Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	3	129	1238	681	179
# contigs (>= 5000 bp)	3	99	5	232	131
# contigs (>= 10000 bp)	3	80	0	71	95
# contigs (>= 25000 bp)	3	45	0	2	46
# contigs (>= 50000 bp)	2	24	0	0	14
Total length (>= 1000 bp)	3486242	3379597	2231388	3205107	3325382
Total length (>= 5000 bp)	3486242	3309077	27620	2066465	3190809
Total length (>= 10000 bp)	3486242	3174210	0	963359	2936340
Total length (>= 25000 bp)	3486242	2627249	0	58568	2146255
Total length (>= 50000 bp)	3446582	1893567	0	0	998172
# contigs	3	142	2167	784	197
Largest contig	2780101	129380	6009	31946	156247
Total length	3486242	3388753	2913946	3281683	3338536
Reference length	3446630	3446630	3446630	3446630	3446630
GC (%)	52.79	52.75	52.77	52.81	52.81
Reference GC (%)	52.87	52.87	52.87	52.87	52.87
N50	2780101	53507	1564	6453	35251
NG50	2780101	53507	1363	6228	33150
N75	2780101	27788	1035	3526	17835
NG75	2780101	26075	758	3163	16637
L50	1	21	619	157	30
LG50	1	21	801	170	32
L75	1	42	1193	326	63
LG75	1	44	1643	364	68
# misassemblies	0	4	0	3	7
# misassembled contigs	0	3	0	3	7
Misassembled contigs length	0	26795	0	22930	120057
# local misassemblies	0	1	33	1	8
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 1 part	0 + 6 part	0 + 4 part	0 + 10 part	0 + 9 part
Unaligned length	38532	43417	3715	1081	5865
Genome fraction (%)	99.999	96.870	80.917	94.919	96.466
Duplication ratio	1.000	1.002	1.044	1.003	1.002
# N's per 100 kbp	0.00	0.00	45.64	27.36	43.88
# mismatches per 100 kbp	0.00	10.39	5.13	58.84	75.37
# indels per 100 kbp	0.00	0.42	0.18	10.48	1.08
Largest alignment	2780101	129379	6009	31946	156247
NA50	2780101	53507	1559	6453	34414
NGA50	2780101	53507	1360	6228	33076
NA75	2780101	27788	1030	3526	17016
NGA75	2780101	25854	755	3163	16479
LA50	1	21	620	157	30
LGA50	1	21	803	170	32
LA75	1	42	1196	326	64
LGA75	1	44	1647	364	69

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).
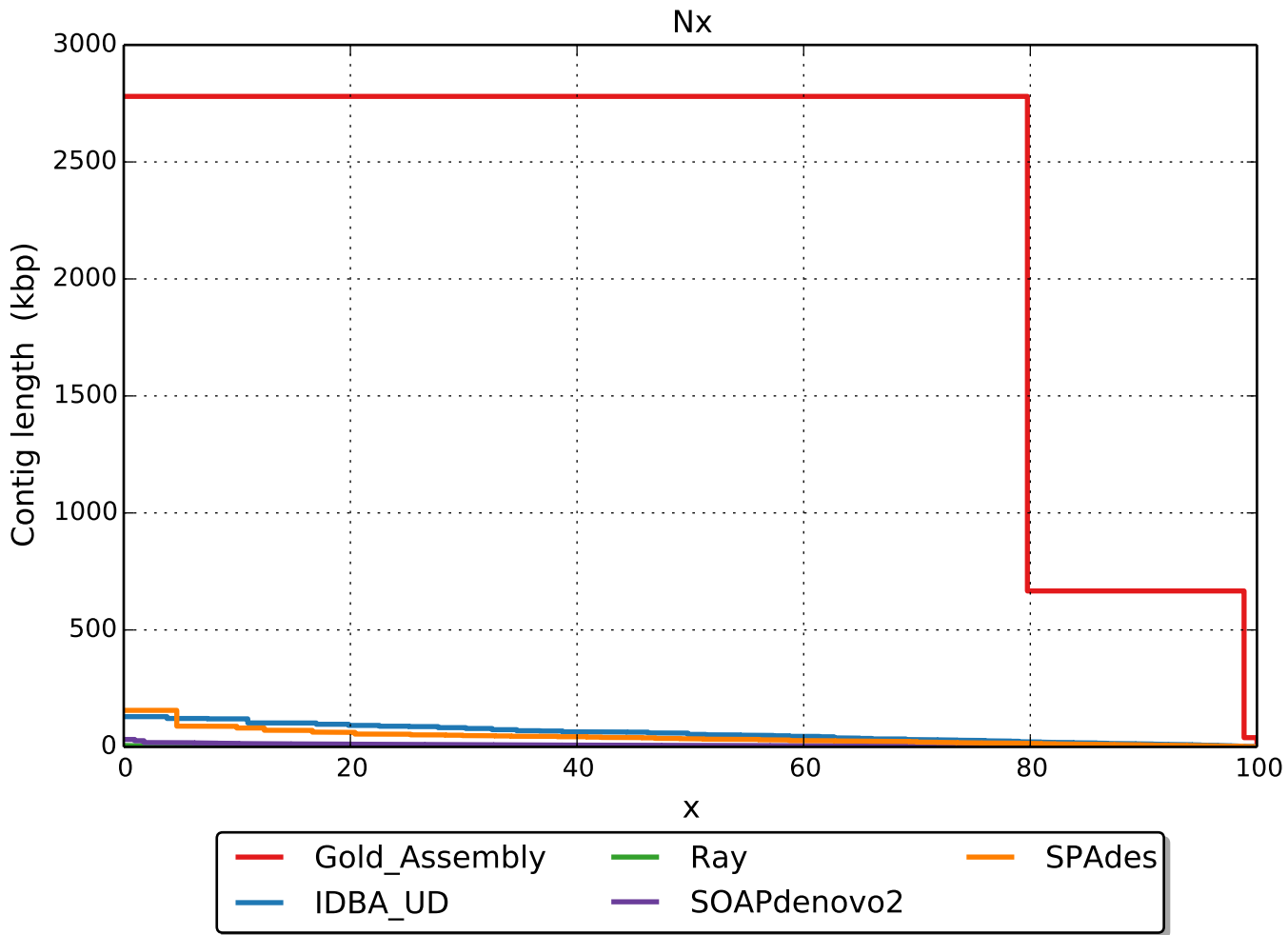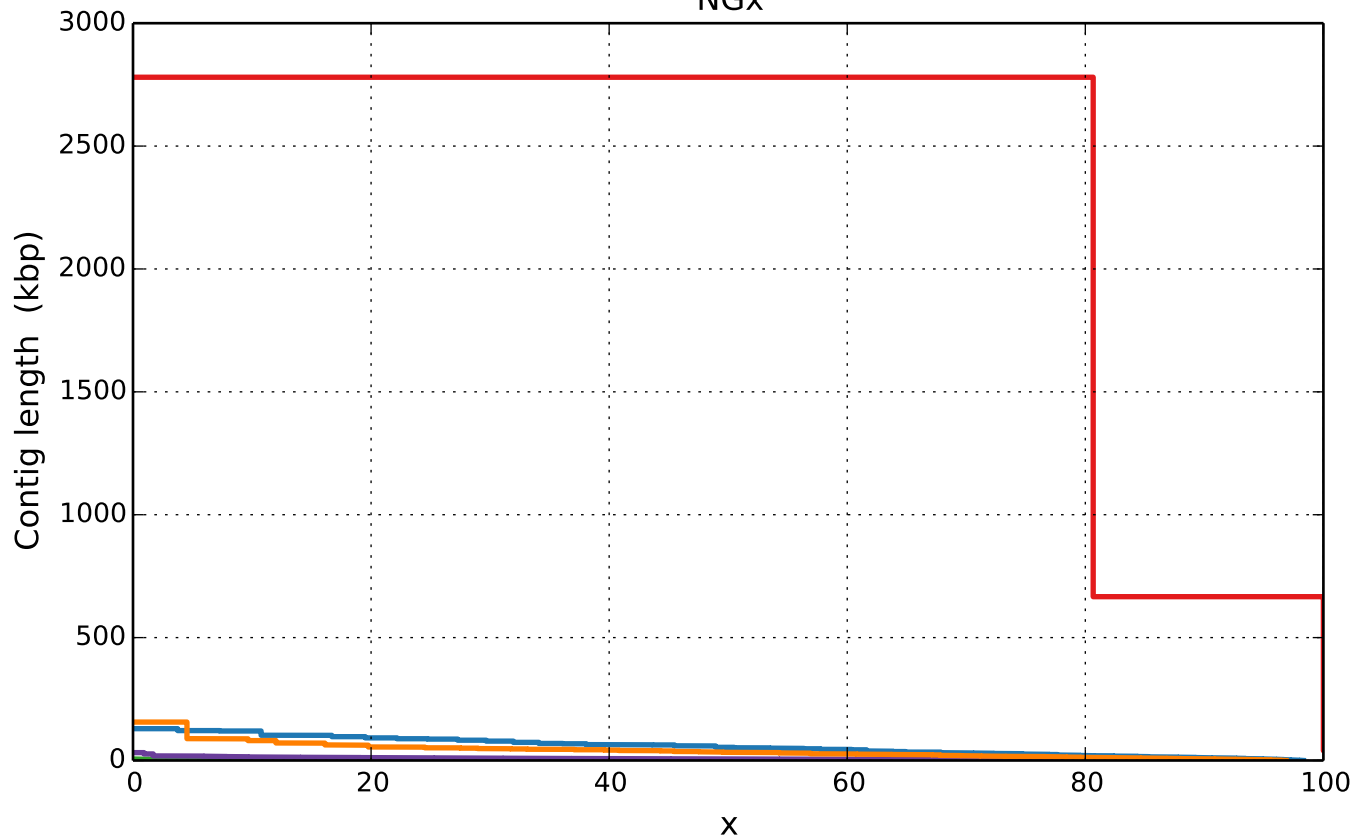
Misassemblies report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	4	0	3	7
# relocations	0	4	0	3	7
# translocations	0	0	0	0	0
# inversions	0	0	0	0	0
# possibly misassembled contigs	1	4	0	0	5
# misassembled contigs	0	3	0	3	7
Misassembled contigs length	0	26795	0	22930	120057
# local misassemblies	0	1	33	1	8
# structural variations	0	0	0	0	0
# mismatches	0	347	143	1925	2506
# indels	0	14	5	343	36
# short indels	0	9	5	149	34
# long indels	0	5	0	194	2
Indels length	0	116	10	2717	106

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).
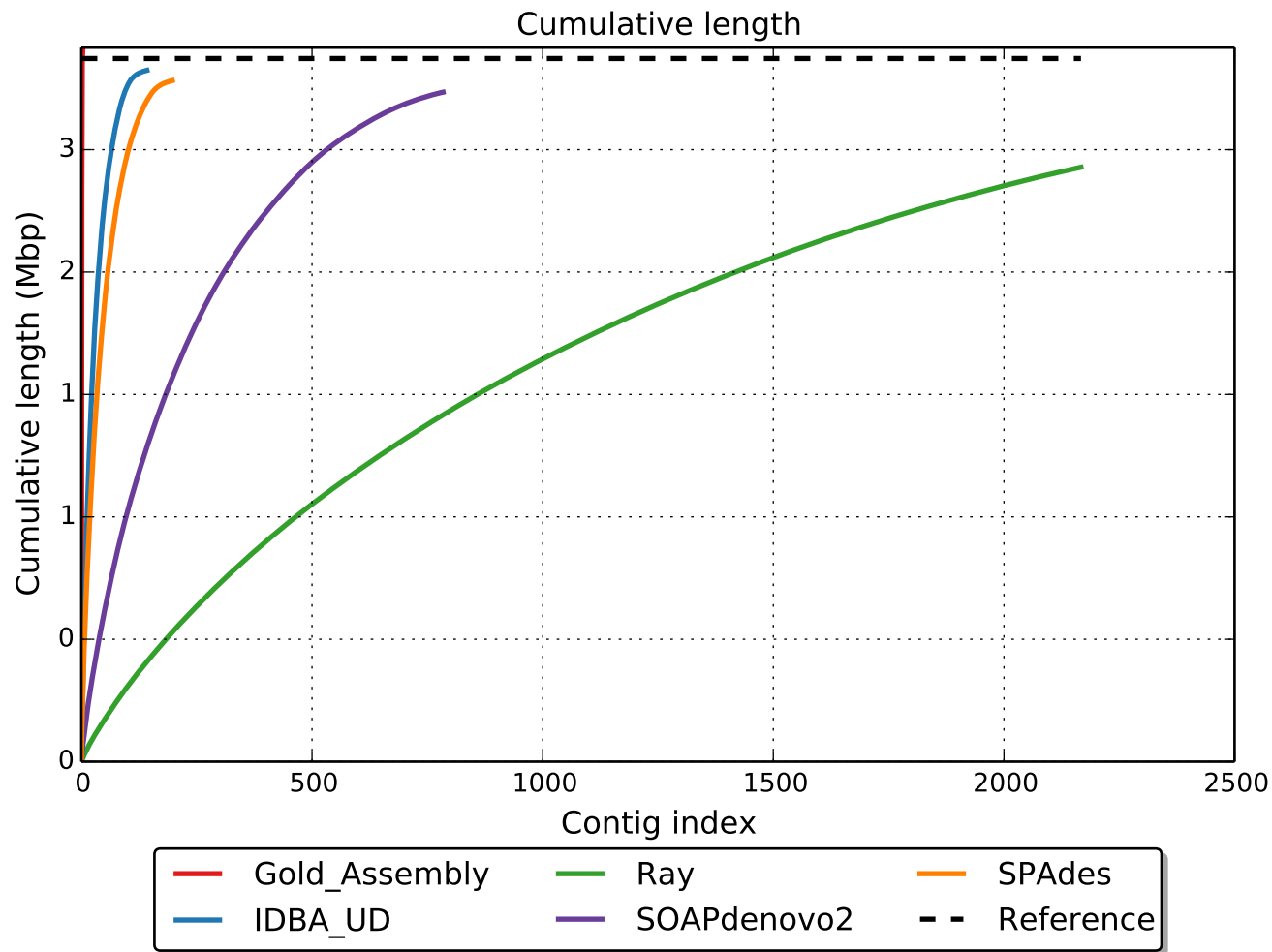
Unaligned report

	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	6	4	10	9
# with misassembly	1	1	0	0	0
# both parts are significant	1	4	0	0	3
Partially unaligned length	38532	43417	3715	1081	5865
# N's	0	0	1330	898	1465

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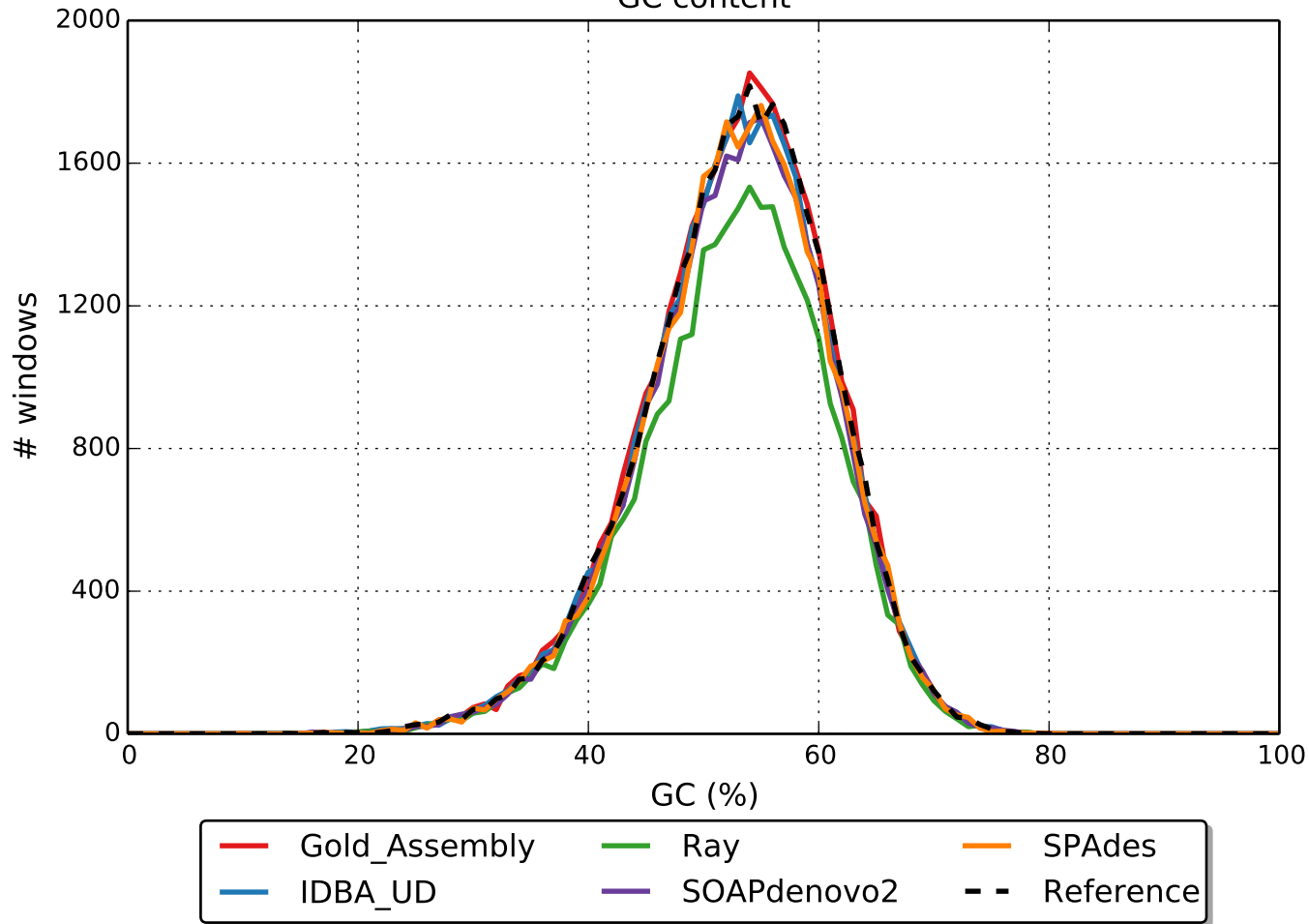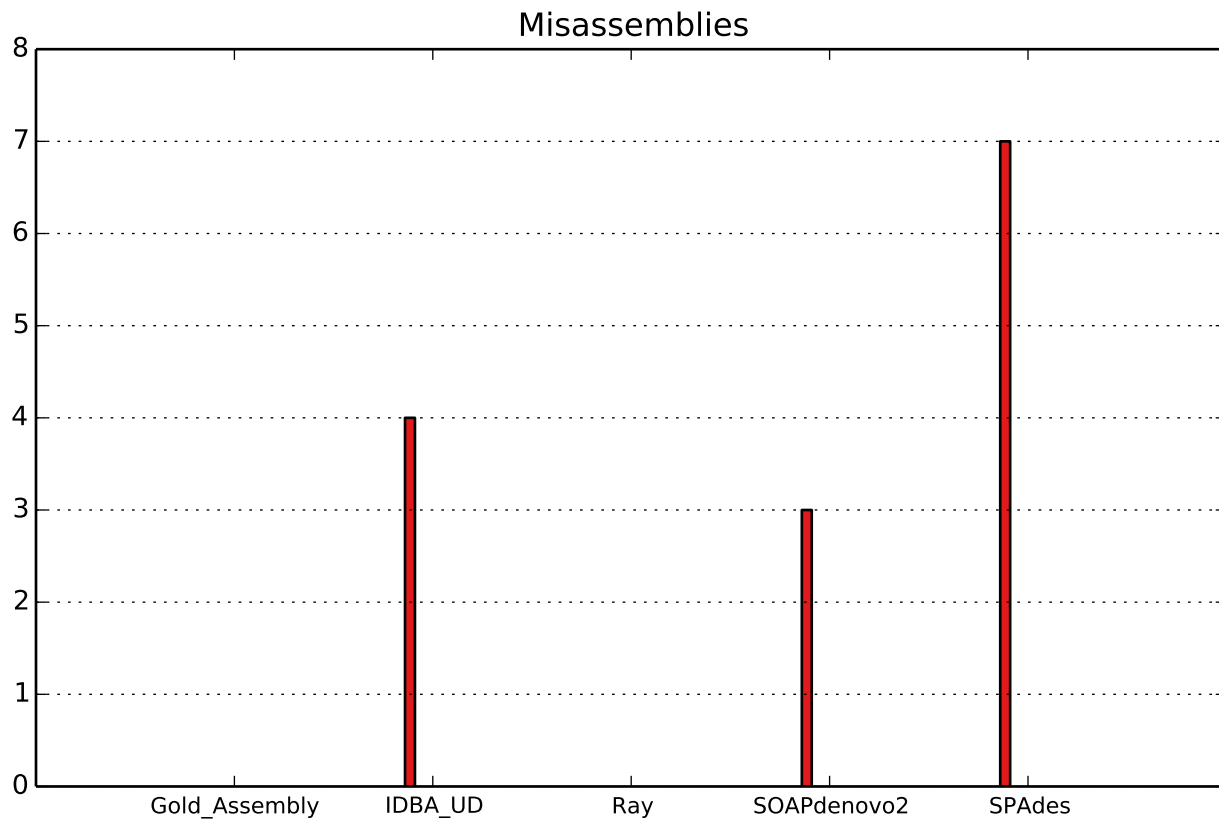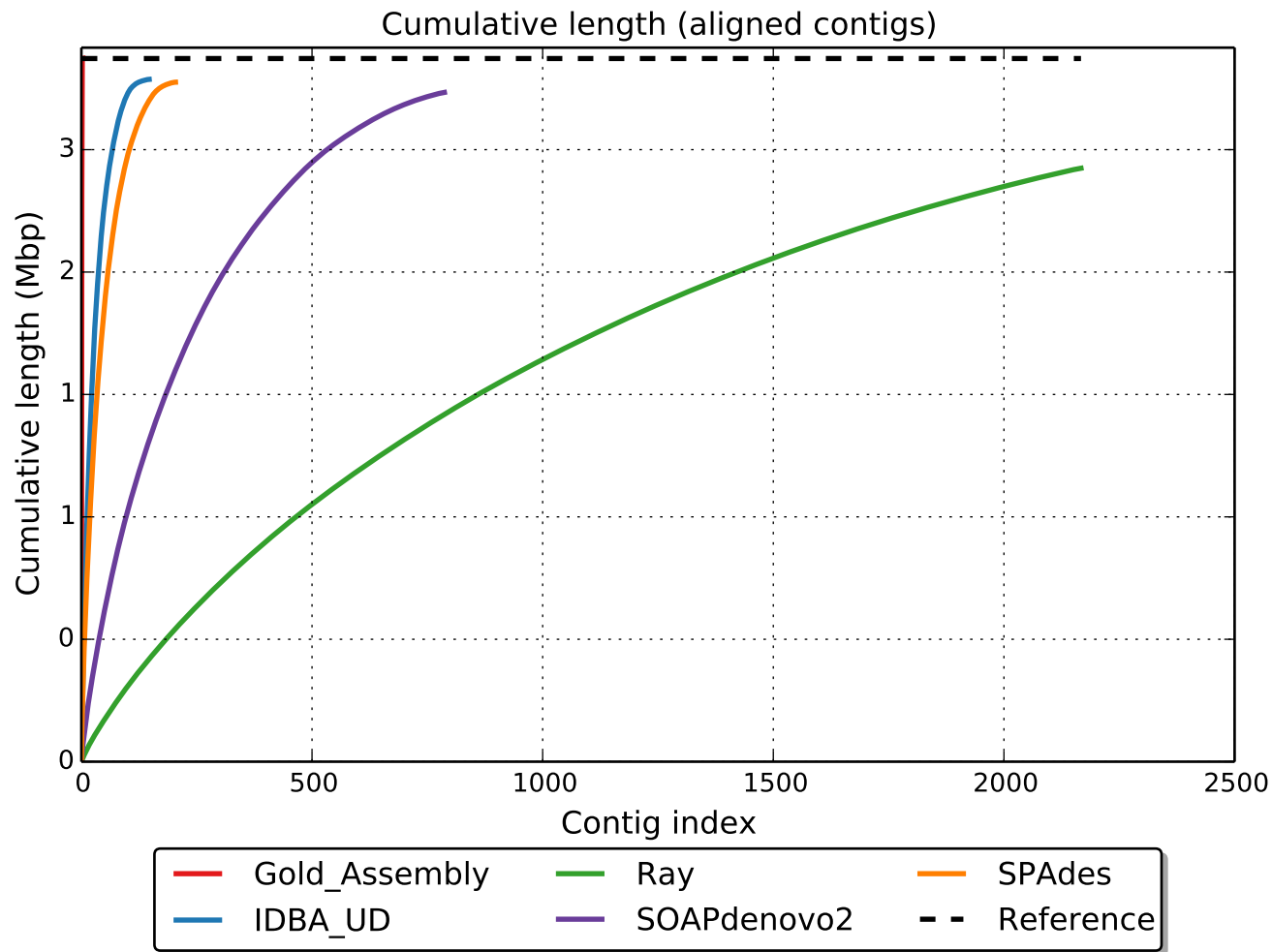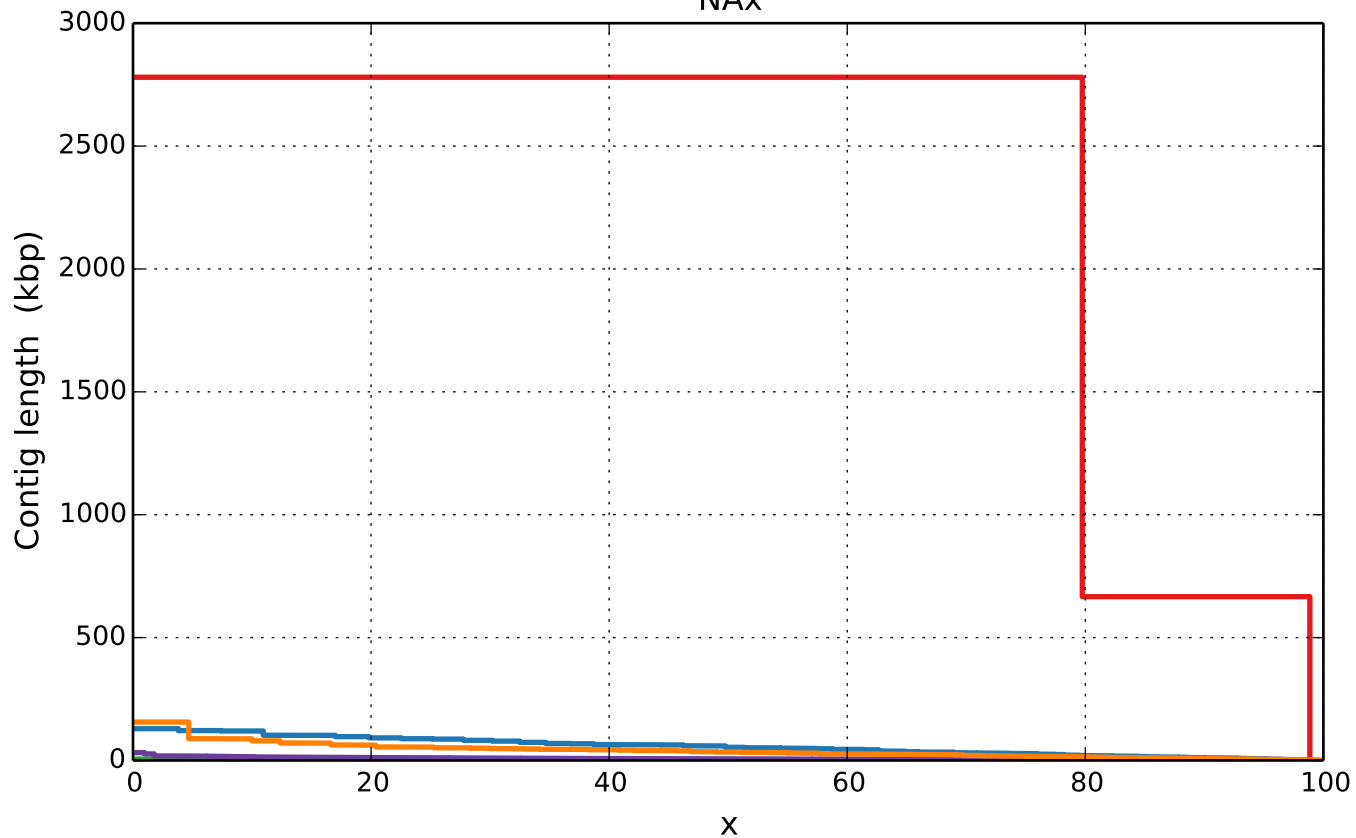(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

NGx

Contig length (kbp) vs x

Legend: Gold_Assembly, Ray, SPAdes, IDBA_UD, SOAPdenovo2

Cumulative length

Gold_Assembly	Ray	SPAdes
IDBA_UD	SOAPdenovo2	Reference

GC content

Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

- Gold_Assembly
- IDBA_UD
- Ray
- SOAPdenovo2
- SPAdes

Genome fraction, %