

## Report

	IDBA_UD	SPAdes
# contigs ( $\geq 1000$ bp)	0	0
# contigs ( $\geq 5000$ bp)	0	0
# contigs ( $\geq 10000$ bp)	0	0
# contigs ( $\geq 25000$ bp)	0	0
# contigs ( $\geq 50000$ bp)	0	0
Total length ( $\geq 1000$ bp)	0	0
Total length ( $\geq 5000$ bp)	0	0
Total length ( $\geq 10000$ bp)	0	0
Total length ( $\geq 25000$ bp)	0	0
Total length ( $\geq 50000$ bp)	0	0
# contigs	6	10
Largest contig	982	956
Total length	4639	6252
Reference length	2439869	2439869
GC (%)	56.46	54.20
Reference GC (%)	60.55	60.55
N50	869	597
N75	770	540
L50	3	5
L75	4	8
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# structural variations	0	0
# unaligned contigs	0 + 2 part	0 + 7 part
Unaligned length	975	2263
Genome fraction (%)	0.150	0.152
Duplication ratio	1.000	1.073
# N's per 100 kbp	0.00	9868.84
# mismatches per 100 kbp	2837.65	2637.24
# indels per 100 kbp	409.28	161.46
Largest alignment	982	744
NA50	869	250
NGA50	-	-
NA75	231	-
LA50	3	7
LA75	5	-

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

## Misassemblies report

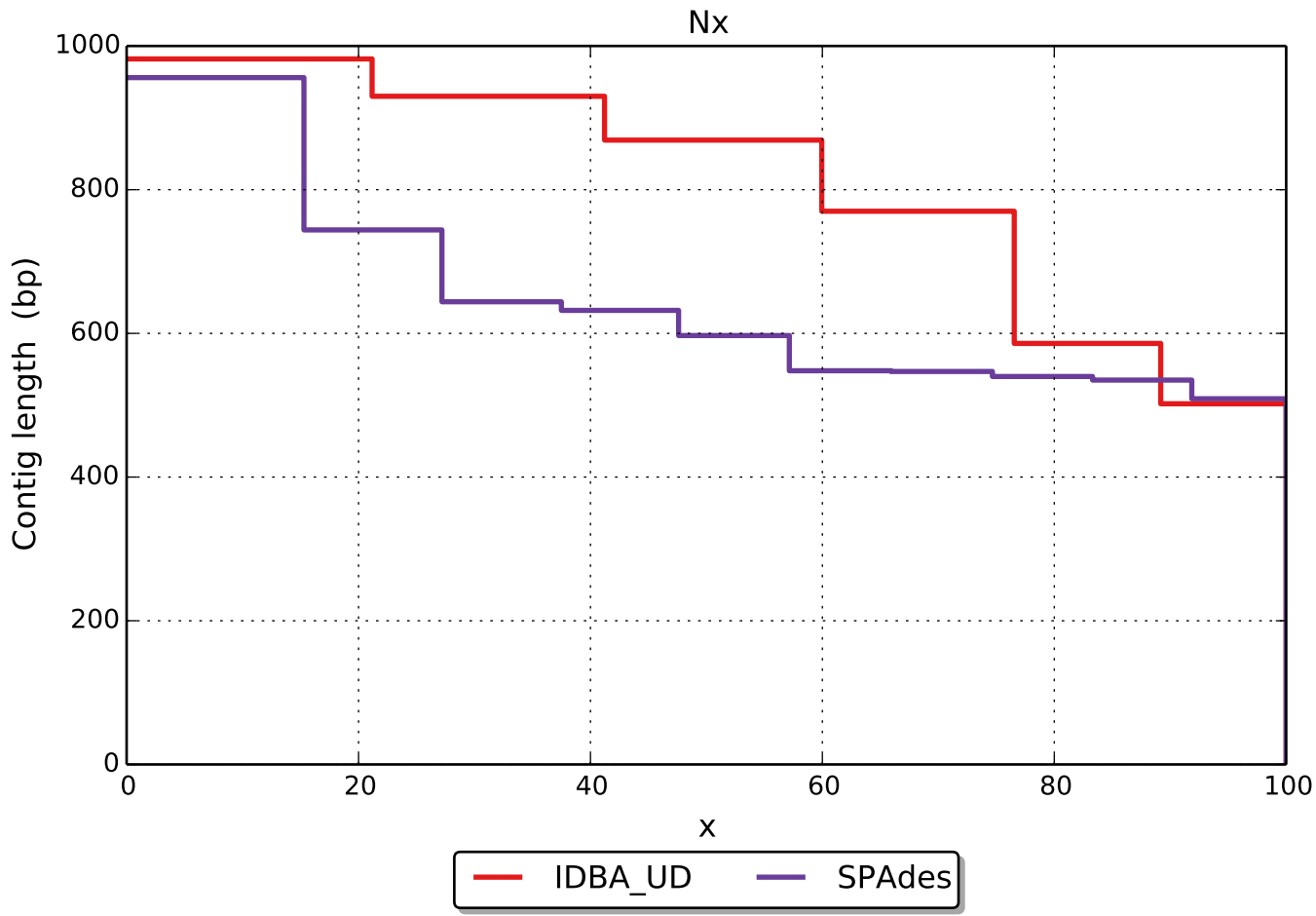
	IDBA_UD	SPAdes
# misassemblies	0	0
# relocations	0	0
# translocations	0	0
# inversions	0	0
# possibly misassembled contigs	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# structural variations	0	0
# mismatches	104	98
# indels	15	6
# short indels	15	6
# long indels	0	0
Indels length	20	11

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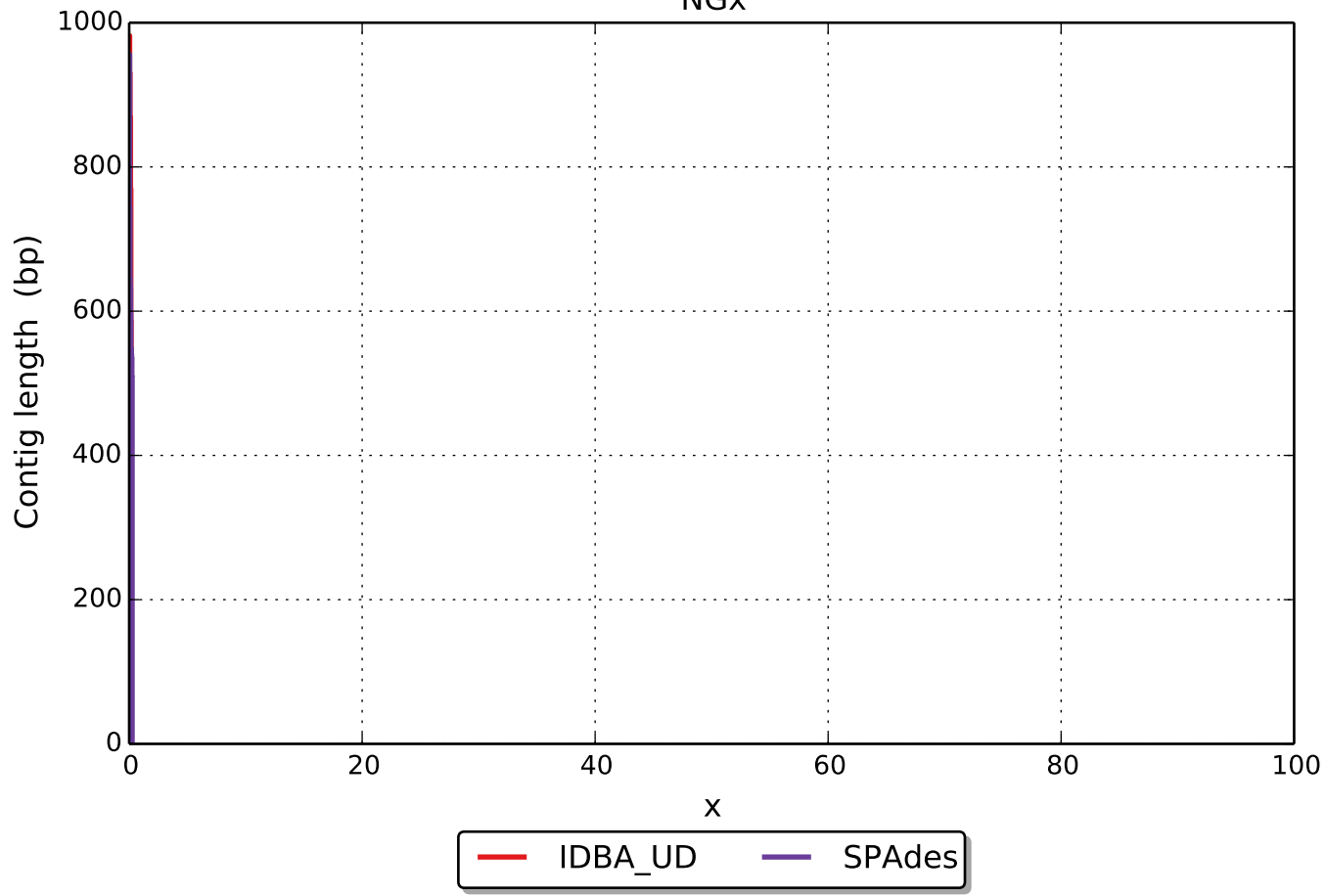
## Unaligned report

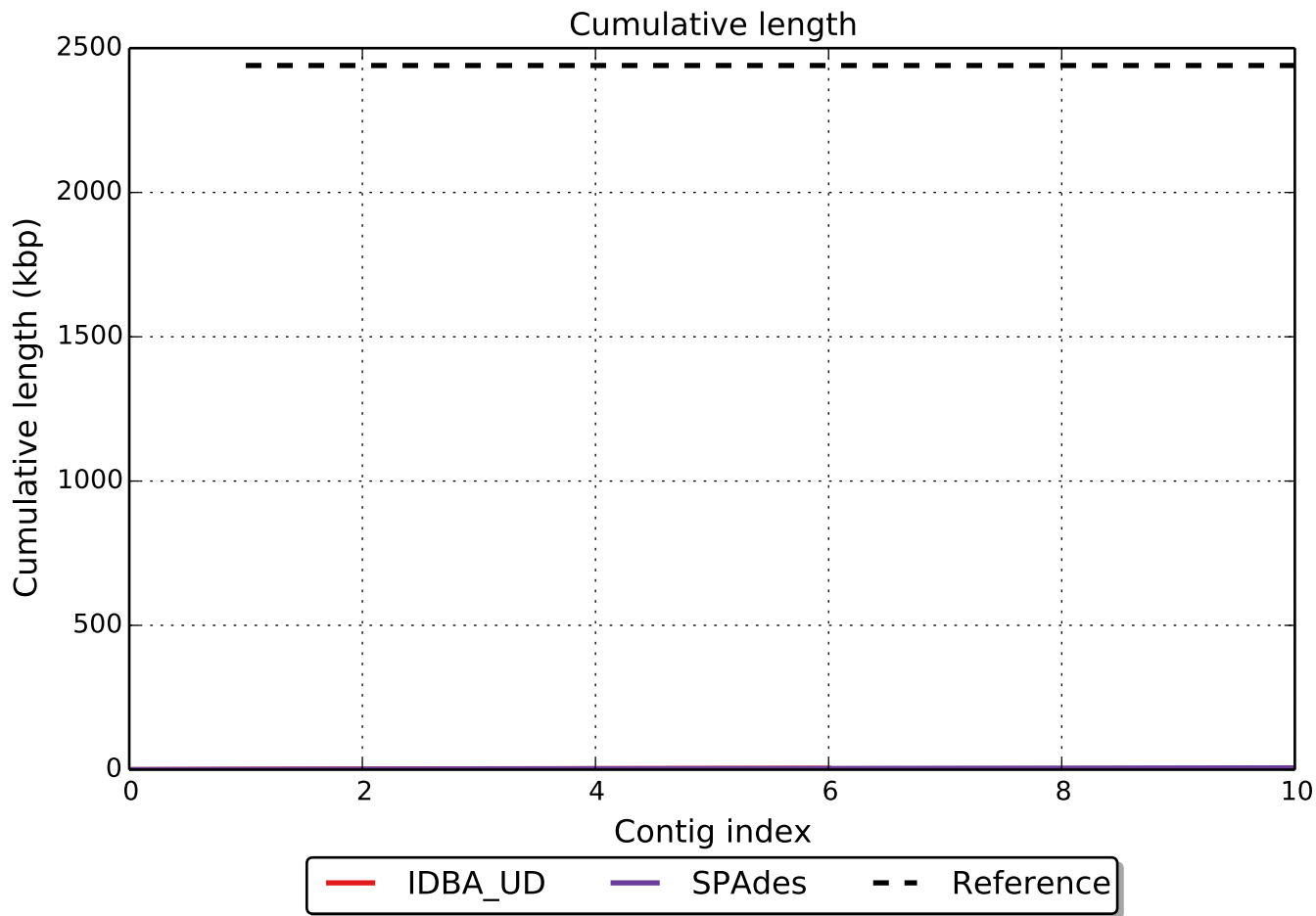
	IDBA_UD	SPAdes
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	2	7
# with misassembly	0	0
# both parts are significant	0	0
Partially unaligned length	975	2263
# N's	0	617

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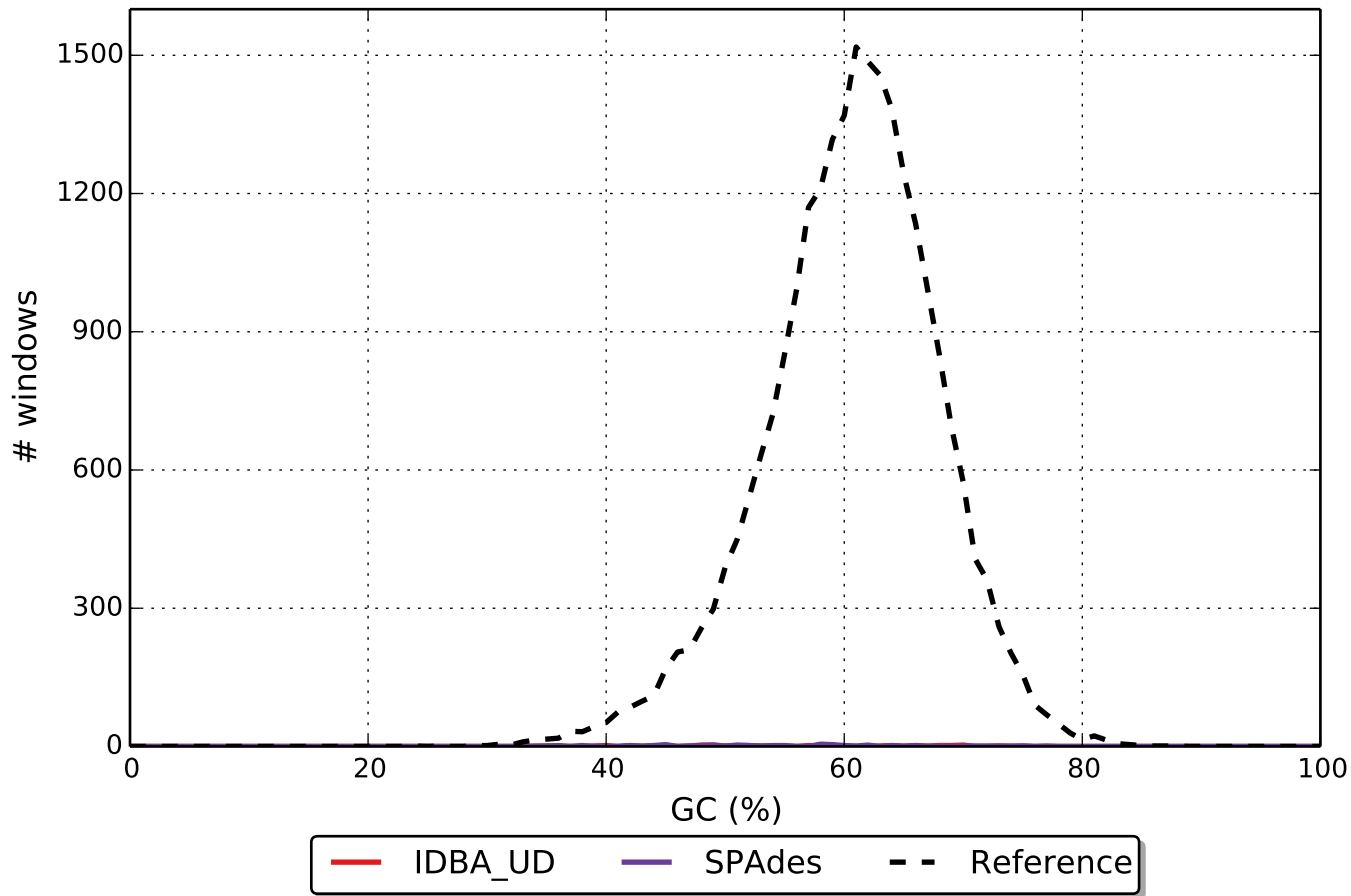


NGx

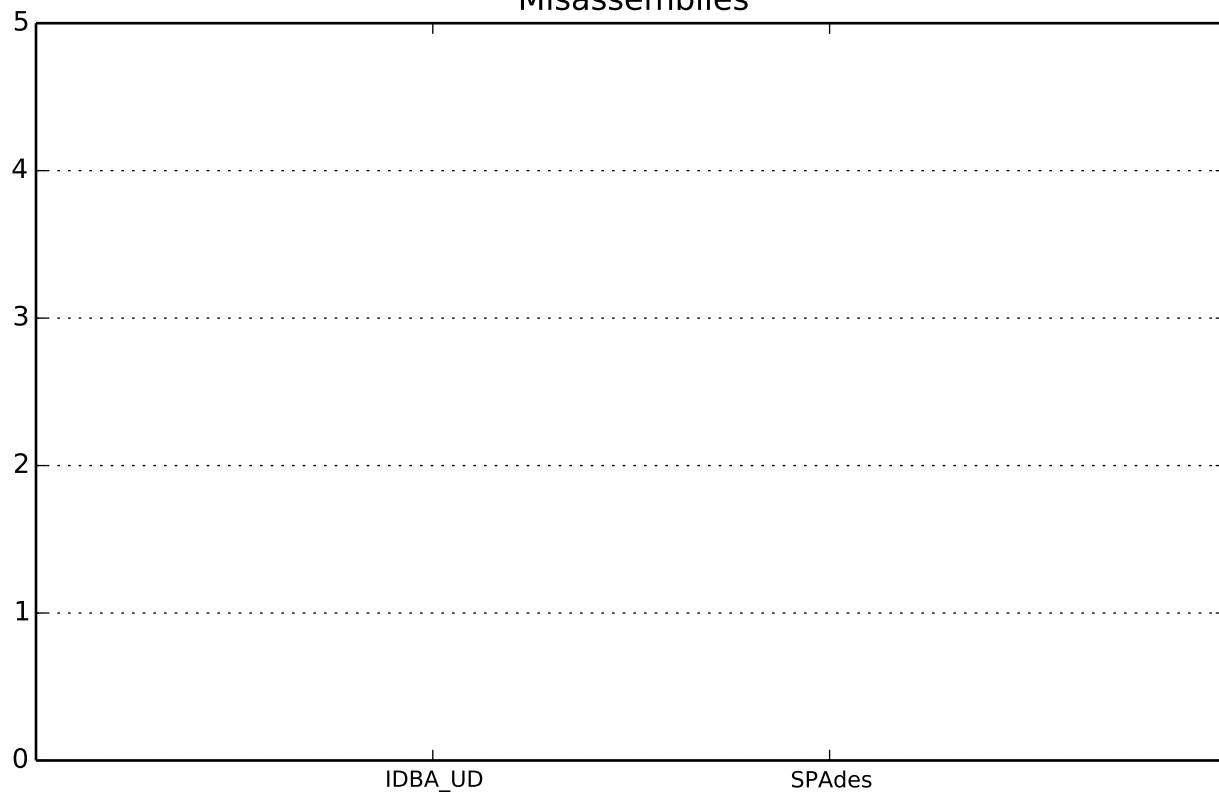




GC content

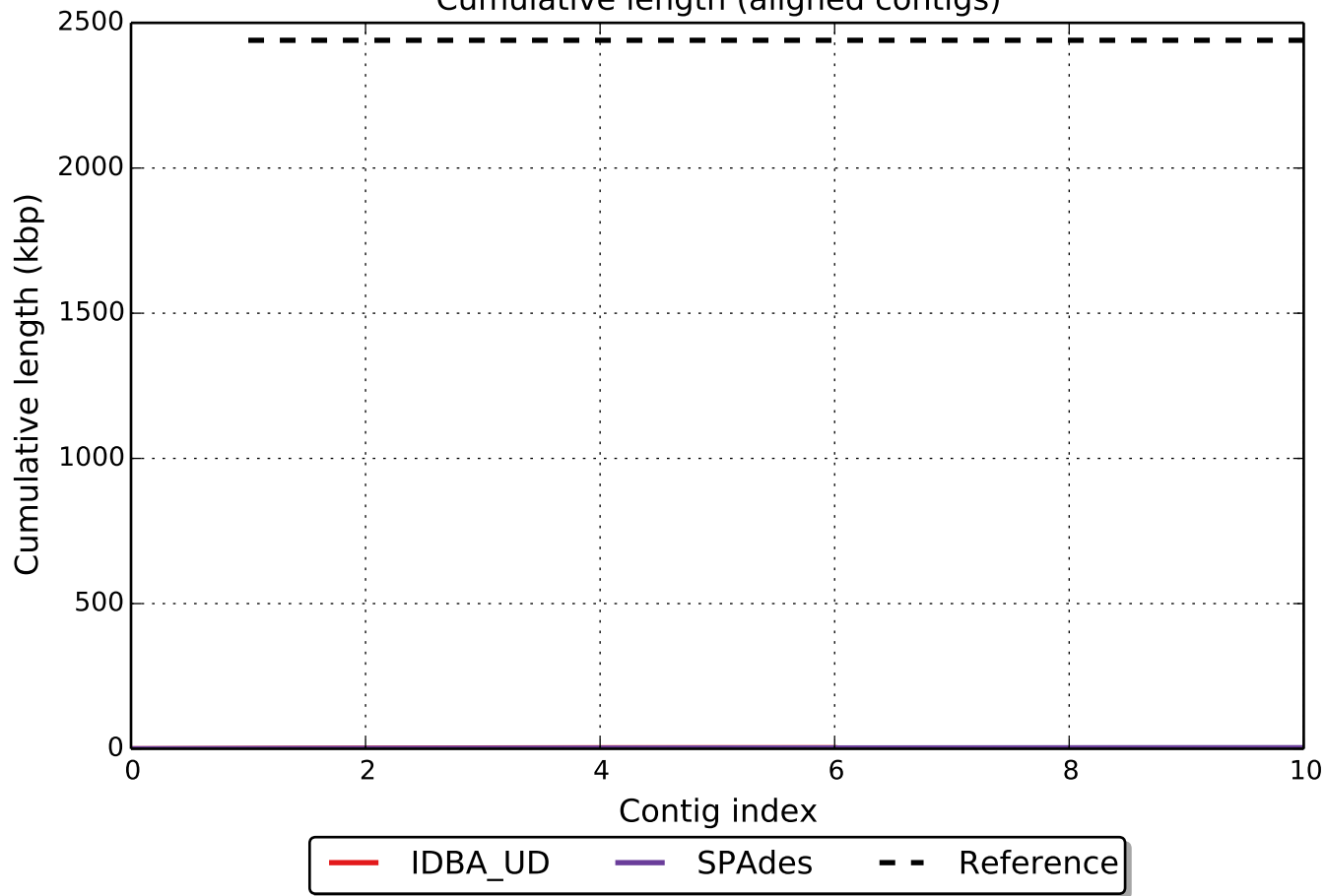


# Misassemblies

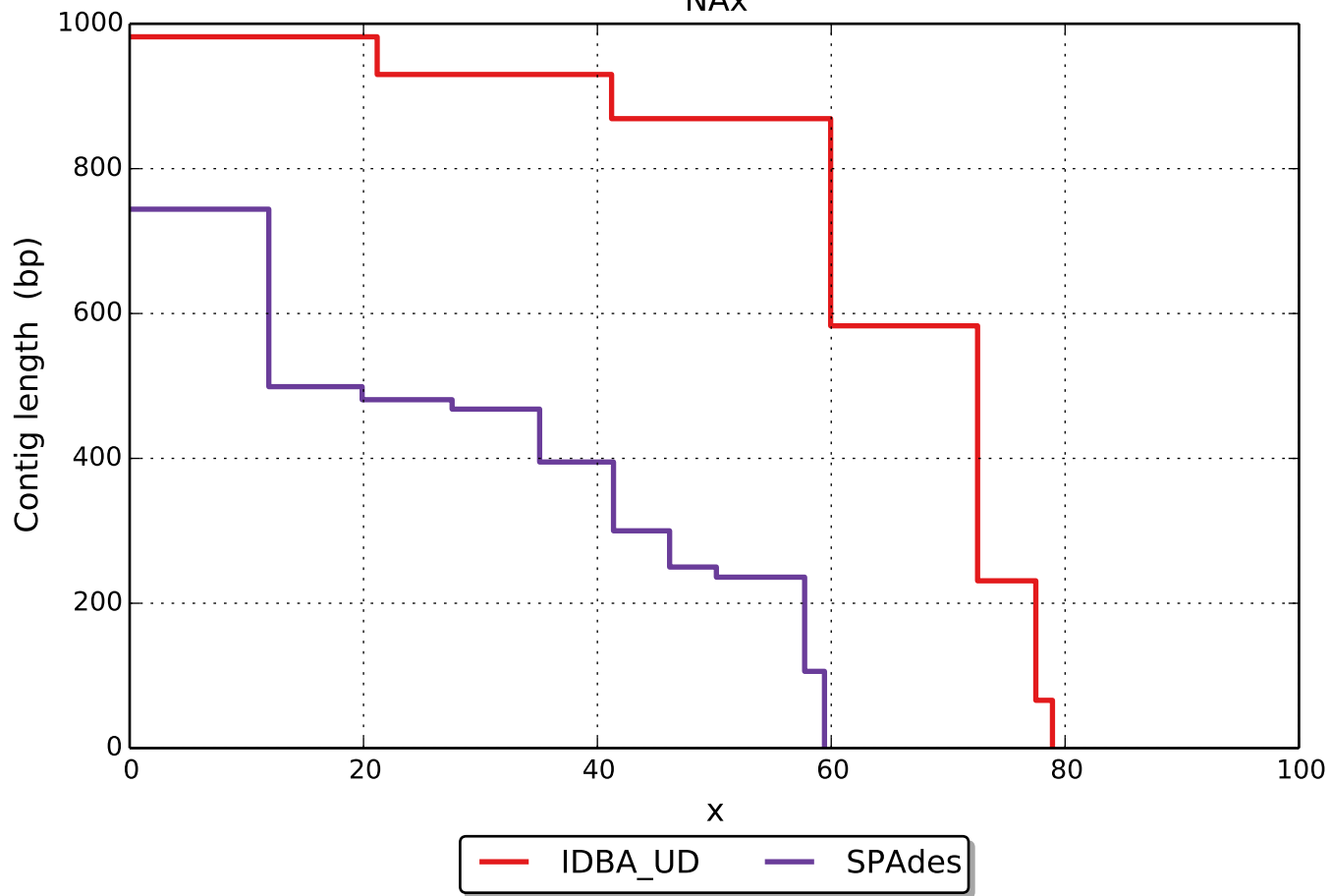




Cumulative length (aligned contigs)



NAx



NGAx

