Report

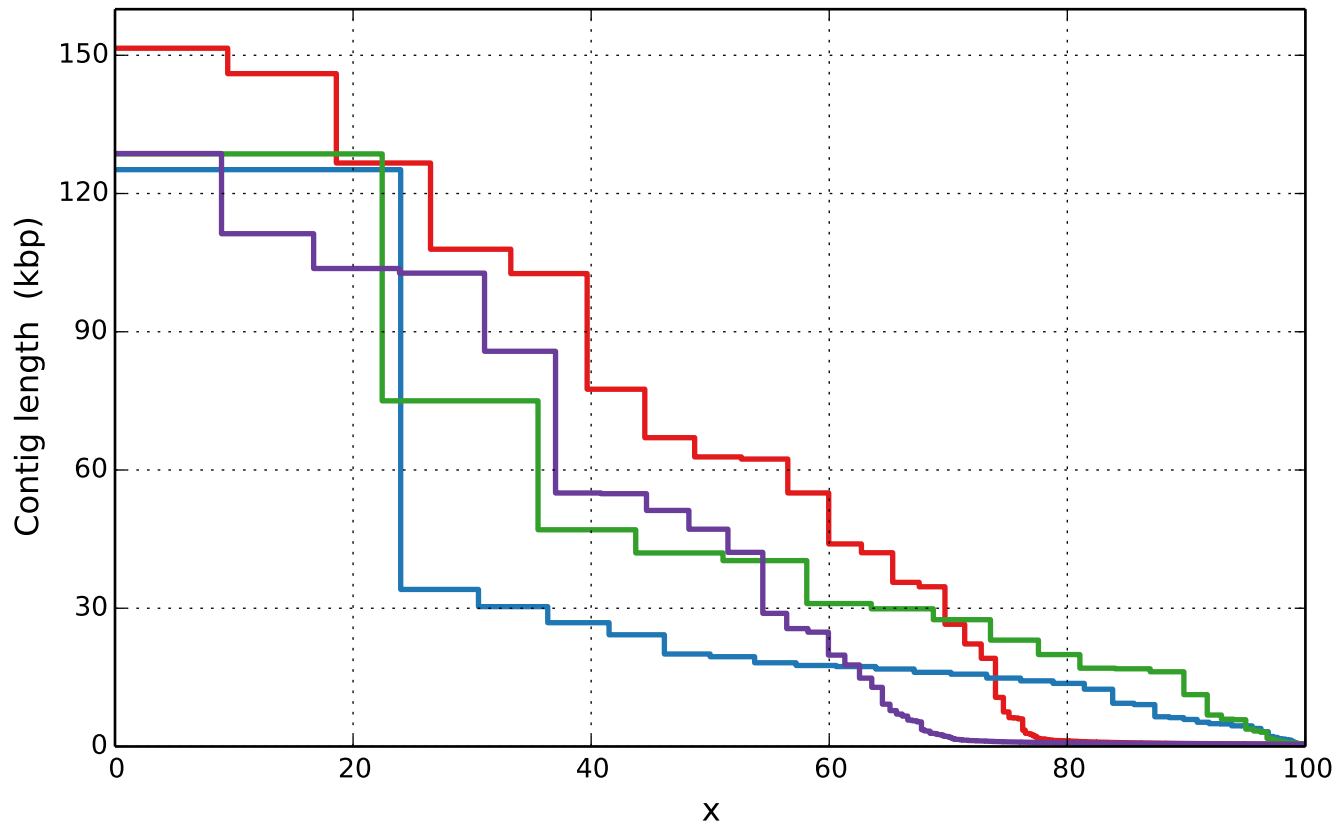|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	86	36	25	95
# contigs (>= 5000 bp)	22	23	17	24
# contigs (>= 10000 bp)	18	17	14	17
# contigs (>= 25000 bp)	15	4	8	12
# contigs (>= 50000 bp)	10	1	2	8
Total length (>= 1000 bp)	1310567	516591	561609	1080186
Total length (>= 5000 bp)	1220221	479398	544245	974211
Total length (>= 10000 bp)	1194293	437117	525708	926990
Total length (>= 25000 bp)	1142266	216464	421374	837002
Total length (>= 50000 bp)	959475	125177	203608	693254
# contigs	537	44	41	649
Largest contig	151531	125177	128598	128675
Total length	1600274	521557	572944	1437971
Reference length	3127600	3127600	3127600	3127600
GC (%)	40.64	44.56	41.29	39.43
Reference GC (%)	37.46	37.46	37.46	37.46
N50	62839	19479	41998	47152
NG50	528	-	-	-
N75	7500	14844	23079	1000
L50	8	7	4	9
LG50	466	-	-	-
L75	19	14	9	94
# misassemblies	17	1	1	23
# misassembled contigs	16	1	1	22
Misassembled contigs length	15004	507	11250	20306
# local misassemblies	5	1	1	4
# structural variations	1	0	0	1
# unaligned contigs	0 + 136 part	0 + 36 part	0 + 26 part	0 + 174 part
Unaligned length	1238684	475781	534940	1012214
Genome fraction (%)	11.356	1.217	1.138	13.501
Duplication ratio	1.018	1.203	1.068	1.008
# N's per 100 kbp	0.00	761.76	961.87	14.81
# mismatches per 100 kbp	1268.66	1618.62	1093.40	1348.27
# indels per 100 kbp	38.57	57.81	75.89	43.10
Largest alignment	10649	15763	10828	7785
NGA50	-	-	-	-

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

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	17	1	1	23
# relocations	5	0	0	8
# translocations	9	1	1	15
# inversions	3	0	0	0
# possibly misassembled contigs	12	8	7	18
# misassembled contigs	16	1	1	22
Misassembled contigs length	15004	507	11250	20306
# local misassemblies	5	1	1	4
# structural variations	1	0	0	1
# mismatches	4506	616	389	5693
# indels	137	22	27	182
# short indels	129	21	11	171
# long indels	8	1	16	11
Indels length	262	35	317	375

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).
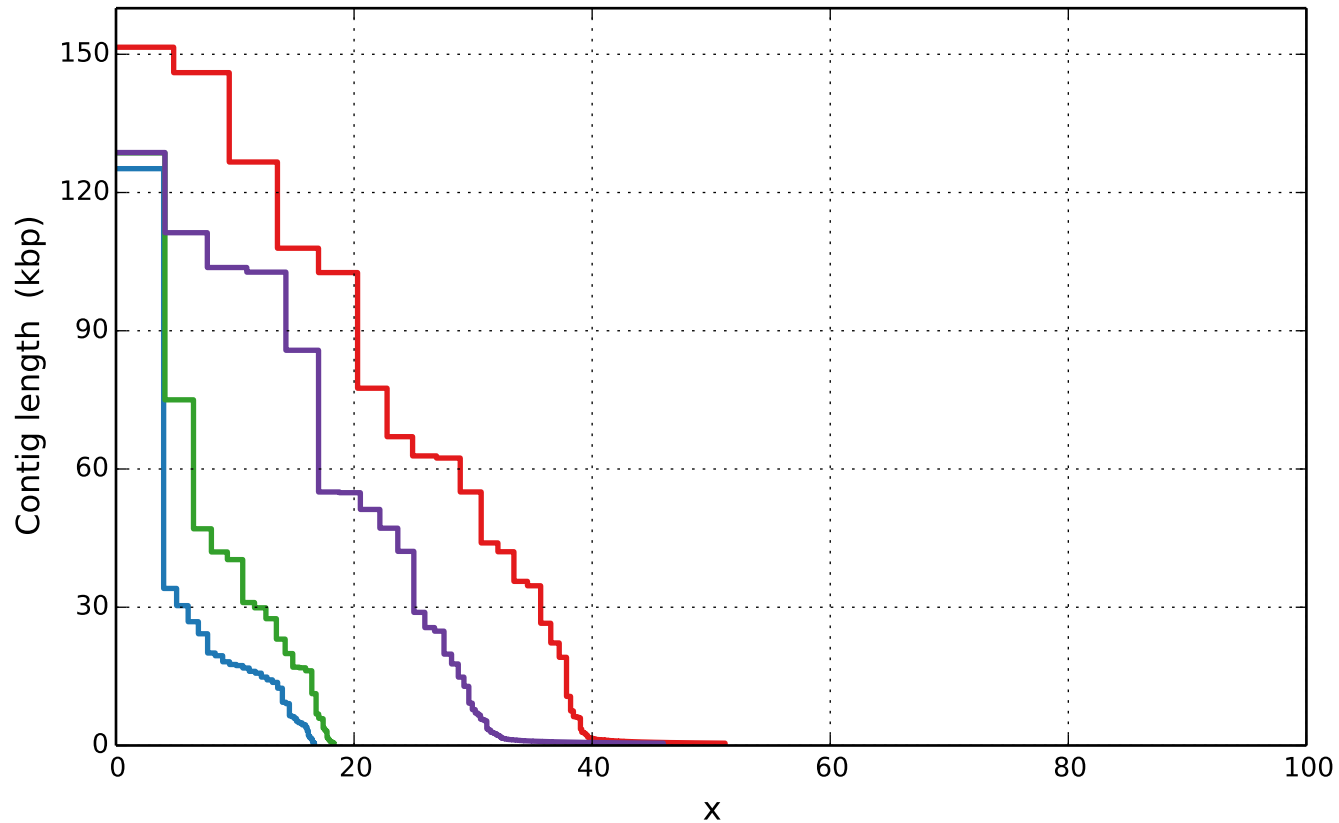
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	136	36	26	174
# with misassembly	10	6	3	9
# both parts are significant	12	8	6	17
Partially unaligned length	1238684	475781	534940	1012214
# N's	0	3973	5511	213

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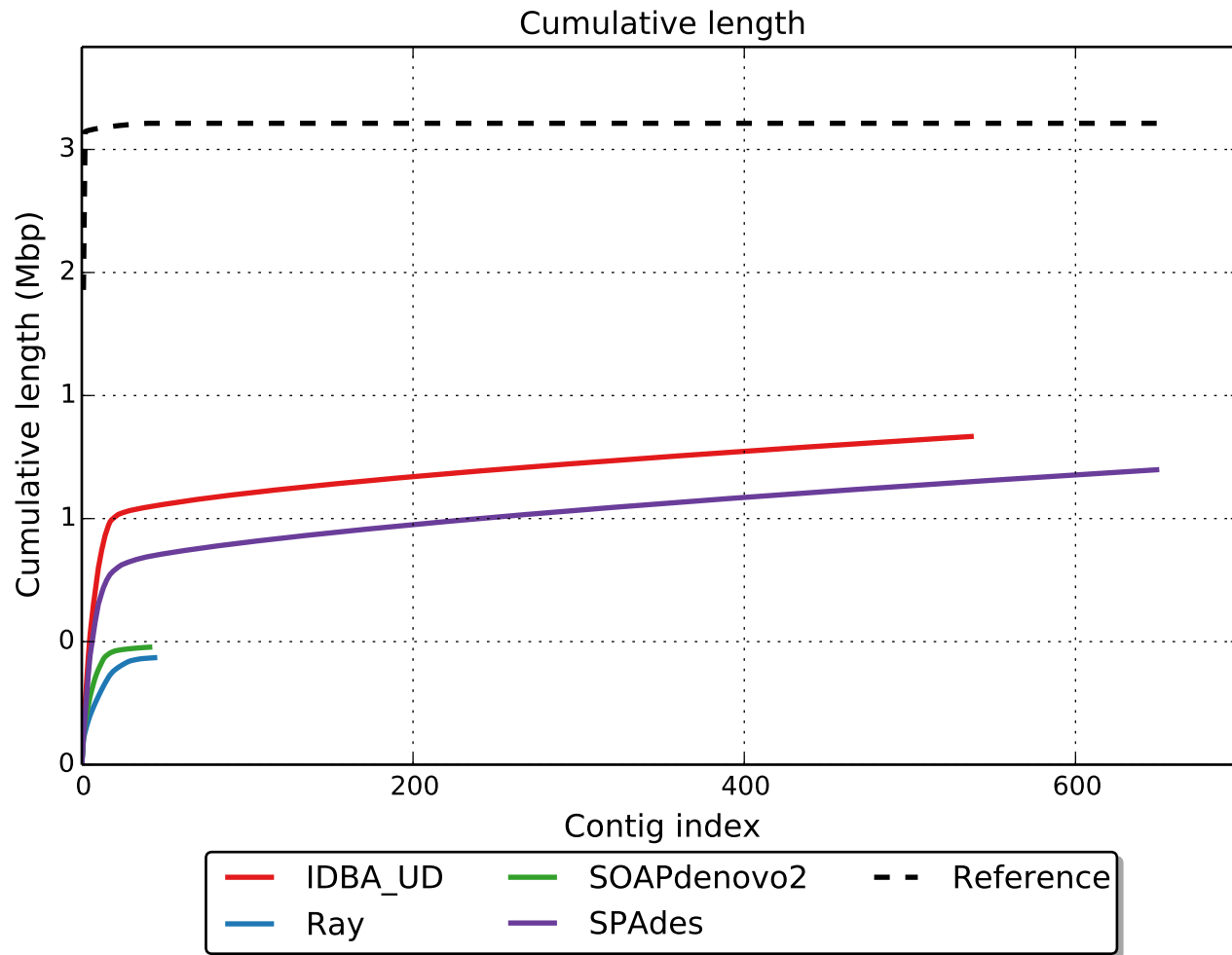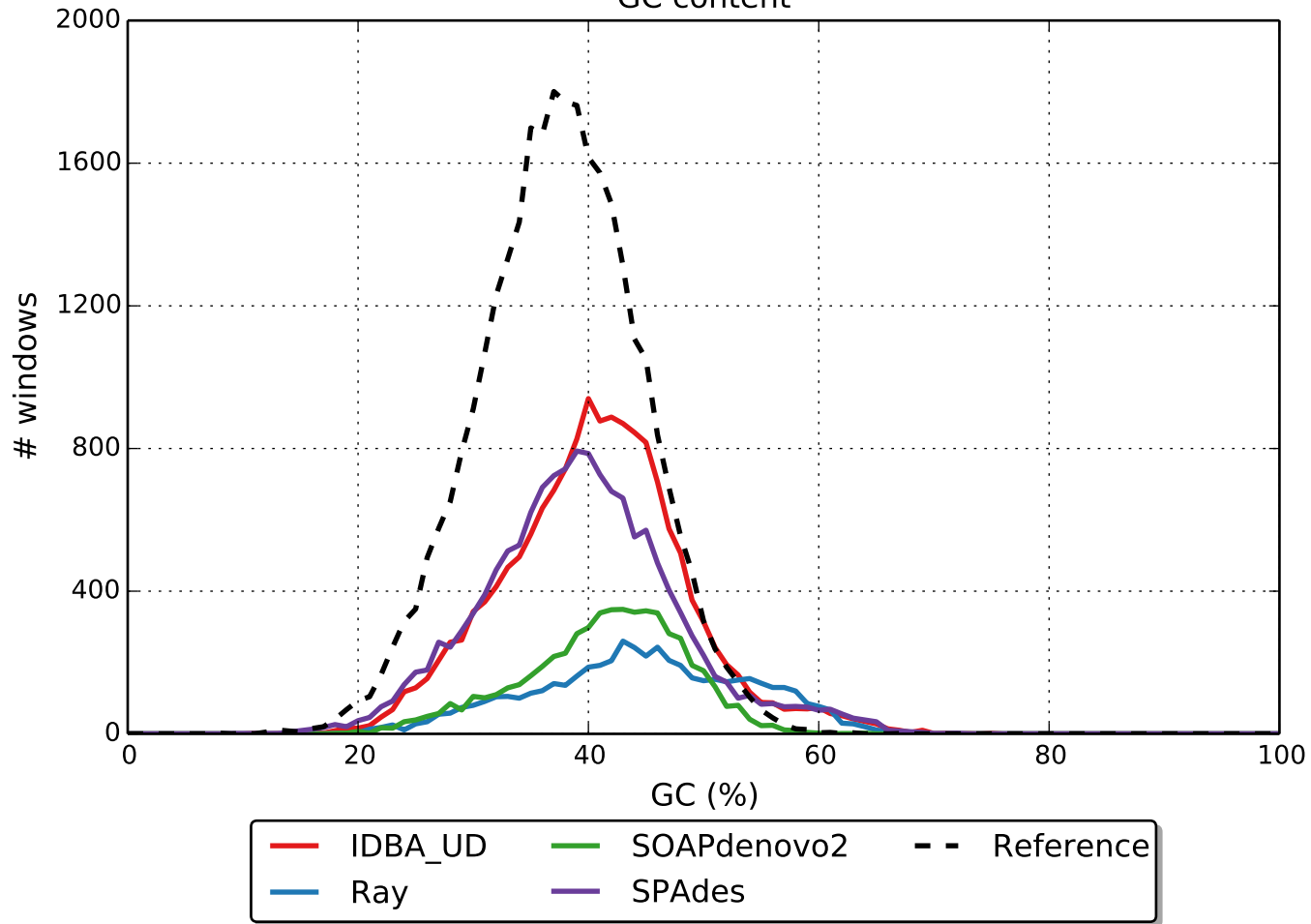(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

Misassemblies

Cumulative length (aligned contigs)

Genome fraction, %

IDBA_UD	SOAPdenovo2	SPAdes
Ray		