Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	13	183	6	48	196
# contigs (>= 5000 bp)	2	37	0	0	36
# contigs (>= 10000 bp)	0	7	0	0	3
# contigs (>= 25000 bp)	0	0	0	0	0
# contigs (>= 50000 bp)	0	0	0	0	0
Total length (>= 1000 bp)	41605	678549	7517	77505	618372
Total length (>= 5000 bp)	13923	308565	0	0	257956
Total length (>= 10000 bp)	0	104061	0	0	39382
Total length (>= 25000 bp)	0	0	0	0	0
Total length (>= 50000 bp)	0	0	0	0	0
# contigs	18	215	112	120	246
Largest contig	8270	21474	1771	3792	14461
Total length	44872	701798	79394	129037	655371
Reference length	5532579	5532579	5532579	5532579	5532579
GC (%)	62.91	65.19	63.79	63.15	65.28
Reference GC (%)	64.39	64.39	64.39	64.39	64.39
N50	3797	4331	717	1155	3806
N75	2004	2613	597	790	2056
L50	5	47	45	37	53
L75	8	99	76	70	111
# misassemblies	0	19	0	0	4
# misassembled contigs	0	19	0	0	3
Misassembled contigs length	0	96428	0	0	19205
# local misassemblies	0	0	2	0	2
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 165 part	0 + 0 part	0 + 11 part	0 + 191 part
Unaligned length	0	111589	0	1299	88734
Genome fraction (%)	0.811	10.454	1.426	2.302	10.181
Duplication ratio	1.000	1.020	1.007	1.003	1.006
# N's per 100 kbp	0.00	0.00	84.39	158.87	31.74
# mismatches per 100 kbp	164.90	2832.26	497.00	748.96	2805.08
# indels per 100 kbp	20.06	47.72	1.27	39.25	47.93
Largest alignment	8270	18643	1764	3792	13857
NA50	3797	2745	717	1155	2806
NGA50	-	-	-	-	-
NA75	2004	1307	597	770	1250
LA50	5	70	45	37	67
LA75	8	160	76	71	155

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).
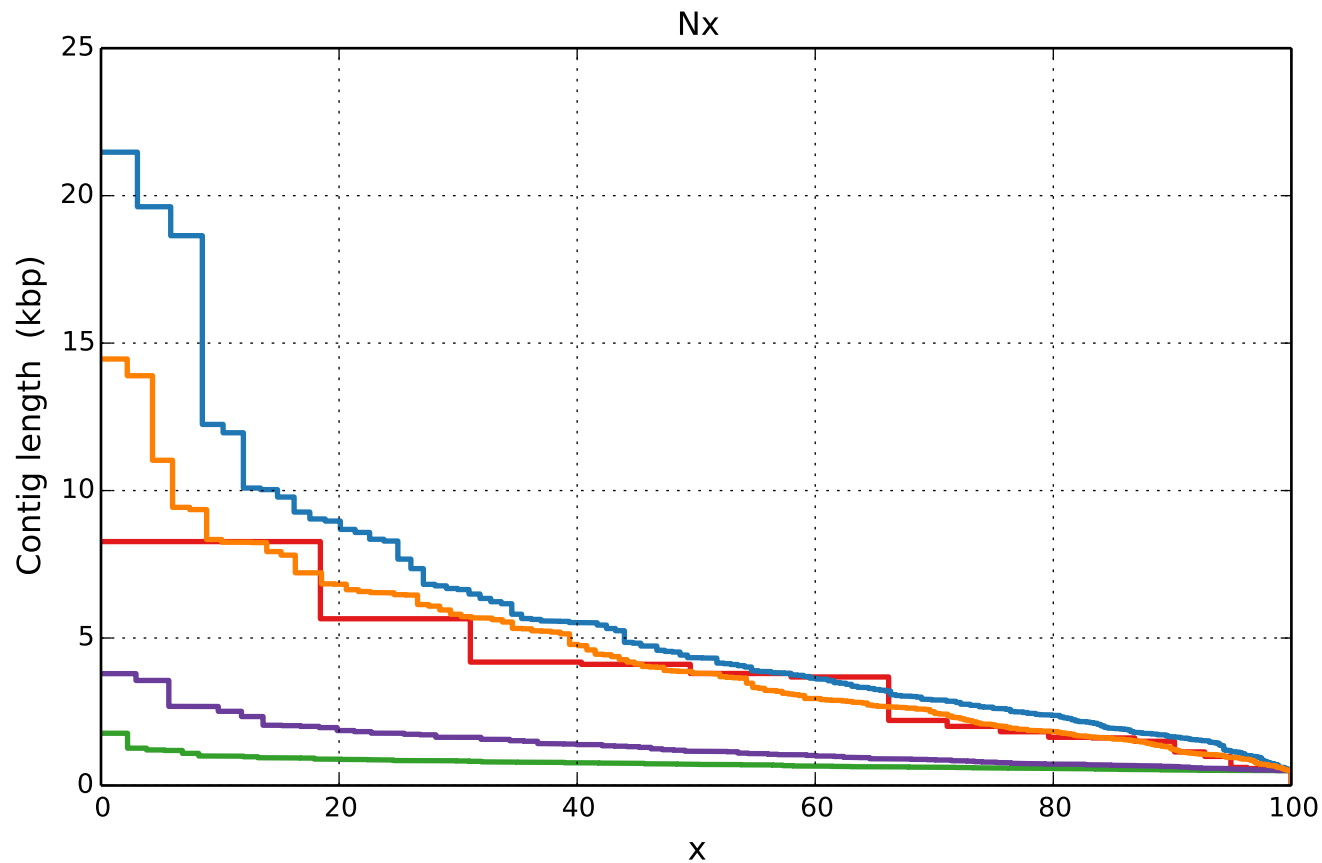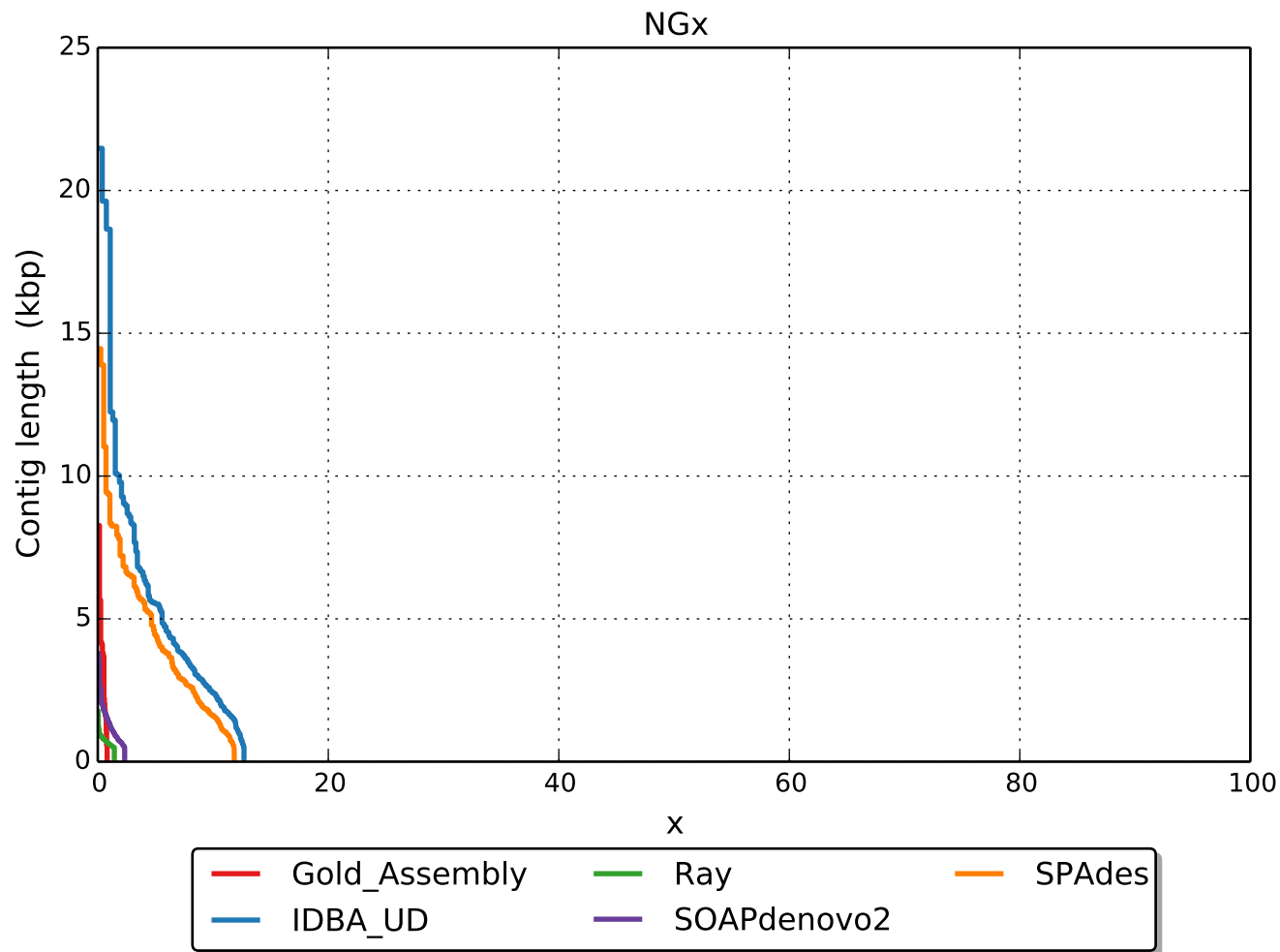
Misassemblies report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	19	0	0	4
# relocations	0	19	0	0	2
# translocations	0	0	0	0	2
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	51	0	1	33
# misassembled contigs	0	19	0	0	3
Misassembled contigs length	0	96428	0	0	19205
# local misassemblies	0	0	2	0	2
# structural variations	0	0	0	0	0
# mismatches	74	16381	392	954	15800
# indels	9	276	1	50	270
# short indels	9	257	0	24	237
# long indels	0	19	1	26	33
Indels length	9	504	6	359	816

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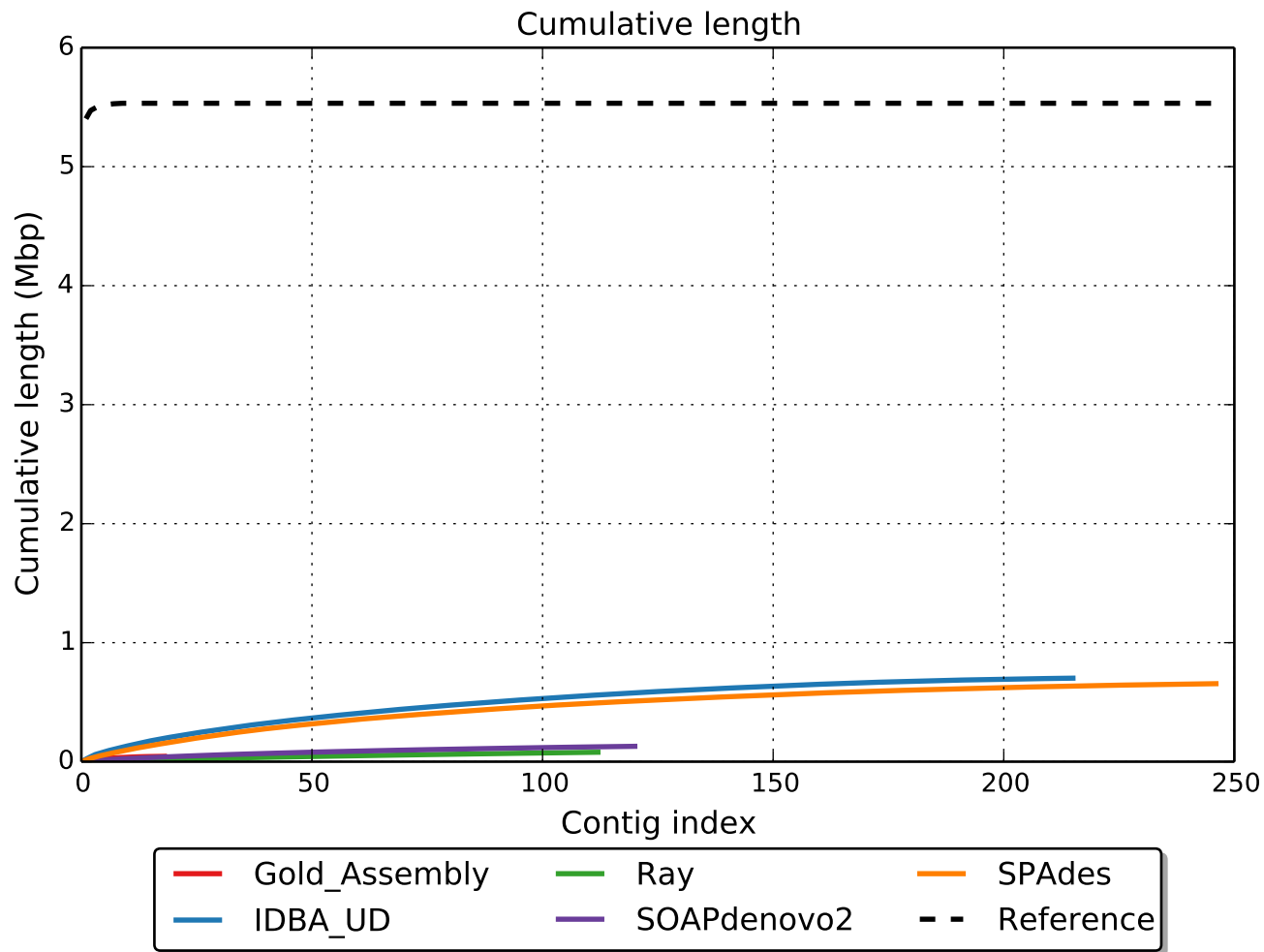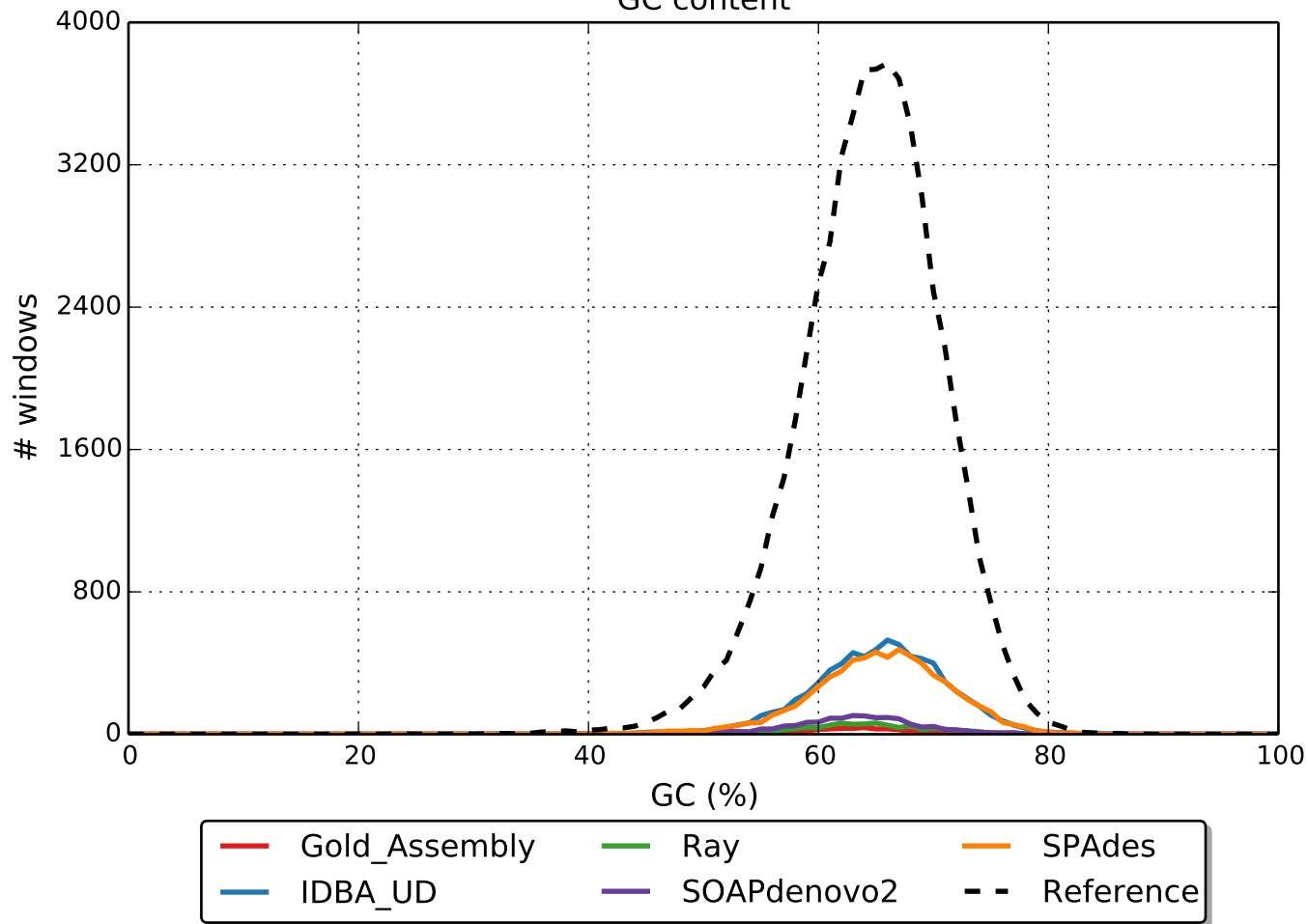(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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	165	0	11	191
# with misassembly	0	0	0	0	0
# both parts are significant	0	49	0	1	32
Partially unaligned length	0	111589	0	1299	88734
# N's	0	0	67	205	208

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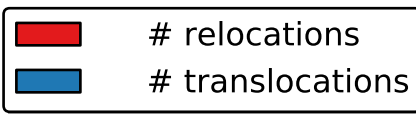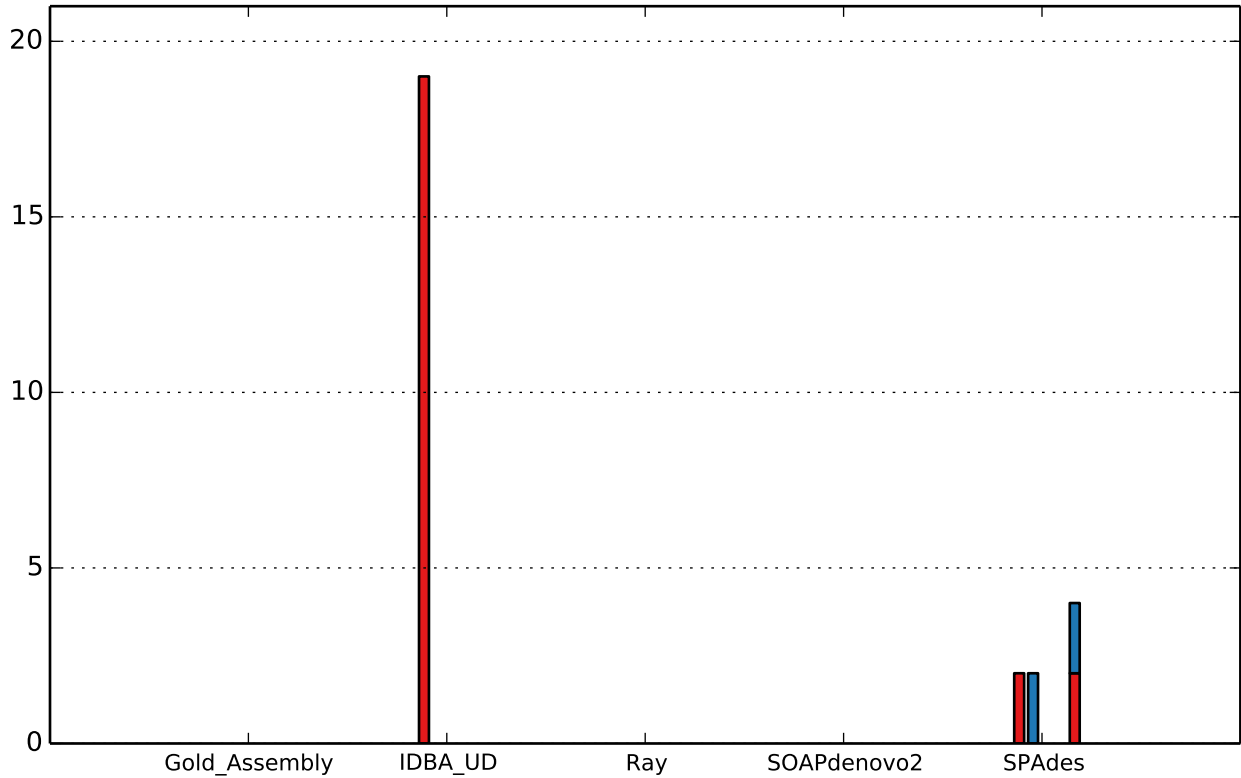(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
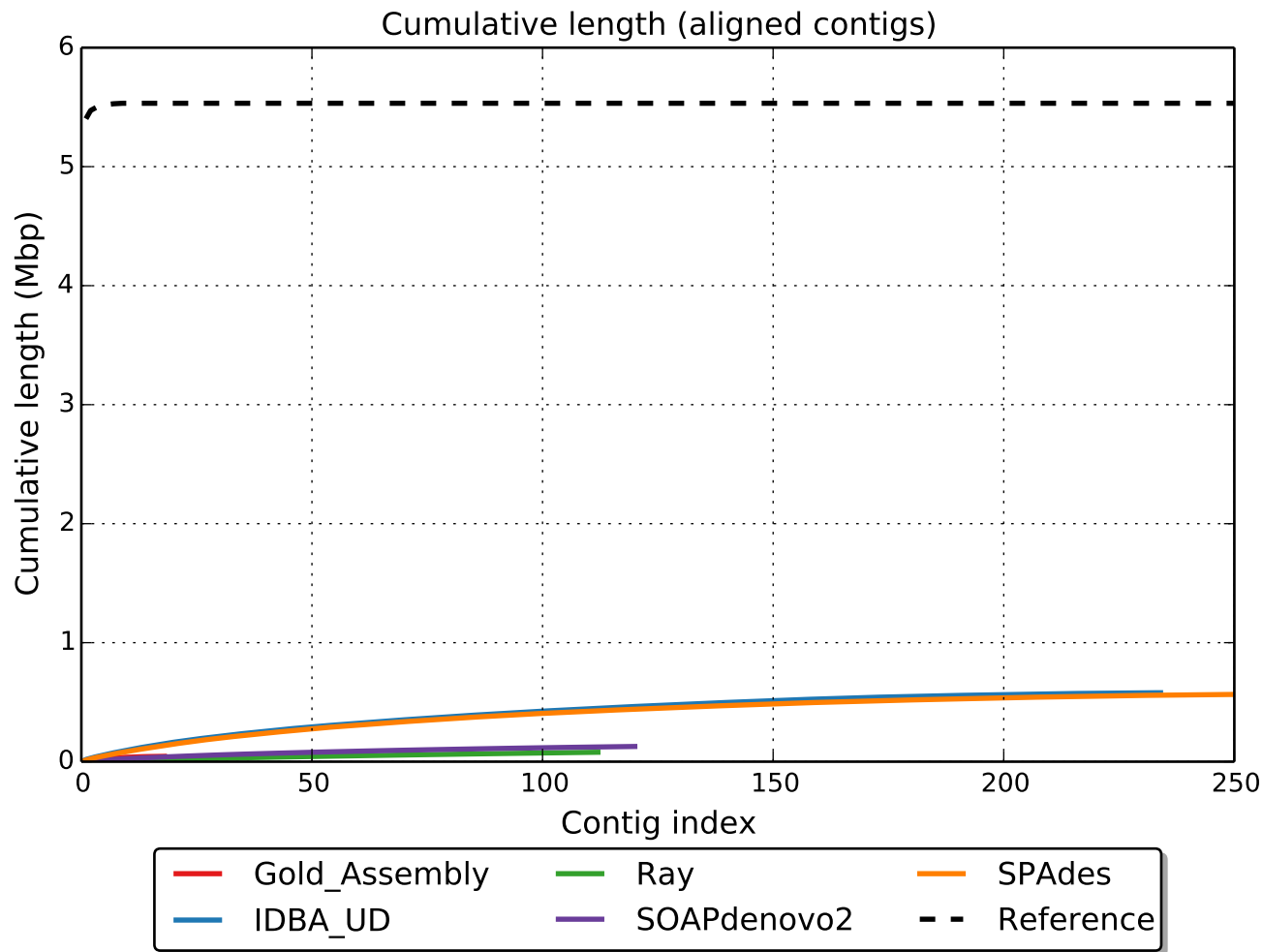
Nx

NGx

Contig length (kbp)

x

— Gold_Assembly   — Ray   — SPAdes

— IDBA_UD   — SOAPdenovo2

Cumulative length

GC content

Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

Gold_Assembly
IDBA_UD
Ray
SOAPdenovo2
SPAdes

NGAx

Genome fraction, %