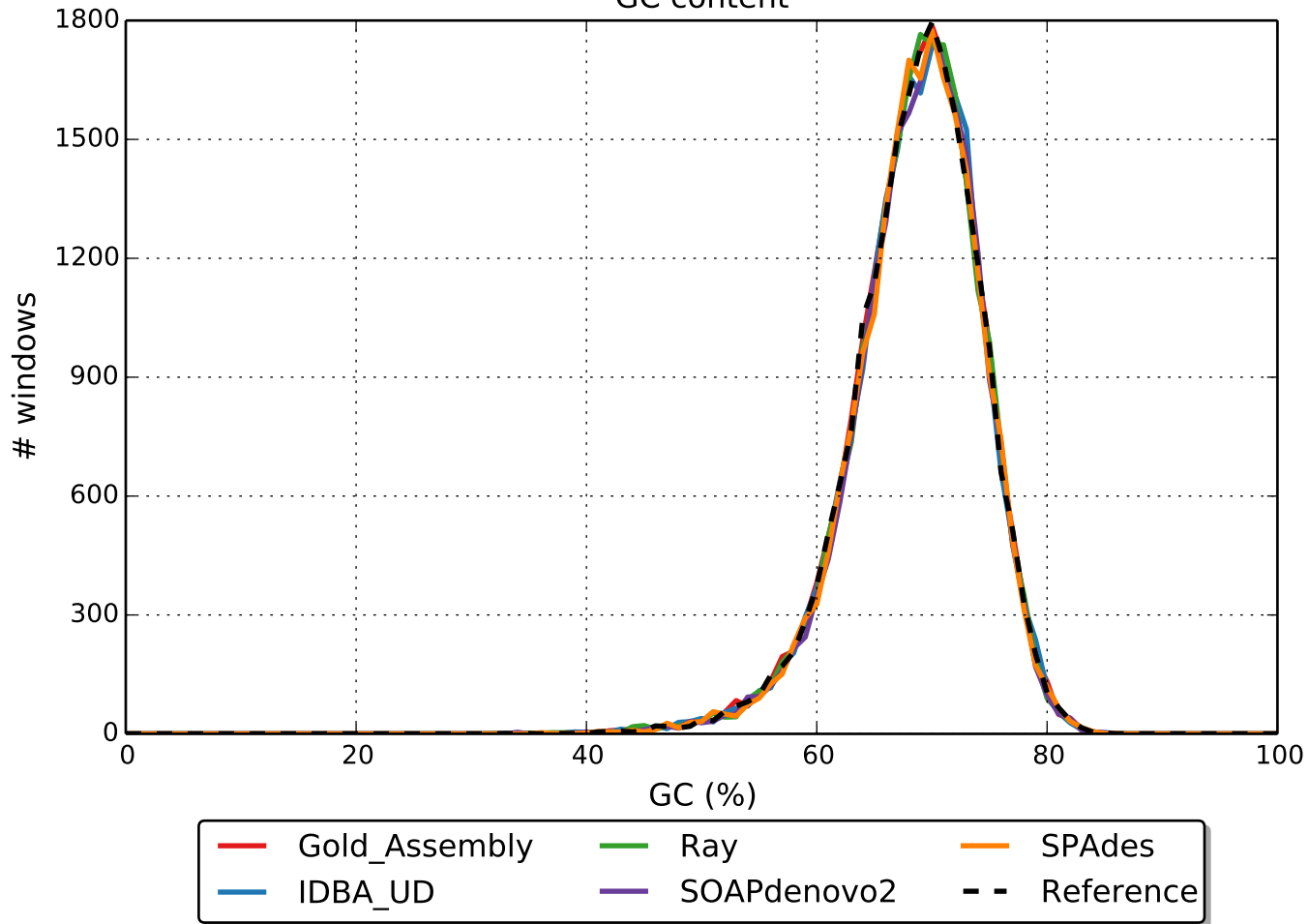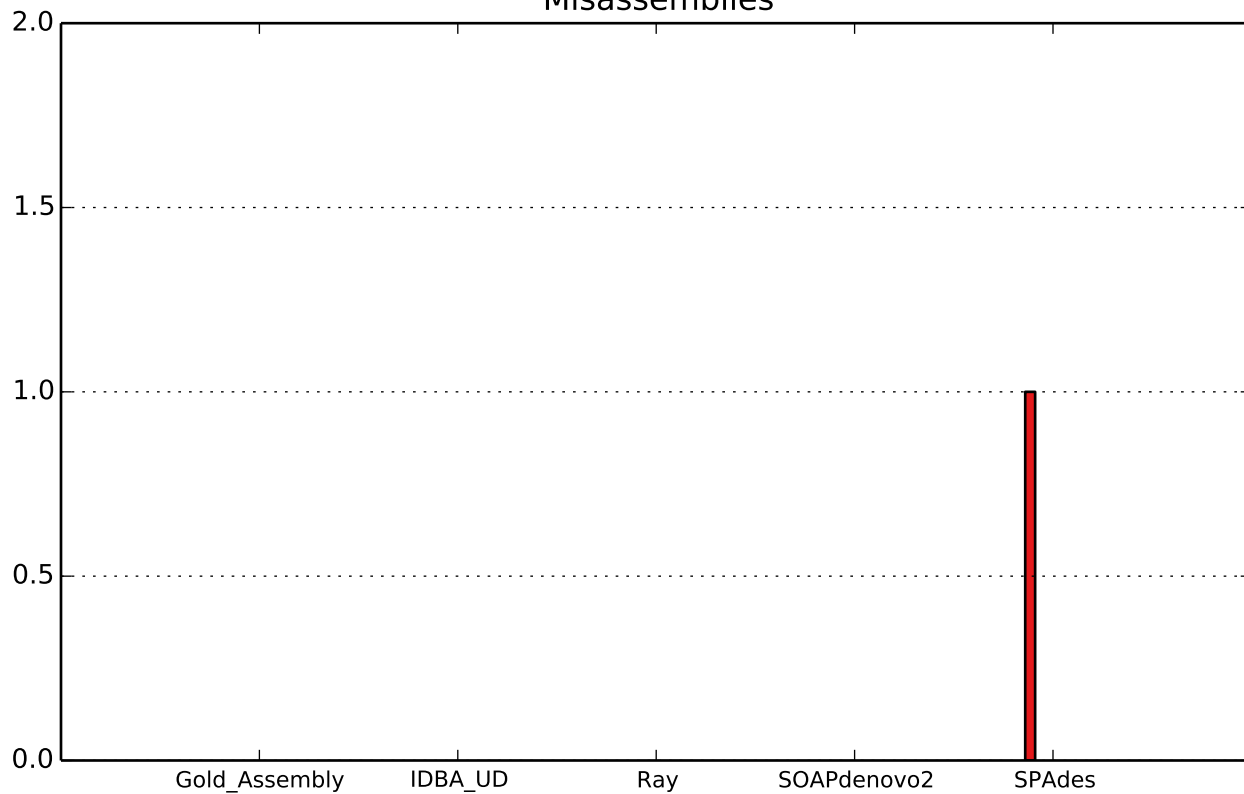(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
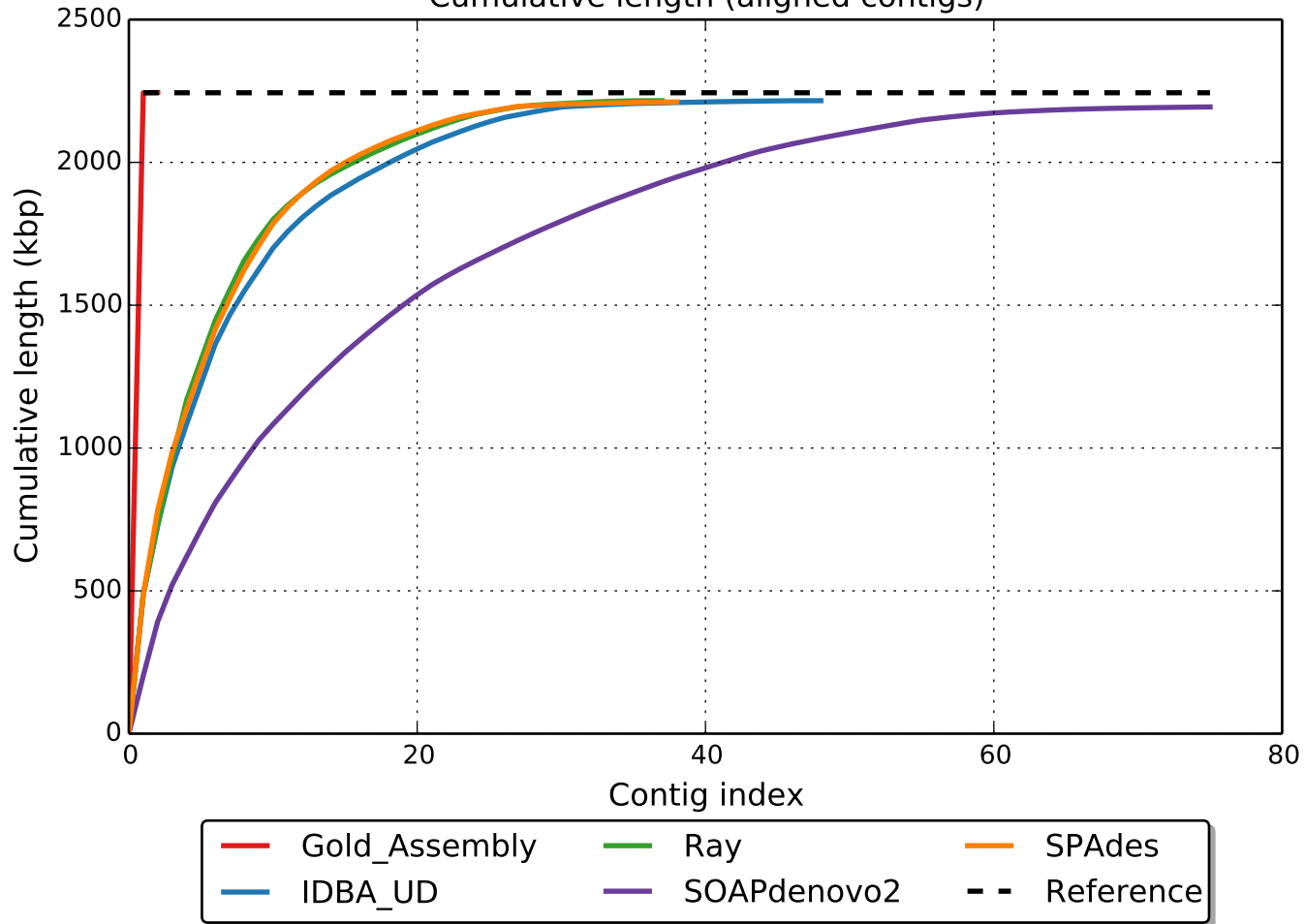
Nx

NGx

Cumulative length

Legend: Gold_Assembly, IDBA_UD, Ray, SOAPdenovo2, SPAdes, Reference
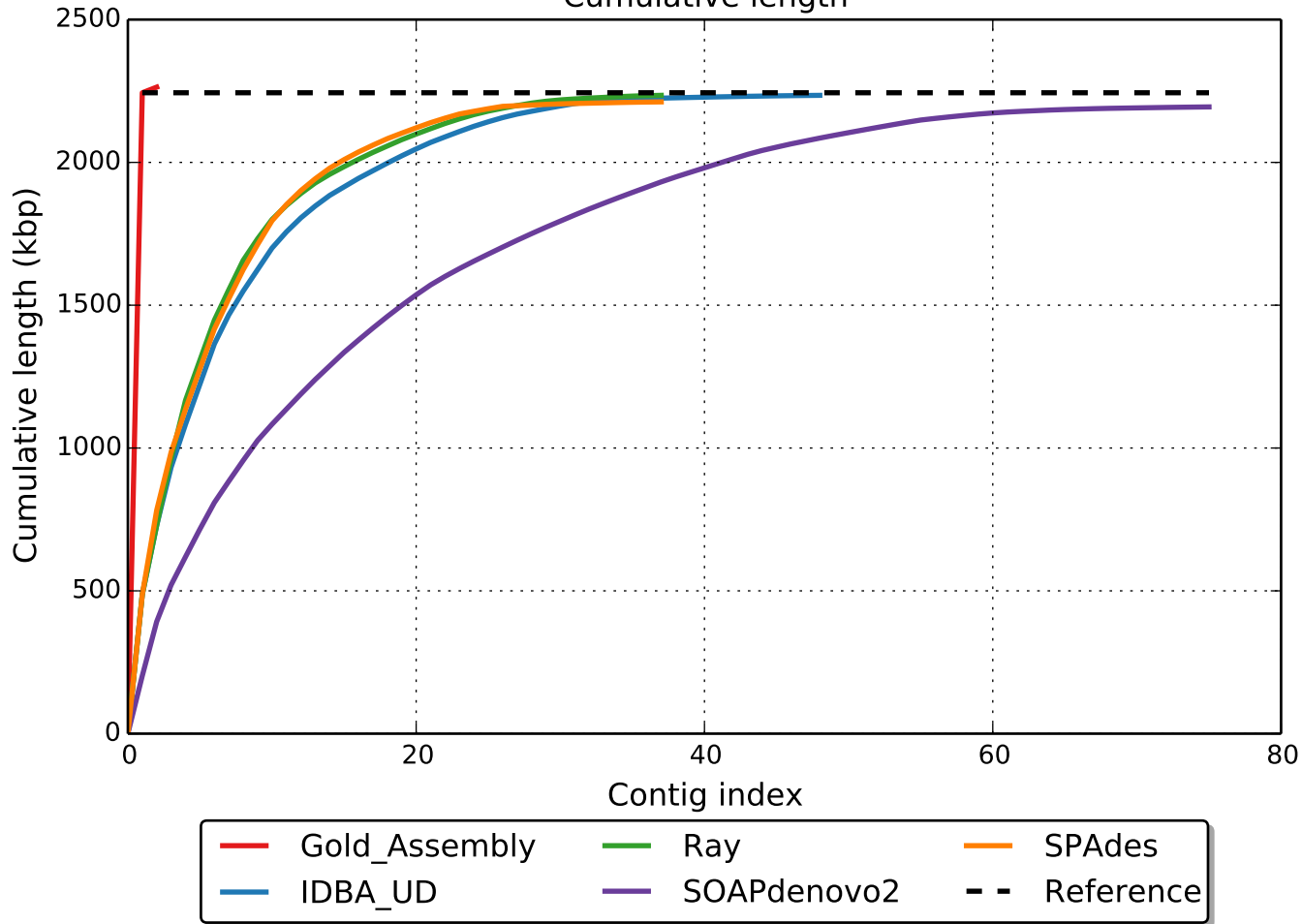
GC content

Misassemblies

Cumulative length (aligned contigs)

Legend:
- Gold_Assembly
- IDBA_UD
- Ray
- SOAPdenovo2
- SPAdes
- Reference

NAx

Contig length (kbp)

x

Gold_Assembly   Ray   SPAdes
IDBA_UD   SOAPdenovo2

Genome fraction, %

Legend: Gold_Assembly, IDBA_UD, Ray, SOAPdenovo2, SPAdes