Report

	IDBA_UD	SPAdes
# contigs (>= 1000 bp)	1	1
# contigs (>= 5000 bp)	0	0
# contigs (>= 10000 bp)	0	0
# contigs (>= 25000 bp)	0	0
# contigs (>= 50000 bp)	0	0
Total length (>= 1000 bp)	3247	1155
Total length (>= 5000 bp)	0	0
Total length (>= 10000 bp)	0	0
Total length (>= 25000 bp)	0	0
Total length (>= 50000 bp)	0	0
# contigs	1	2
Largest contig	3247	1155
Total length	3247	1730
Reference length	2664102	2664102
GC (%)	52.91	50.16
Reference GC (%)	55.76	55.76
N50	3247	1155
N75	3247	575
L50	1	1
L75	1	2
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# structural variations	0	0
# unaligned contigs	0 + 1 part	0 + 2 part
Unaligned length	3164	1428
Genome fraction (%)	0.003	0.011
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	9075.14
# mismatches per 100 kbp	4819.28	2649.01
# indels per 100 kbp	0.00	0.00
Largest alignment	83	228
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).
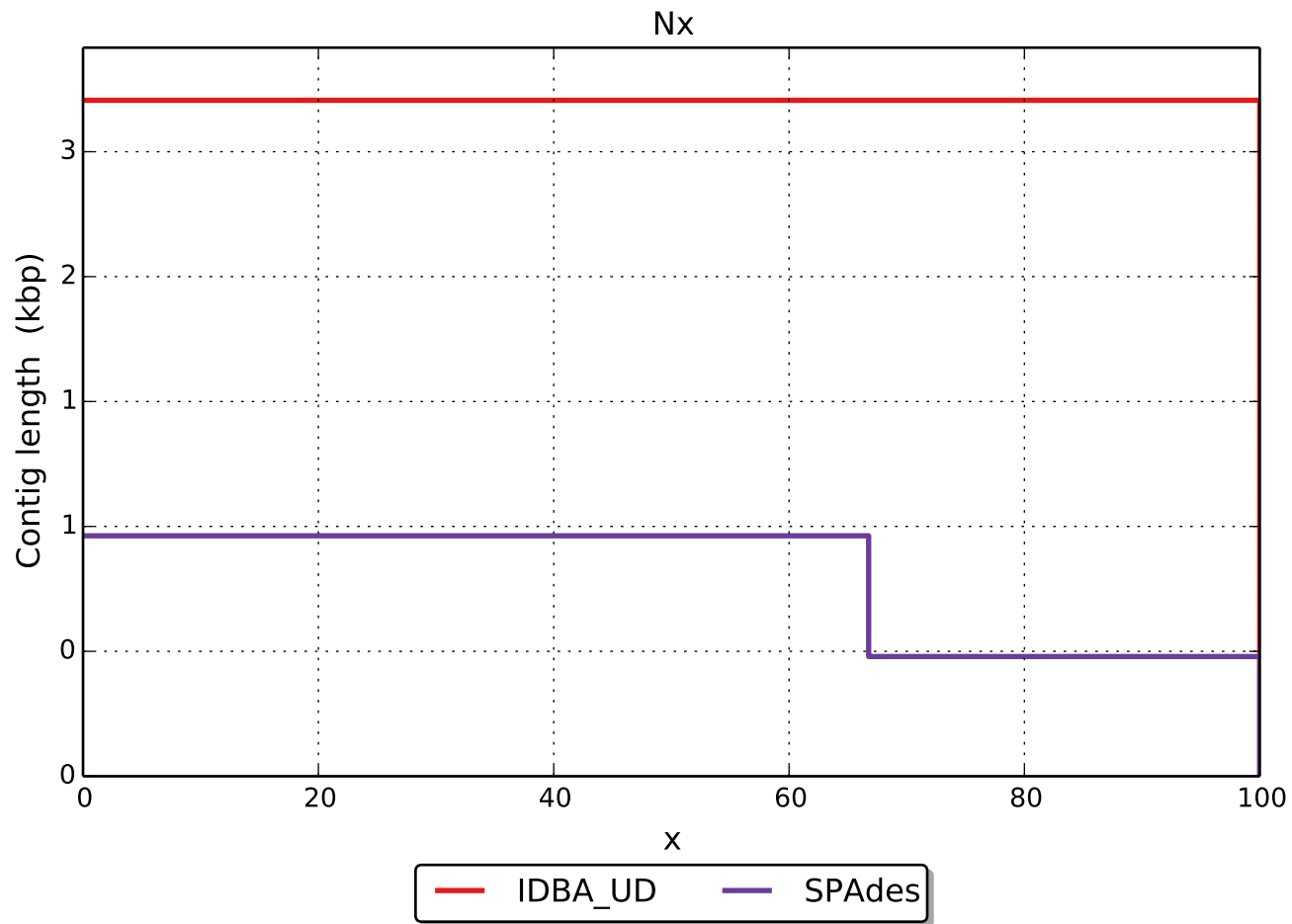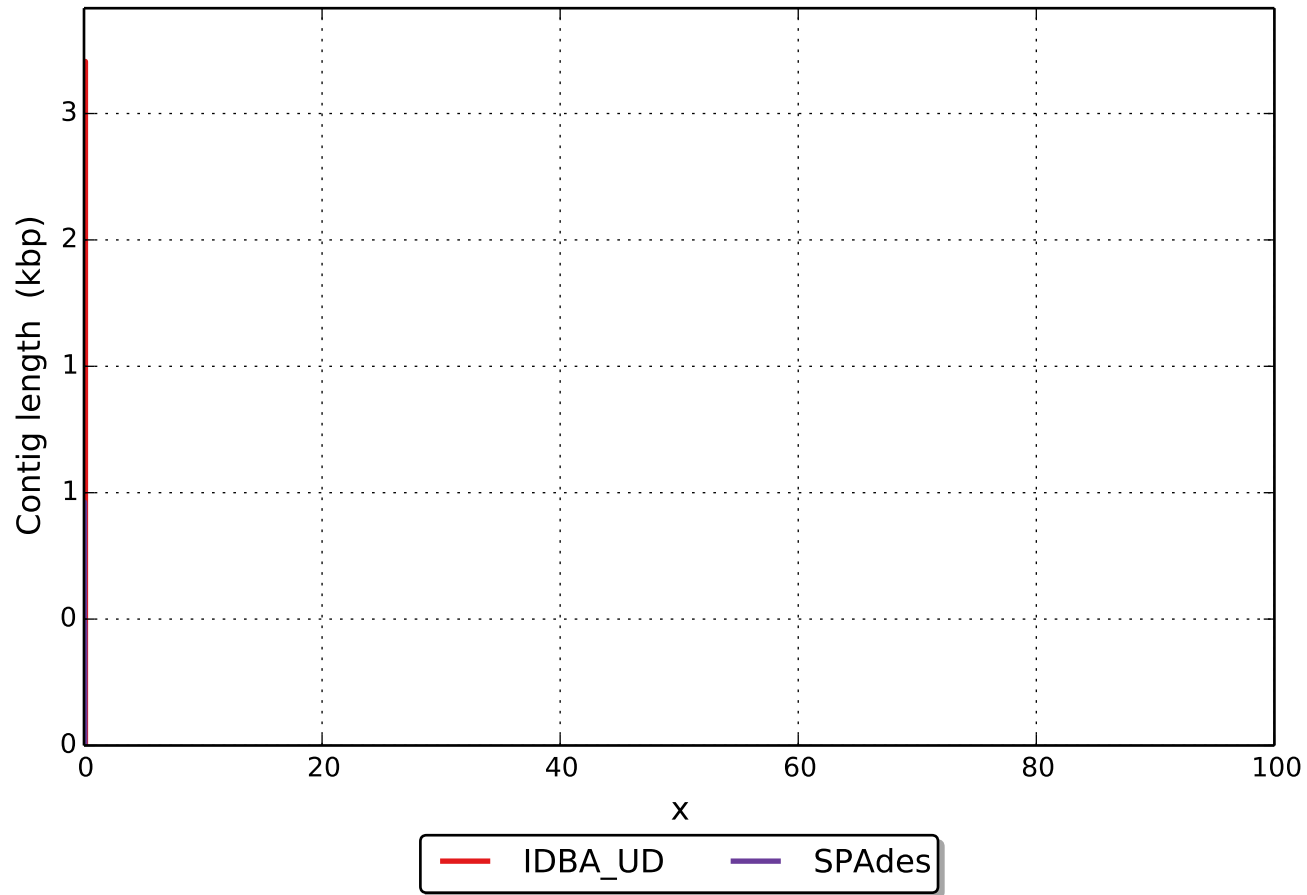
Misassemblies report

	IDBA_UD	SPAdes
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# structural variations	0	0
# mismatches	4	8
# indels	0	0
# short indels	0	0
# long indels	0	0
Indels length	0	0

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	SPAdes
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	1	2
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	3164	1428
# N's	0	157

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

Cumulative length

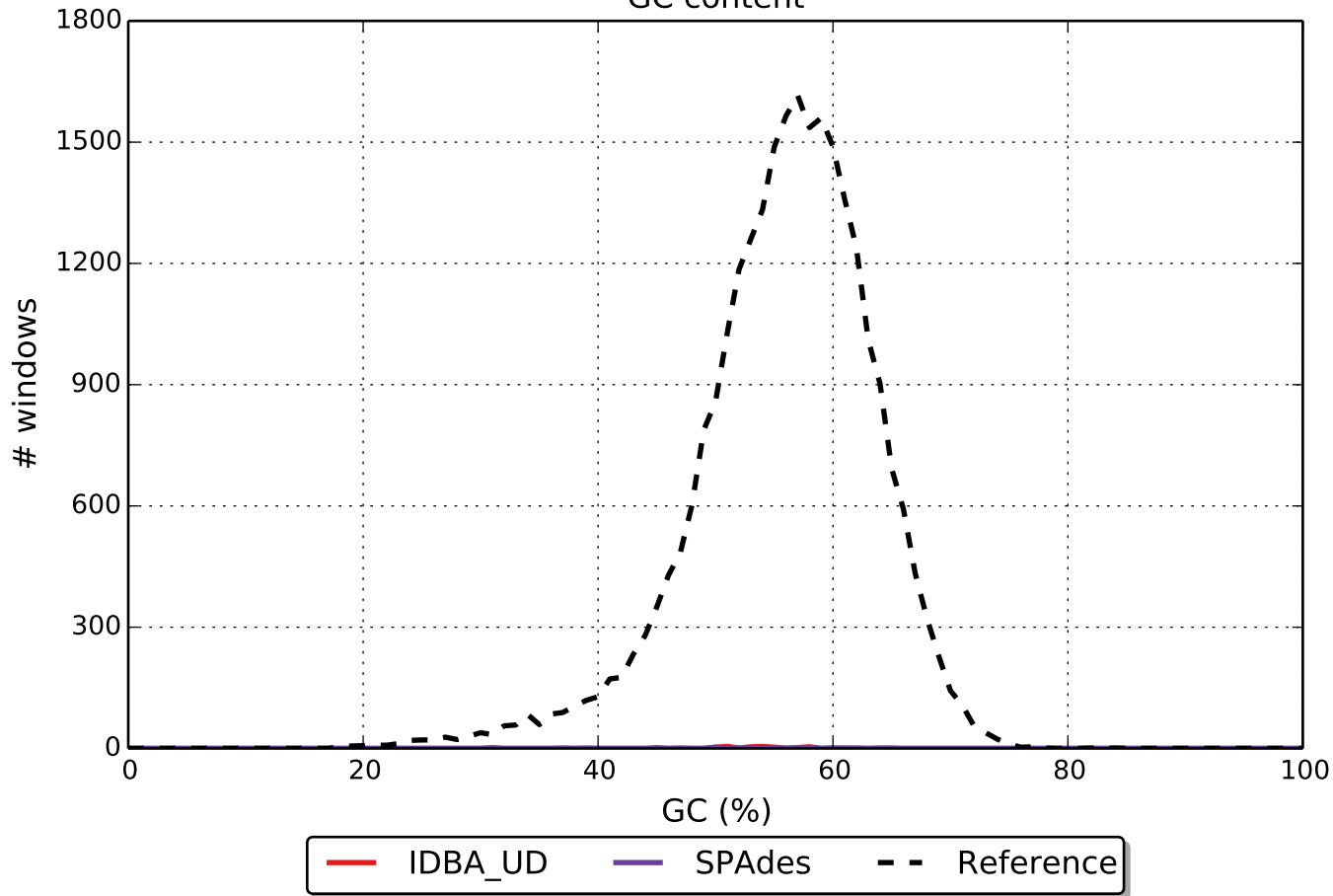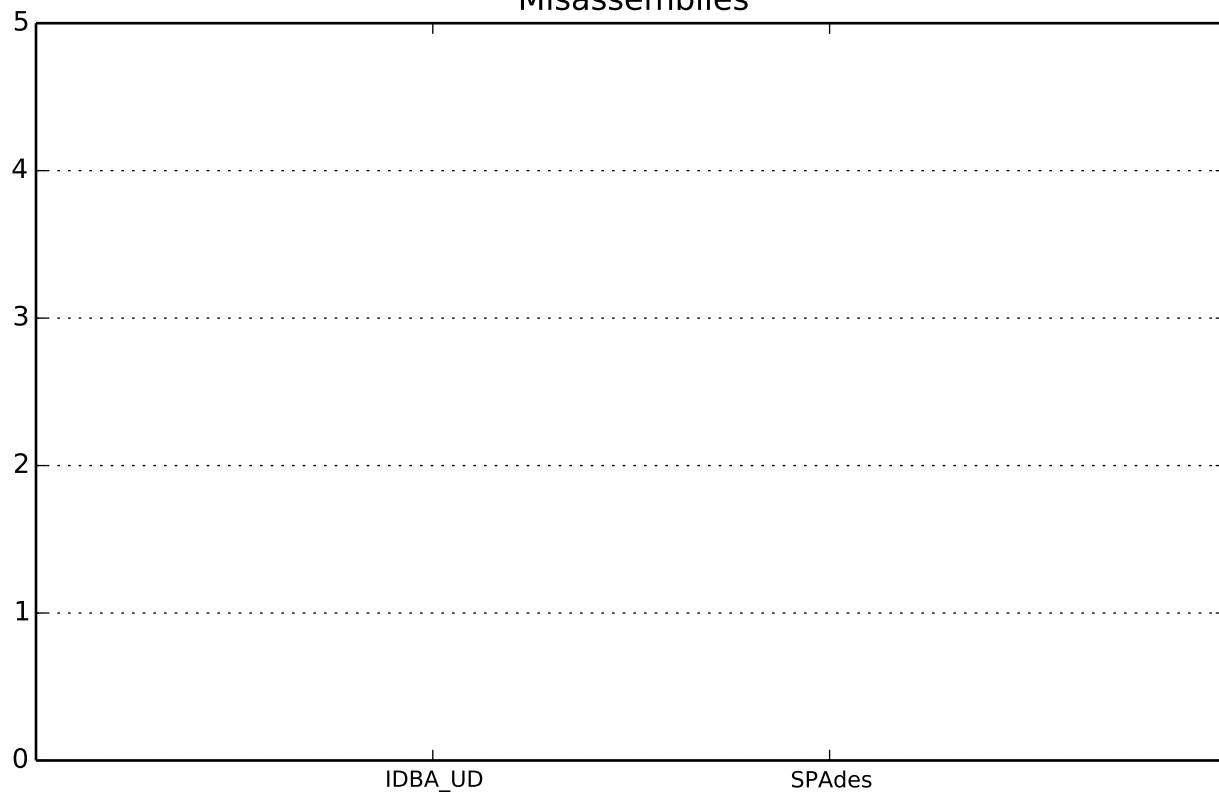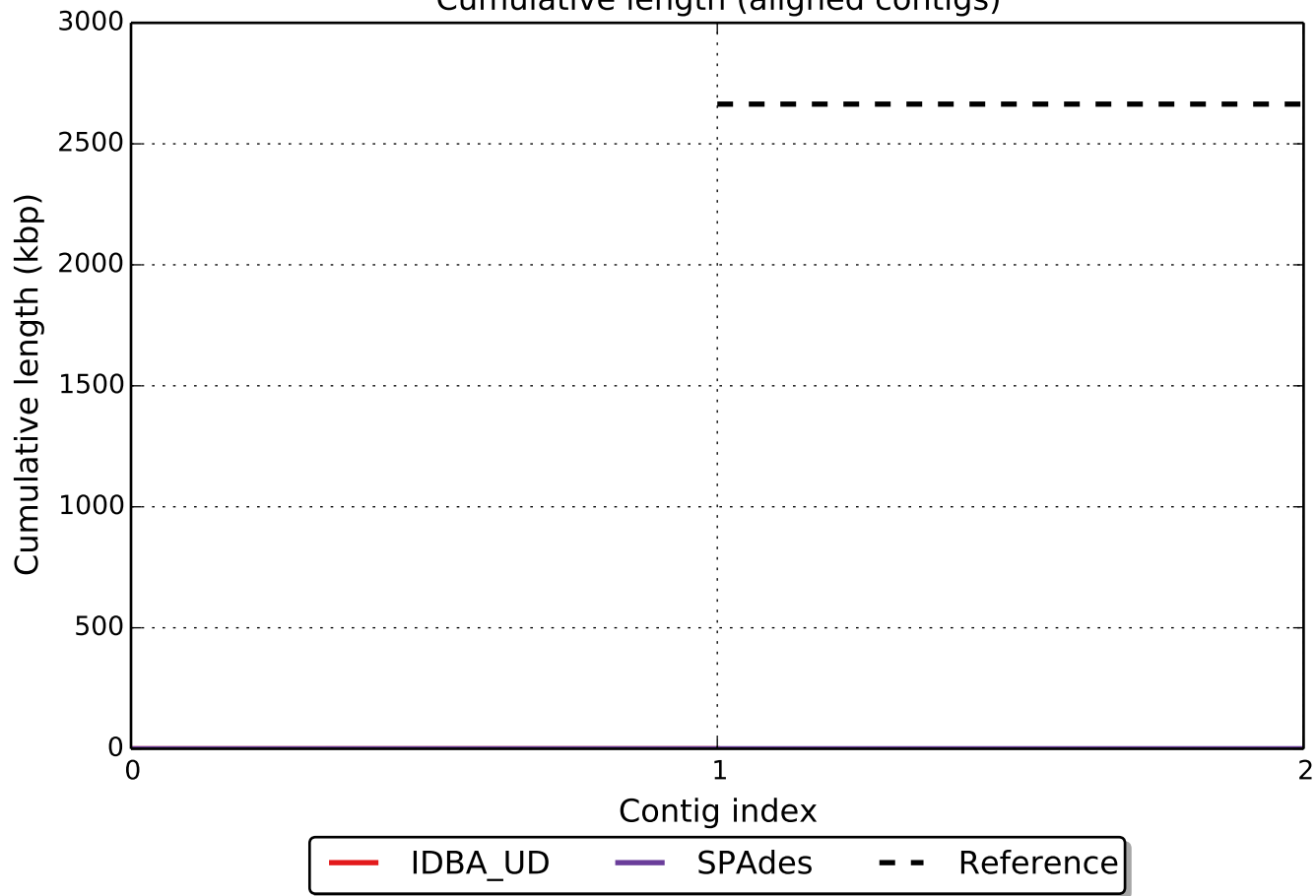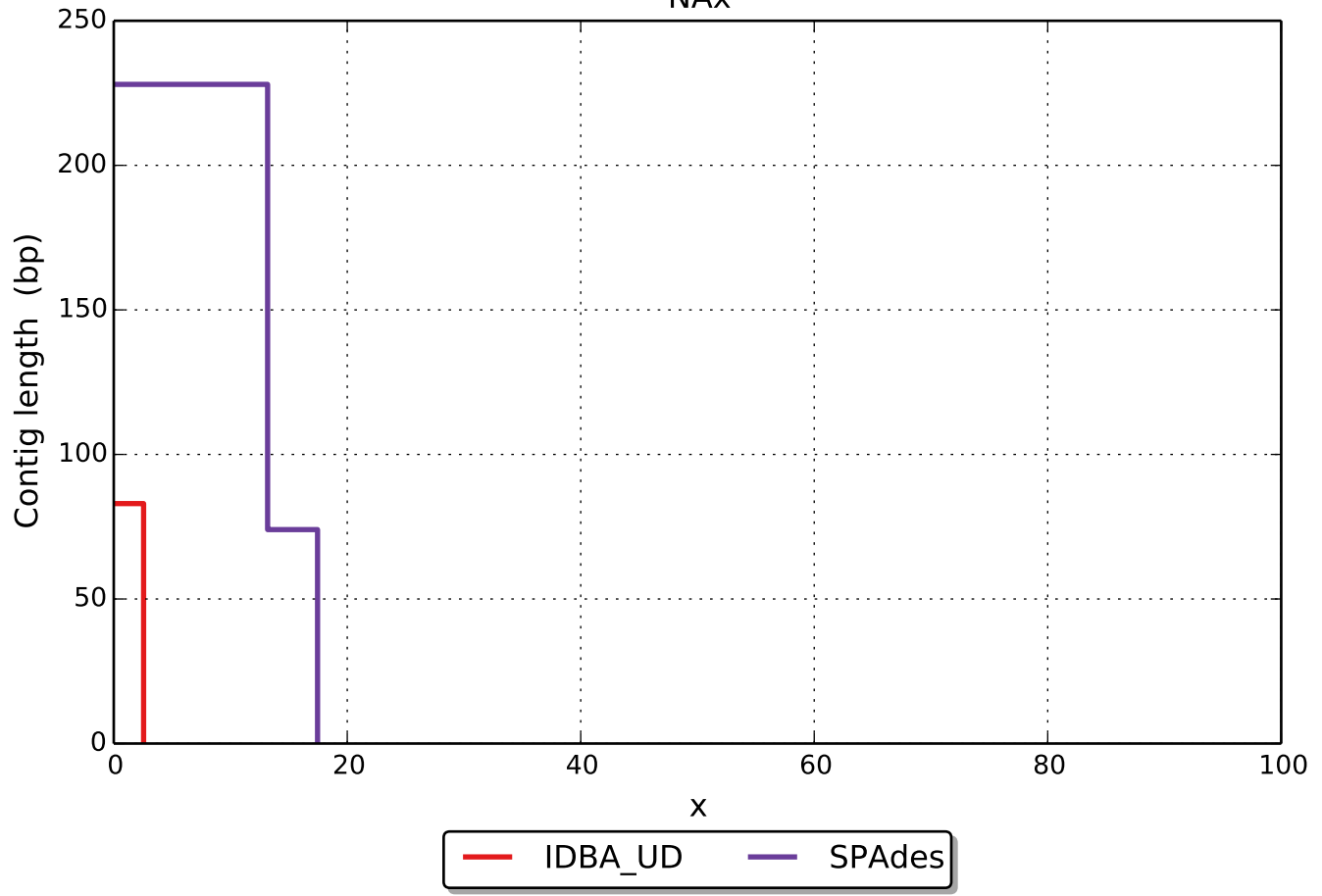Cumulative length (kbp)

Contig index

IDBA_UD SPAdes - - Reference
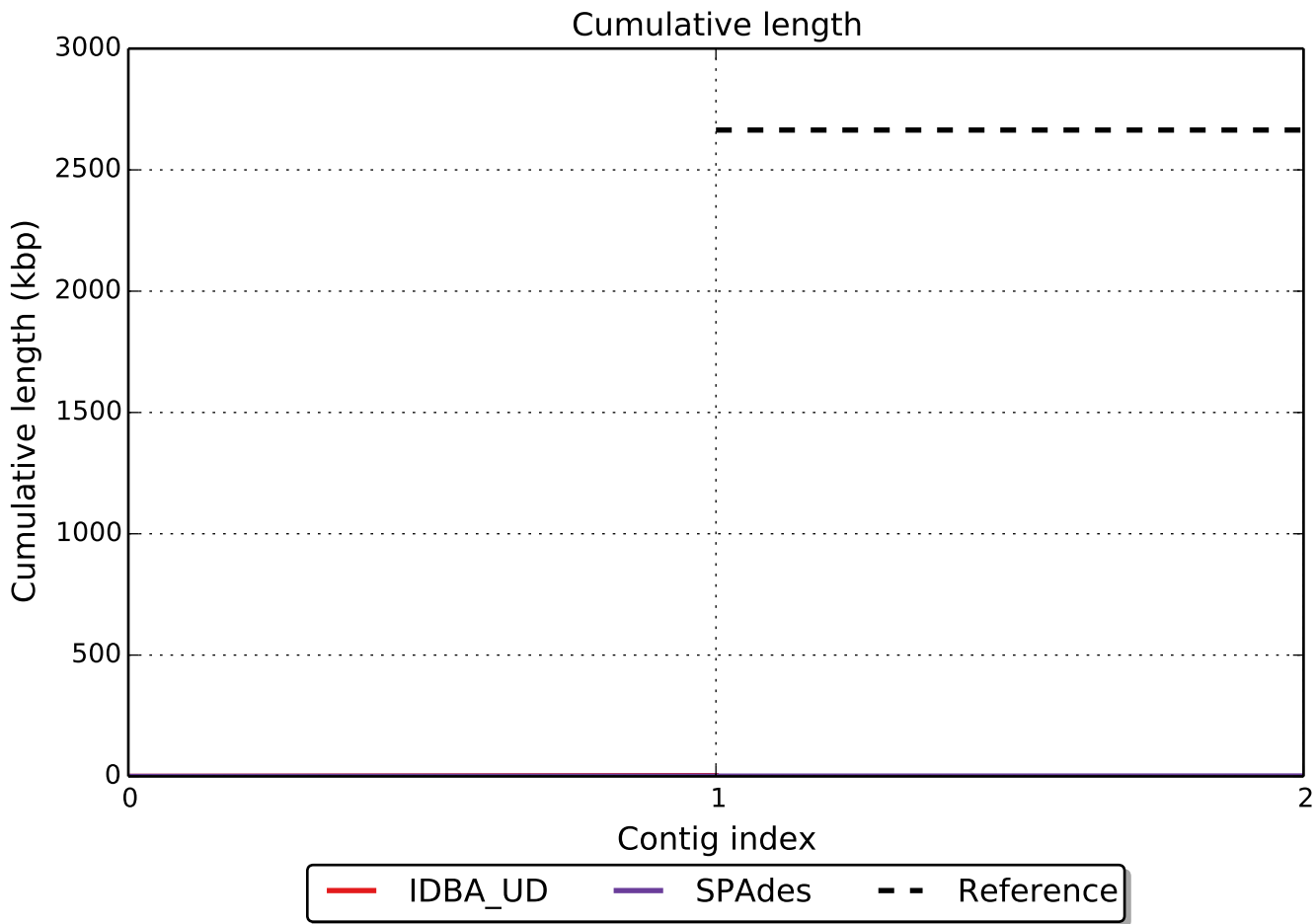
GC content

Misassemblies

Cumulative length (aligned contigs)

NAx

Genome fraction, %

	IDBA_UD	SPAdes