

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	7	6	6	7
# contigs (>= 5000 bp)	1	0	0	1
# contigs (>= 10000 bp)	0	0	0	0
# contigs (>= 25000 bp)	0	0	0	0
# contigs (>= 50000 bp)	0	0	0	0
Total length (>= 1000 bp)	19937	15775	8134	21889
Total length (>= 5000 bp)	8007	0	0	9516
Total length (>= 10000 bp)	0	0	0	0
Total length (>= 25000 bp)	0	0	0	0
Total length (>= 50000 bp)	0	0	0	0
# contigs	16	8	13	12
Largest contig	8007	4916	2005	9516
Total length	27209	17402	13576	24829
Reference length	3270209	3270209	3270209	3270209
GC (%)	44.96	45.09	45.91	43.67
Reference GC (%)	50.19	50.19	50.19	50.19
N50	1855	2427	1133	2462
N75	911	1561	865	2289
L50	3	3	5	3
L75	8	5	9	5
# misassemblies	0	0	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	1	0	4	0
# structural variations	0	0	0	0
# unaligned contigs	0 + 10 part	0 + 3 part	0 + 3 part	0 + 9 part
Unaligned length	8089	2441	1904	18537
Genome fraction (%)	0.582	0.431	0.348	0.191
Duplication ratio	1.004	1.062	1.025	1.008
# N's per 100 kbp	106.58	0.00	3506.19	0.00
# mismatches per 100 kbp	876.73	425.74	281.07	1217.75
# indels per 100 kbp	26.25	42.57	0.00	64.09
Largest alignment	8007	3947	2005	2289
NA50	933	2427	1133	-
NGA50	-	-	-	-
NA75	-	1561	633	-
LA50	5	3	5	-
LA75	-	5	9	-

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

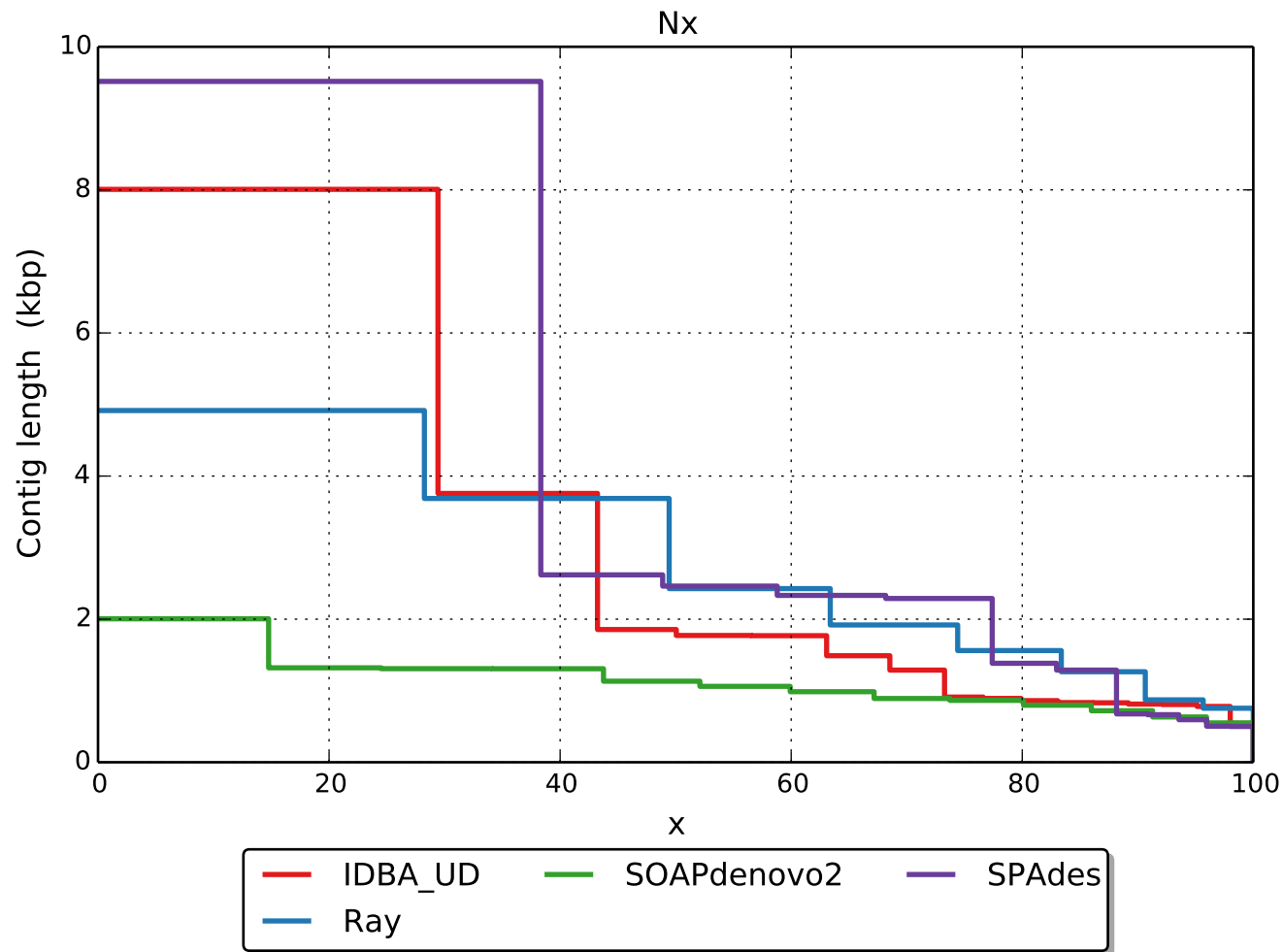
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	0	0	0
# relocations	0	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# possibly misassembled contigs	1	1	0	0
# misassembled contigs	0	0	0	0
Misassembled contigs length	0	0	0	0
# local misassemblies	1	0	4	0
# structural variations	0	0	0	0
# mismatches	167	60	32	76
# indels	5	6	0	4
# short indels	5	6	0	4
# long indels	0	0	0	0
Indels length	6	6	0	4

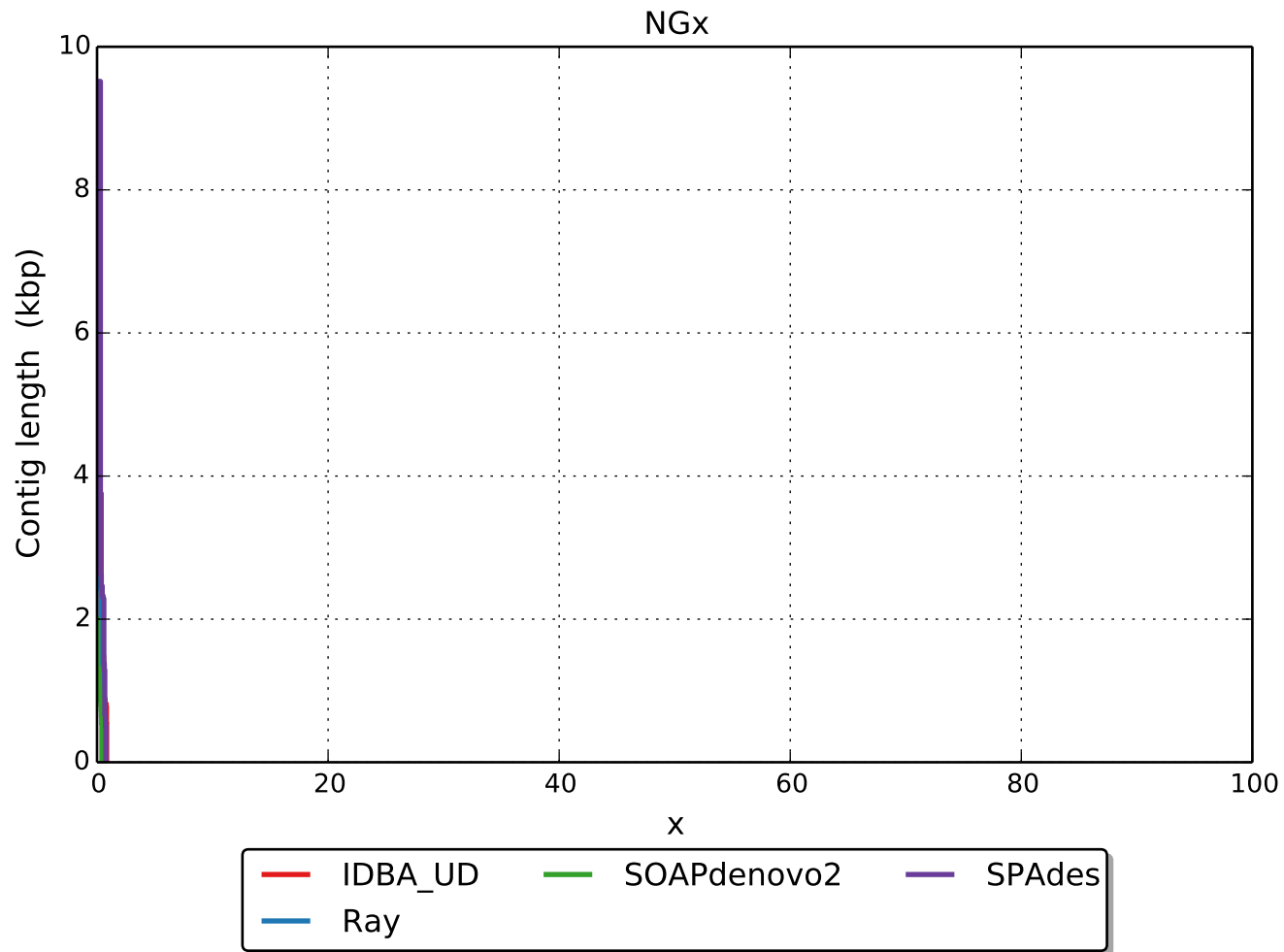
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

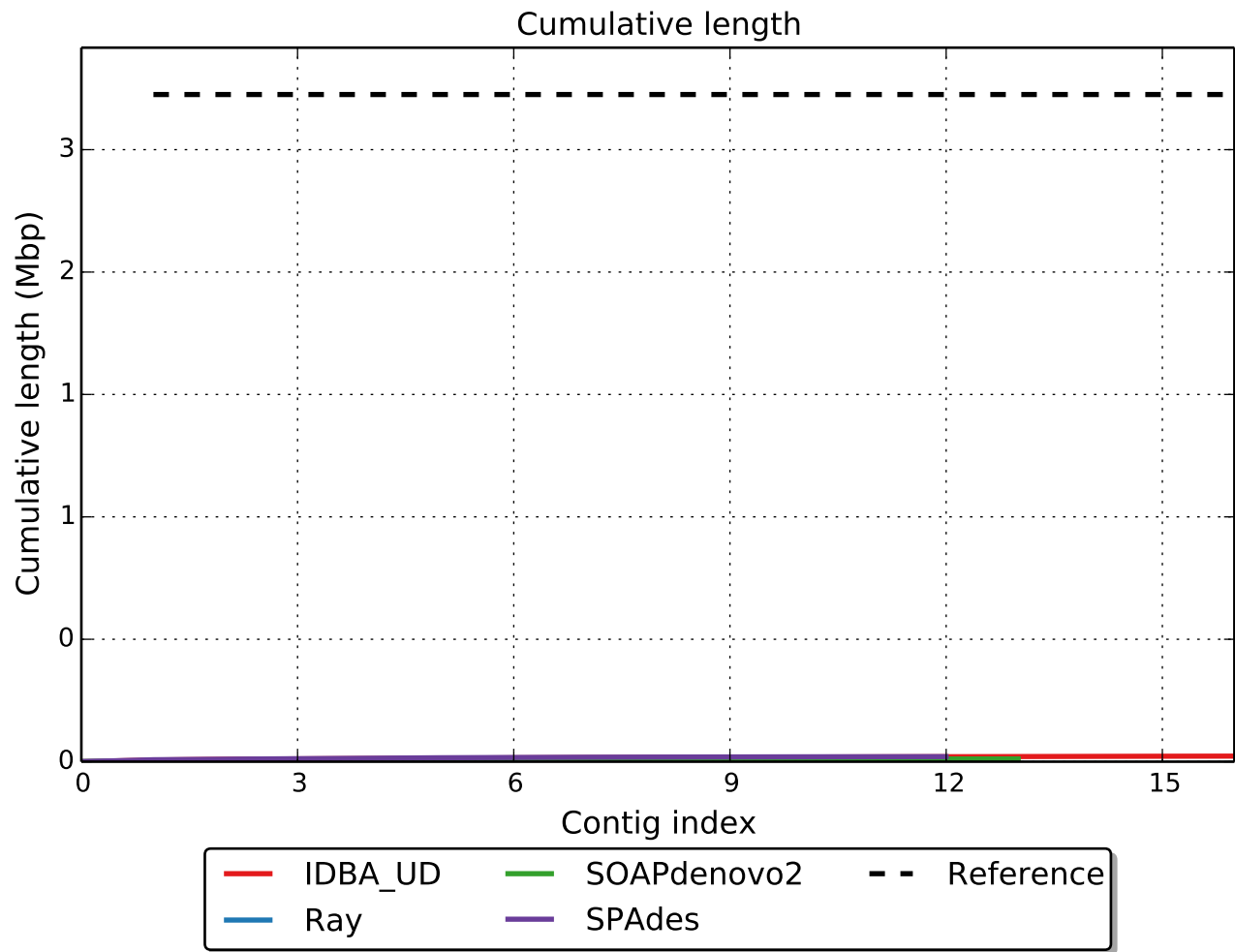
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	10	3	3	9
# with misassembly	0	0	0	0
# both parts are significant	1	1	0	0
Partially unaligned length	8089	2441	1904	18537
# N's	29	0	476	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).







GC content

