Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	381	134	379	337
# contigs (>= 5000 bp)	72	51	23	93
# contigs (>= 10000 bp)	36	33	0	55
# contigs (>= 25000 bp)	12	4	0	22
# contigs (>= 50000 bp)	2	2	0	10
Total length (>= 1000 bp)	1893837	924406	780382	2354673
Total length (>= 5000 bp)	1240366	745922	151049	1832682
Total length (>= 10000 bp)	992986	621398	0	1559985
Total length (>= 25000 bp)	581314	170000	0	1042610
Total length (>= 50000 bp)	217961	108204	0	637731
# contigs	639	220	989	523
Largest contig	125793	54754	9696	126159
Total length	2085384	982740	1207331	2486305
Reference length	6060928	6060928	6060928	6060928
GC (%)	42.49	41.86	42.11	42.76
Reference GC (%)	42.20	42.20	42.20	42.20
N50	8618	13246	1368	19052
N75	2439	5408	829	4695
L50	42	23	229	32
L75	168	50	517	100
# misassemblies	18	11	7	30
# misassembled contigs	14	8	7	19
Misassembled contigs length	117364	151605	14017	454680
# local misassemblies	10	94	657	20
# structural variations	4	4	4	5
# unaligned contigs	0 + 121 part	0 + 40 part	0 + 95 part	0 + 174 part
Unaligned length	667599	174458	63601	633695
Genome fraction (%)	22.920	12.284	18.095	27.906
Duplication ratio	1.021	1.086	1.043	1.095
# N's per 100 kbp	140.89	1780.12	2715.16	398.46
# mismatches per 100 kbp	1022.12	2041.27	919.45	1696.83
# indels per 100 kbp	41.46	43.25	16.23	58.77
Largest alignment	37090	29014	9696	50956
NA50	1614	5109	1181	3123
NGA50	-	-	-	-
NA75	-	593	669	-
LA50	226	42	264	123
LA75	-	197	610	-

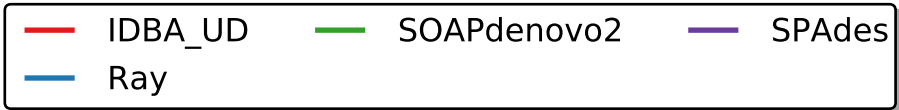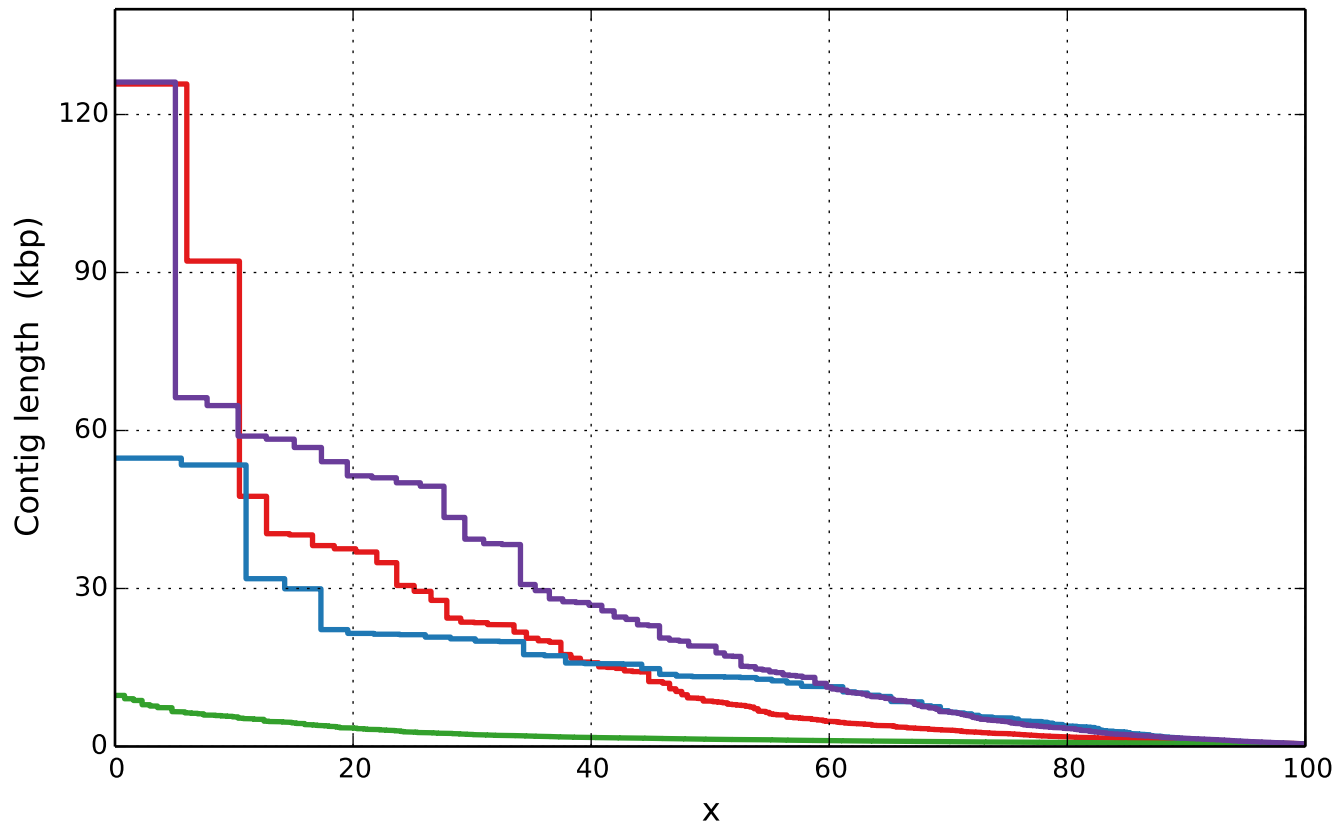All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	18	11	7	30
# relocations	6	5	2	19
# translocations	12	6	3	10
# inversions	0	0	2	1
# possibly misassembled contigs	40	33	16	70
# misassembled contigs	14	8	7	19
Misassembled contigs length	117364	151605	14017	454680
# local misassemblies	10	94	657	20
# structural variations	4	4	4	5
# mismatches	14199	15198	10084	28700
# indels	576	322	178	994
# short indels	522	302	166	865
# long indels	54	20	12	129
Indels length	1433	651	428	2958

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).
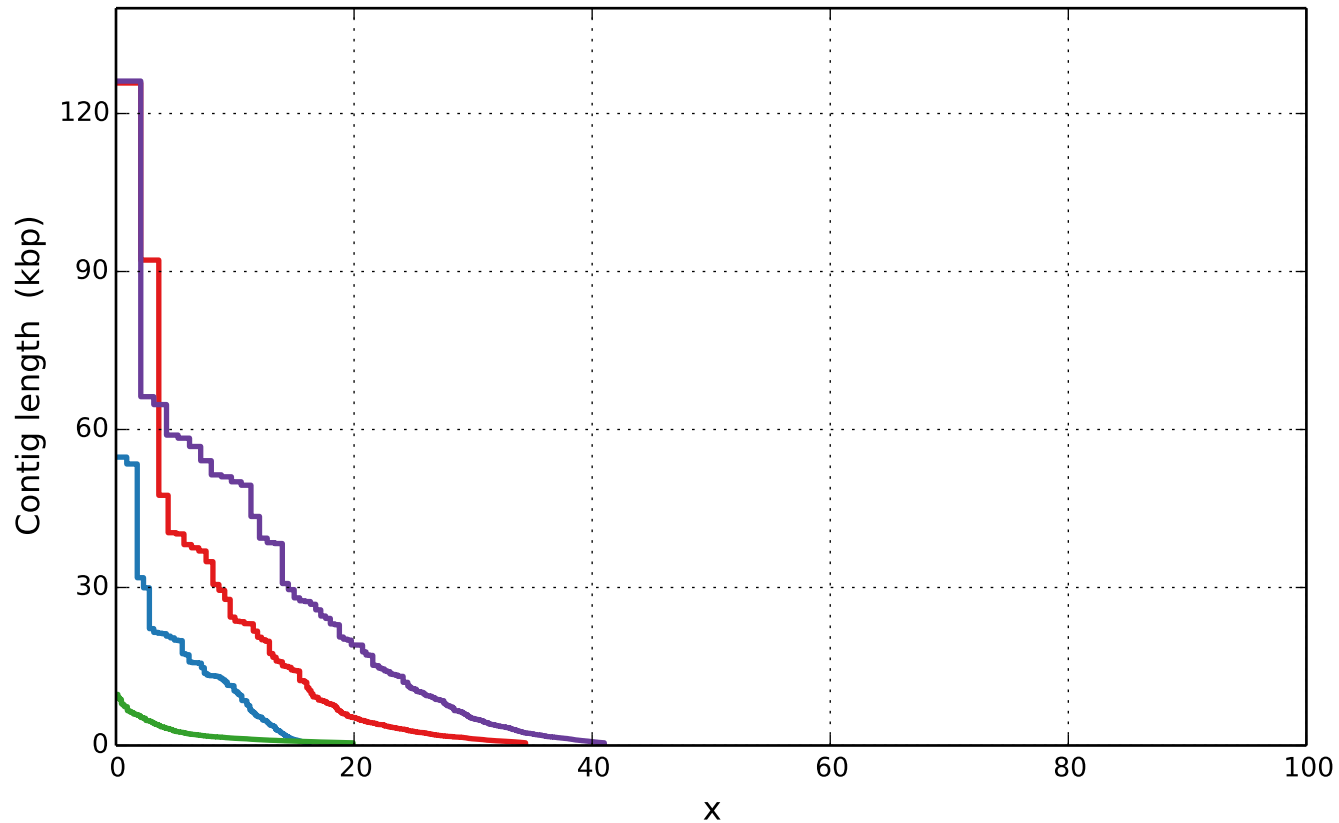
Unaligned report

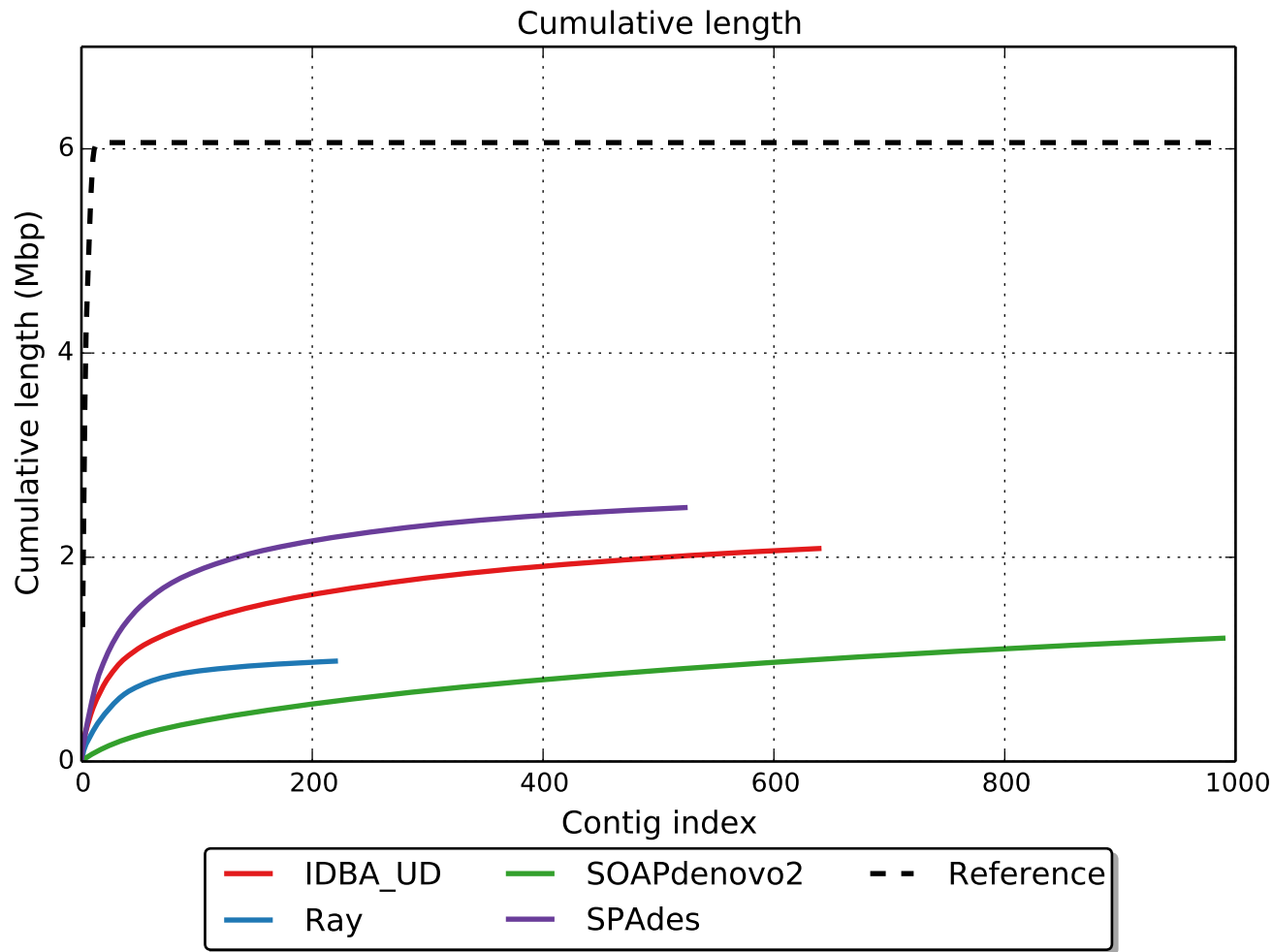|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	121	40	95	174
# with misassembly	11	7	12	6
# both parts are significant	33	18	10	56
Partially unaligned length	667599	174458	63601	633695
# N's	2938	17494	32781	9907

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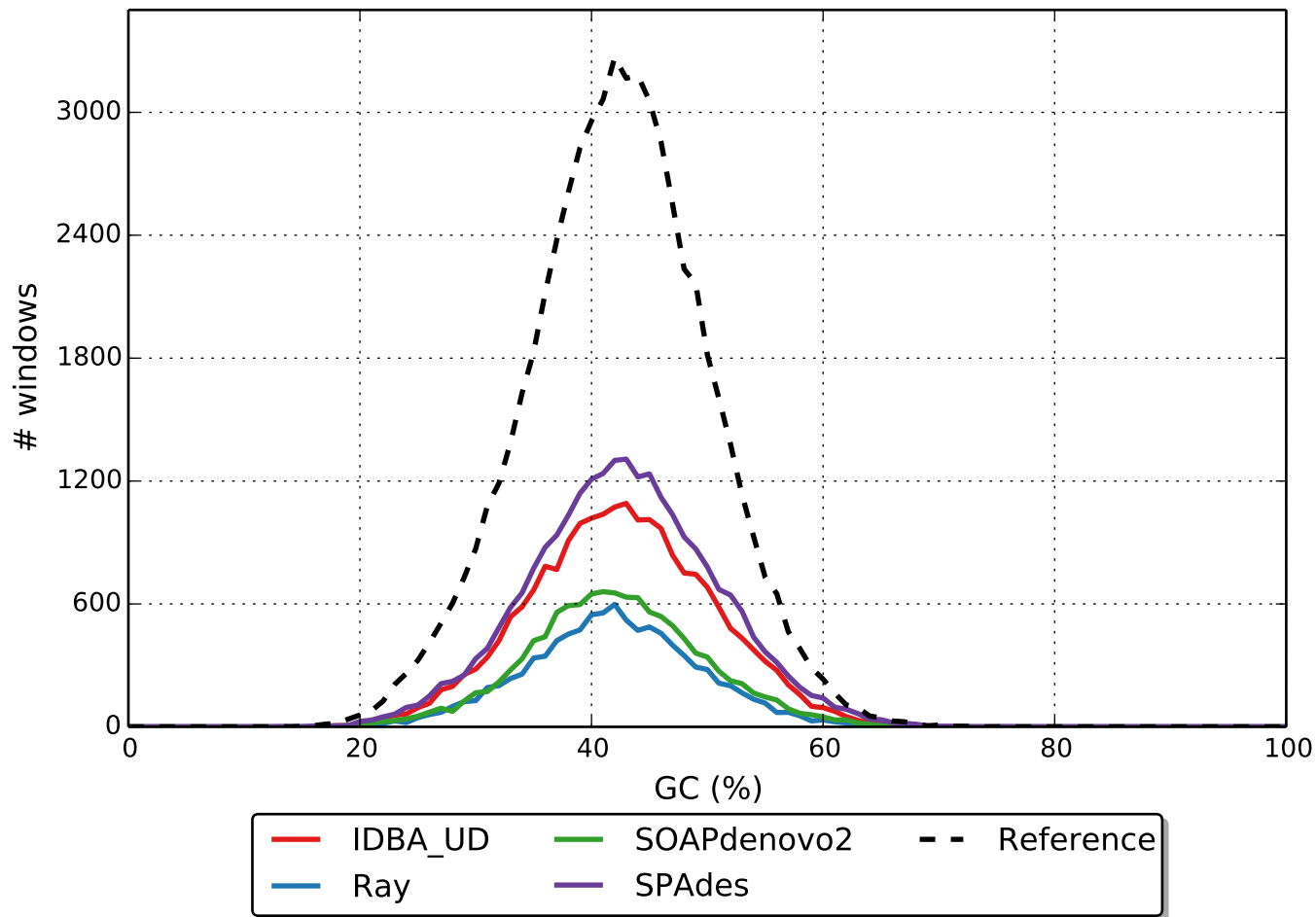(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

Cumulative length (aligned contigs)

Genome fraction, %

Legend: IDBA_UD, Ray, SOAPdenovo2, SPAdes