Report

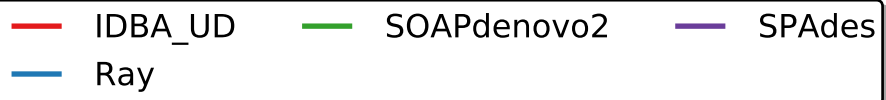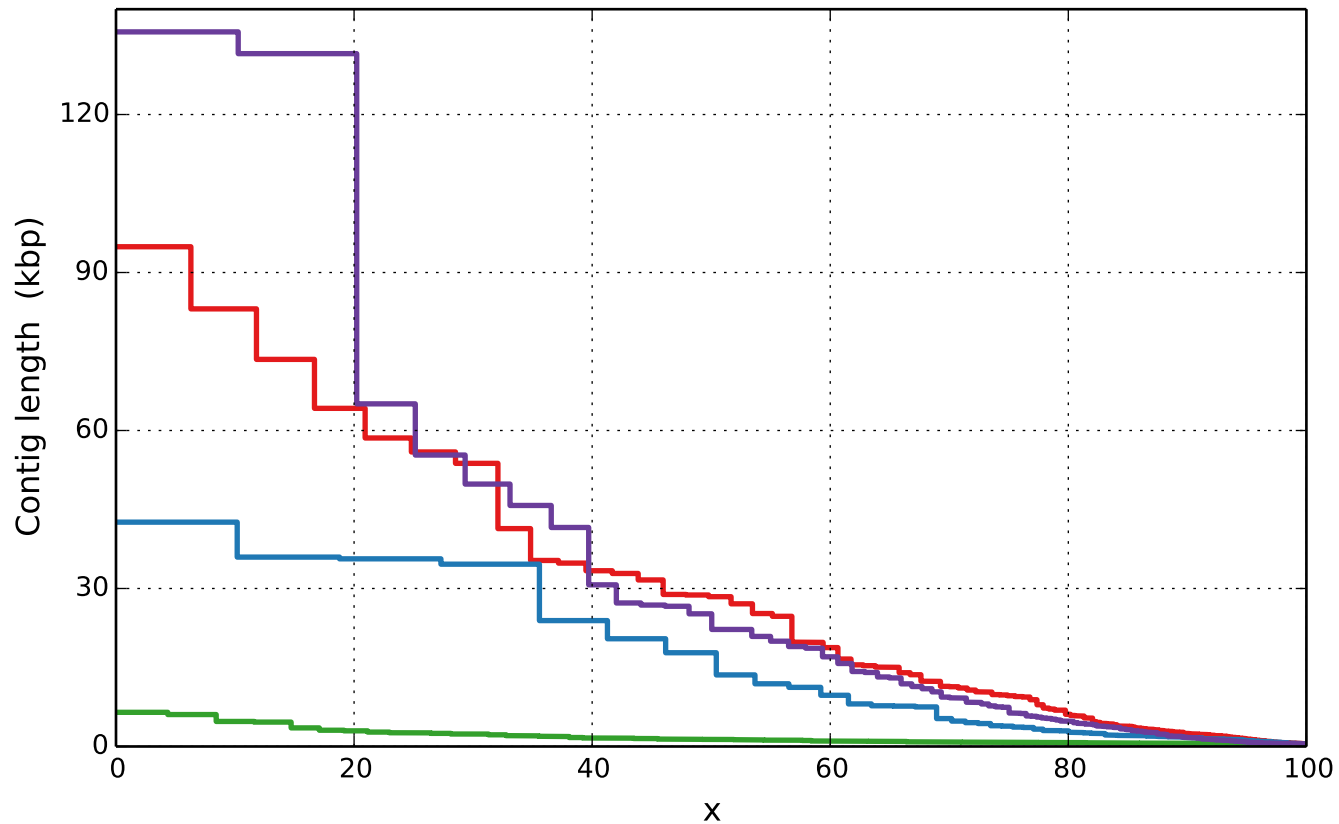|	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	149	65	44	135
# contigs (>= 5000 bp)	54	16	2	47
# contigs (>= 10000 bp)	37	10	0	28
# contigs (>= 25000 bp)	18	4	0	12
# contigs (>= 50000 bp)	7	0	0	4
Total length (>= 1000 bp)	1459141	401264	91169	1244225
Total length (>= 5000 bp)	1237519	293674	12549	1048561
Total length (>= 10000 bp)	1110008	247678	0	916292
Total length (>= 25000 bp)	831729	148802	0	661433
Total length (>= 50000 bp)	483963	0	0	387650
# contigs	220	89	126	255
Largest contig	94894	42596	6486	135693
Total length	1508421	418337	149083	1321670
Reference length	3698419	3698419	3698419	3698419
GC (%)	41.18	42.10	38.74	40.65
Reference GC (%)	40.55	40.55	40.55	40.55
N50	28442	17800	1344	25191
N75	9629	3859	790	7436
L50	16	7	30	12
L75	40	21	68	37
# misassemblies	11	3	5	3
# misassembled contigs	6	2	5	3
Misassembled contigs length	37824	5076	9945	16246
# local misassemblies	4	7	23	4
# structural variations	0	0	0	0
# unaligned contigs	0 + 153 part	0 + 58 part	0 + 53 part	0 + 165 part
Unaligned length	1295788	319522	41485	1085232
Genome fraction (%)	5.270	2.364	2.762	6.102
Duplication ratio	1.091	1.130	1.053	1.048
# N's per 100 kbp	56.95	2003.17	3370.61	582.52
# mismatches per 100 kbp	1540.30	1354.41	1269.64	1615.95
# indels per 100 kbp	53.87	21.73	18.60	48.74
Largest alignment	8202	9719	4753	8204
NA50	-	-	628	-
NGA50	-	-	-	-
LA50	-	-	60	-

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	11	3	5	3
# relocations	10	3	5	3
# translocations	0	0	0	0
# inversions	1	0	0	0
# possibly misassembled contigs	45	21	9	51
# misassembled contigs	6	2	5	3
Misassembled contigs length	37824	5076	9945	16246
# local misassemblies	4	7	23	4
# structural variations	0	0	0	0
# mismatches	3002	1184	1297	3647
# indels	105	19	19	110
# short indels	97	19	19	81
# long indels	8	0	0	29
Indels length	252	25	31	485

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).
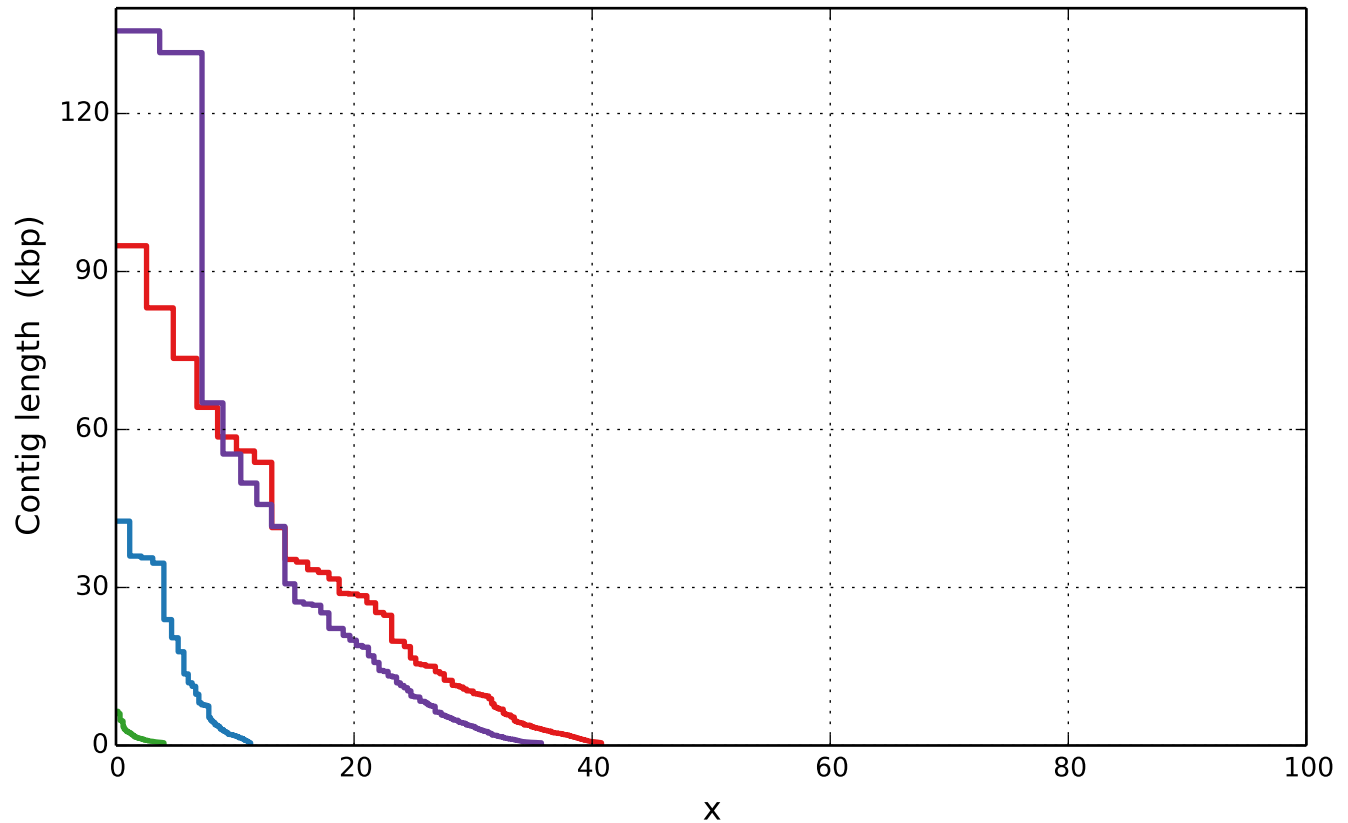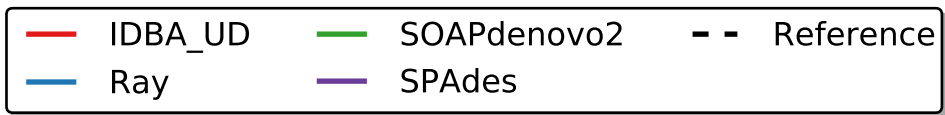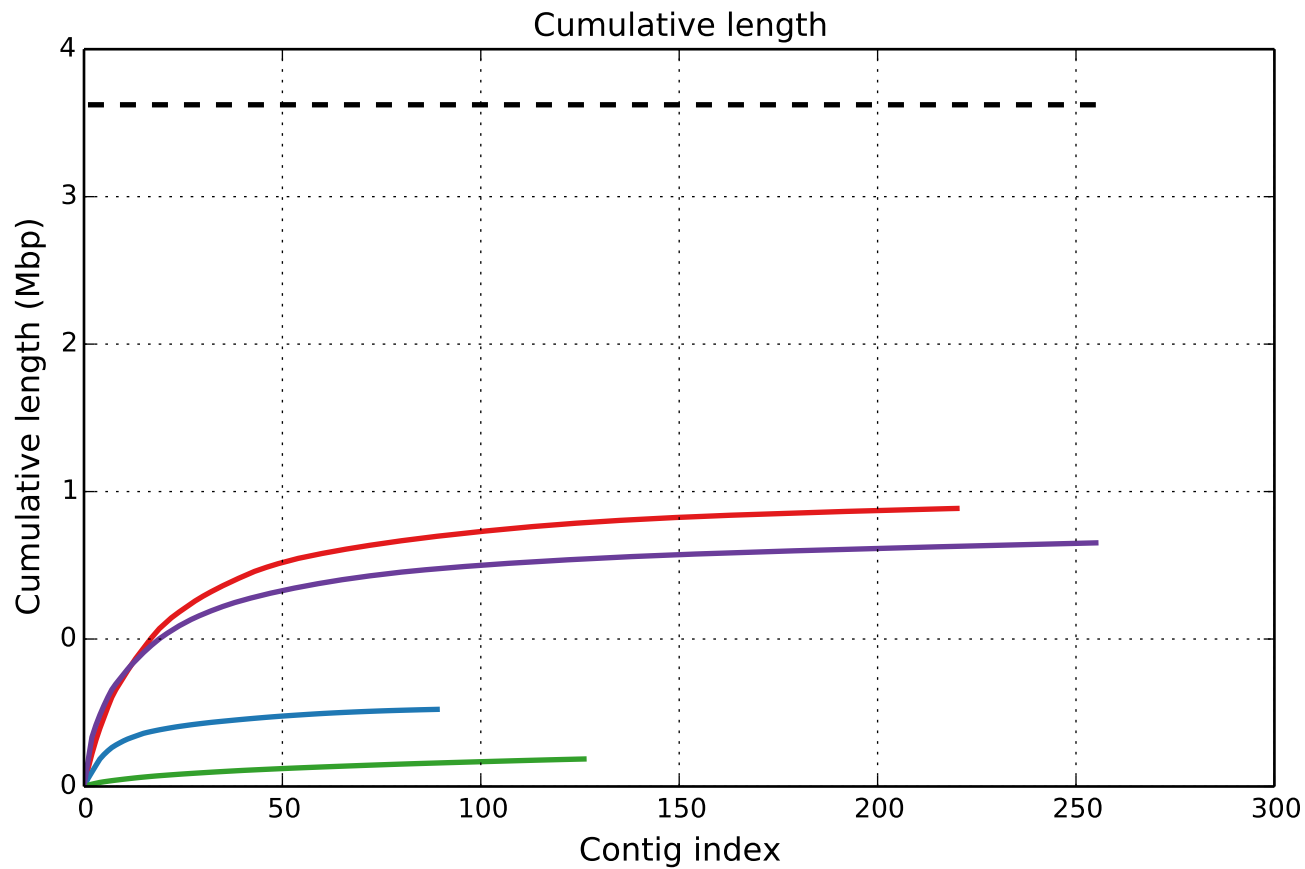
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	153	58	53	165
# with misassembly	24	11	9	19
# both parts are significant	41	17	6	47
Partially unaligned length	1295788	319522	41485	1085232
# N's	859	8380	5025	7699

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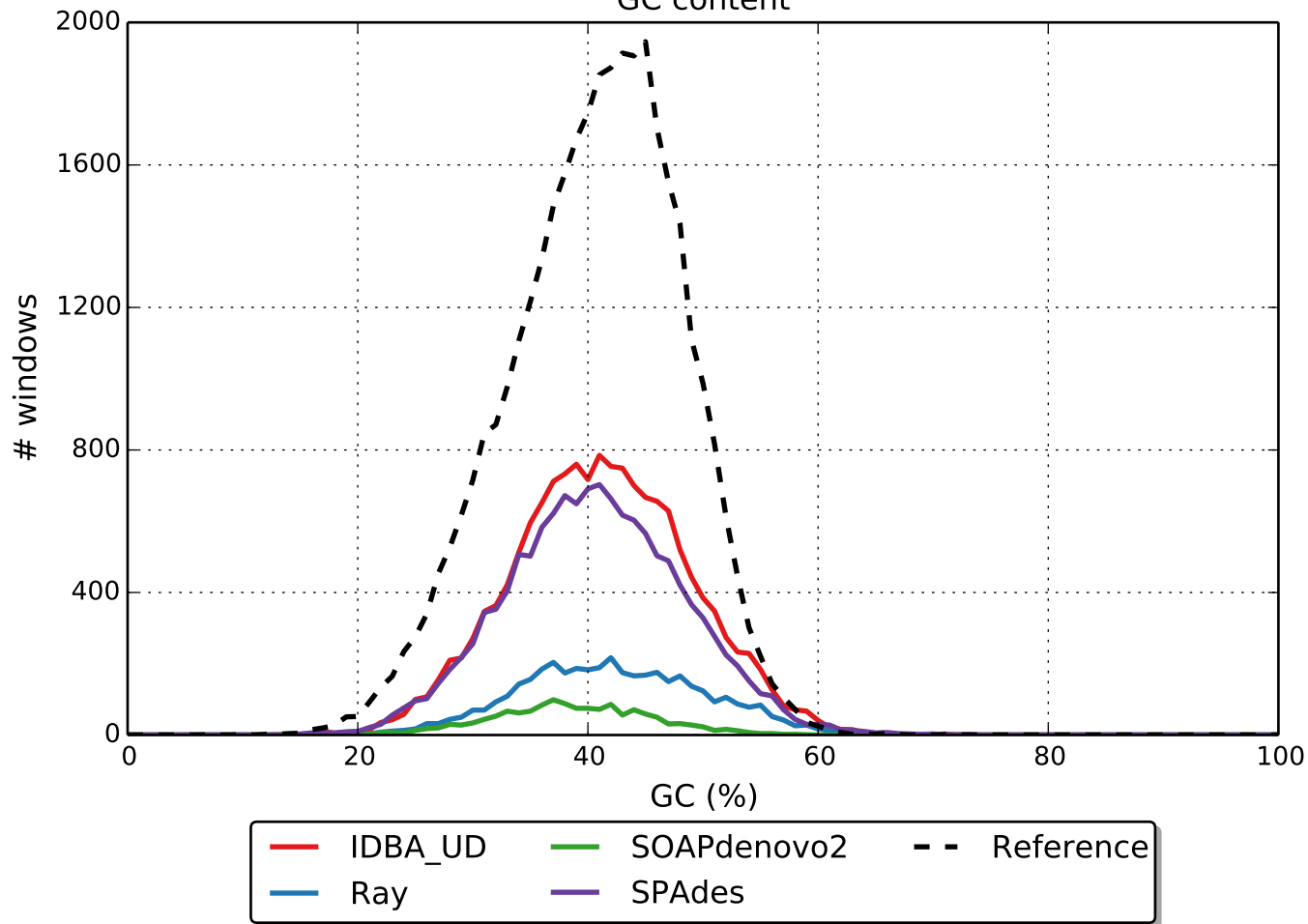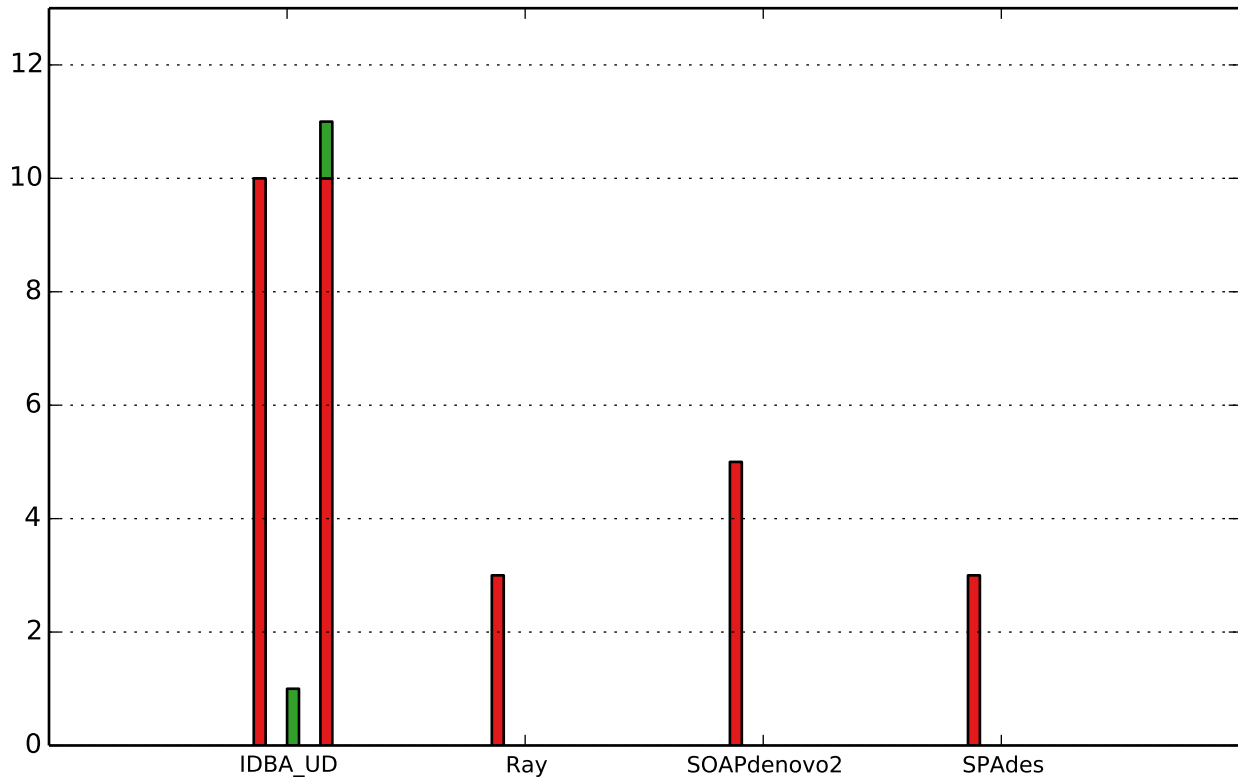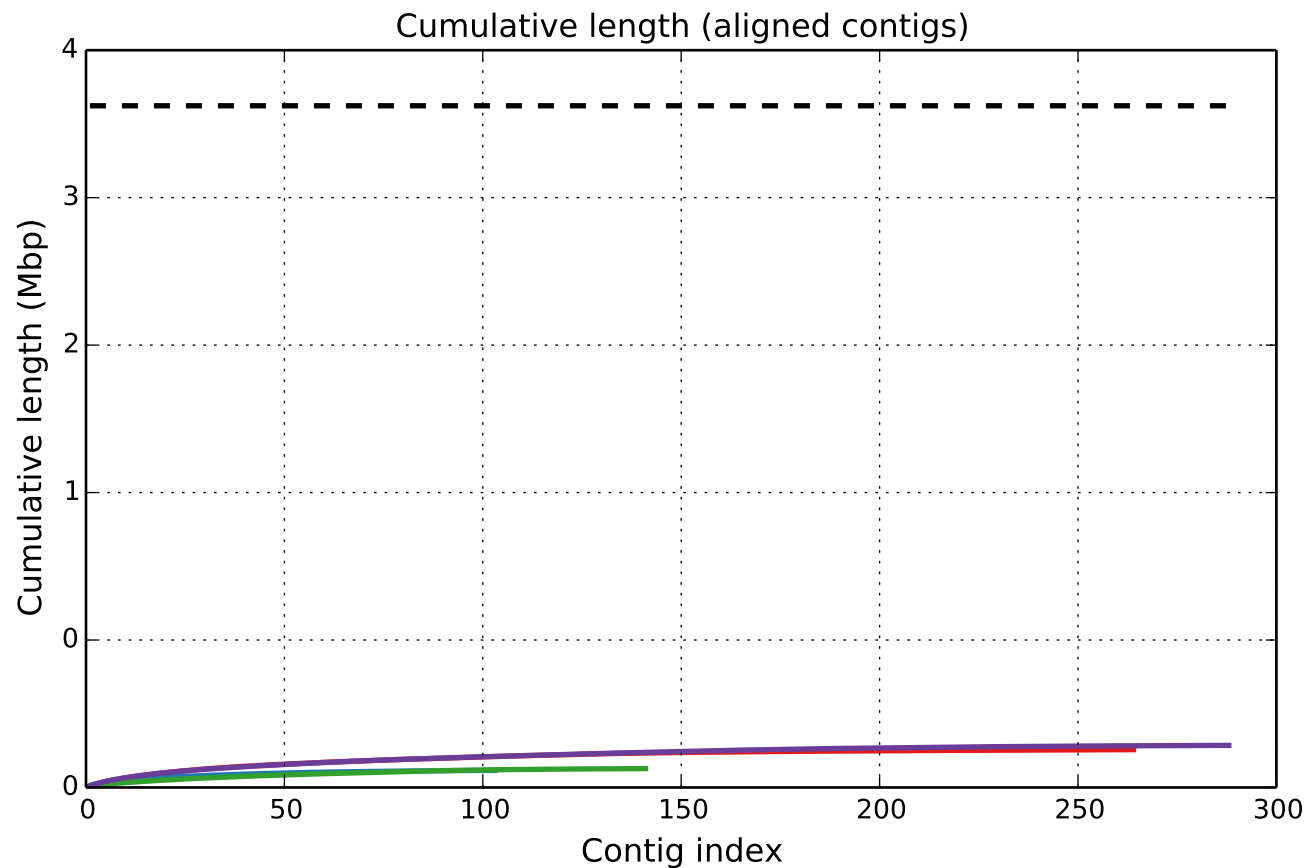(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

IDBA_UD	SOAPdenovo2	Reference
Ray	SPAdes	

Misassemblies

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

IDBA_UD — SOAPdenovo2 — SPAdes — Ray

Genome fraction, %