

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	409	165	55	190
# contigs (>= 5000 bp)	33	79	3	67
# contigs (>= 10000 bp)	5	52	0	26
# contigs (>= 25000 bp)	0	30	0	7
# contigs (>= 50000 bp)	0	12	0	2
Total length (>= 1000 bp)	969818	2429057	118320	1133647
Total length (>= 5000 bp)	252276	2205488	18497	910888
Total length (>= 10000 bp)	62628	2016729	0	613342
Total length (>= 25000 bp)	0	1672466	0	334714
Total length (>= 50000 bp)	0	1054317	0	172901
# contigs	932	192	312	434
Largest contig	15597	127463	6744	87691
Total length	1341028	2448098	289479	1304291
Reference length	2124757	2124757	2124757	2124757
GC (%)	39.17	40.19	38.77	41.00
Reference GC (%)	39.18	39.18	39.18	39.18
N50	1807	40900	836	9622
NG50	849	47818	-	1390
N75	937	16042	651	2948
NG75	-	27995	-	-
L50	183	16	84	30
LG50	510	13	-	128
L75	447	38	183	85
LG75	-	28	-	-
# misassemblies	15	9	2	21
# misassembled contigs	15	6	2	14
Misassembled contigs length	31319	103846	6363	235102
# local misassemblies	59	18	2	24
# structural variations	2	8	0	4
# unaligned contigs	0 + 293 part	0 + 96 part	0 + 65 part	0 + 103 part
Unaligned length	439141	1607862	48784	431227
Genome fraction (%)	33.984	29.736	11.097	35.646
Duplication ratio	1.249	1.330	1.021	1.153
# N's per 100 kbp	0.00	290.88	1616.35	1803.05
# mismatches per 100 kbp	3476.13	4031.01	2512.42	3683.81
# indels per 100 kbp	53.04	55.24	43.26	53.34
Largest alignment	15524	28228	6744	20423
NA50	694	-	691	869
NGA50	-	-	-	-
NA75	-	-	514	-
LA50	513	-	118	228
LA75	-	-	240	-

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	15	9	2	21
# relocations	7	6	2	18
# translocations	8	3	0	3
# inversions	0	0	0	0
# possibly misassembled contigs	115	69	4	64
# misassembled contigs	15	6	2	14
Misassembled contigs length	31319	103846	6363	235102
# local misassemblies	59	18	2	24
# structural variations	2	8	0	4
# mismatches	25100	25469	5924	27901
# indels	383	349	102	404
# short indels	352	340	98	377
# long indels	31	9	4	27
Indels length	1122	607	156	1533

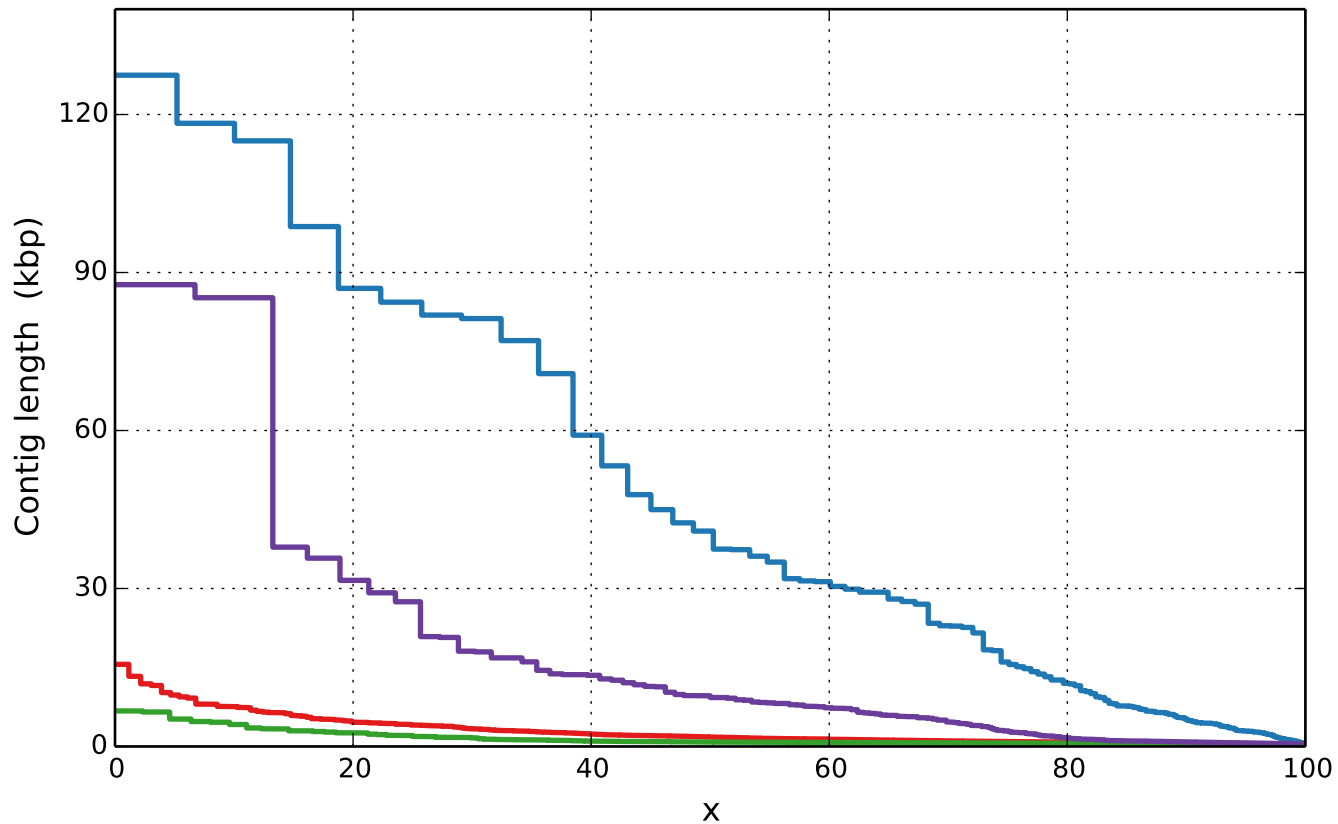
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	293	96	65	103
# with misassembly	23	24	2	11
# both parts are significant	102	59	4	45
Partially unaligned length	439141	1607862	48784	431227
# N's	0	7121	4679	23517

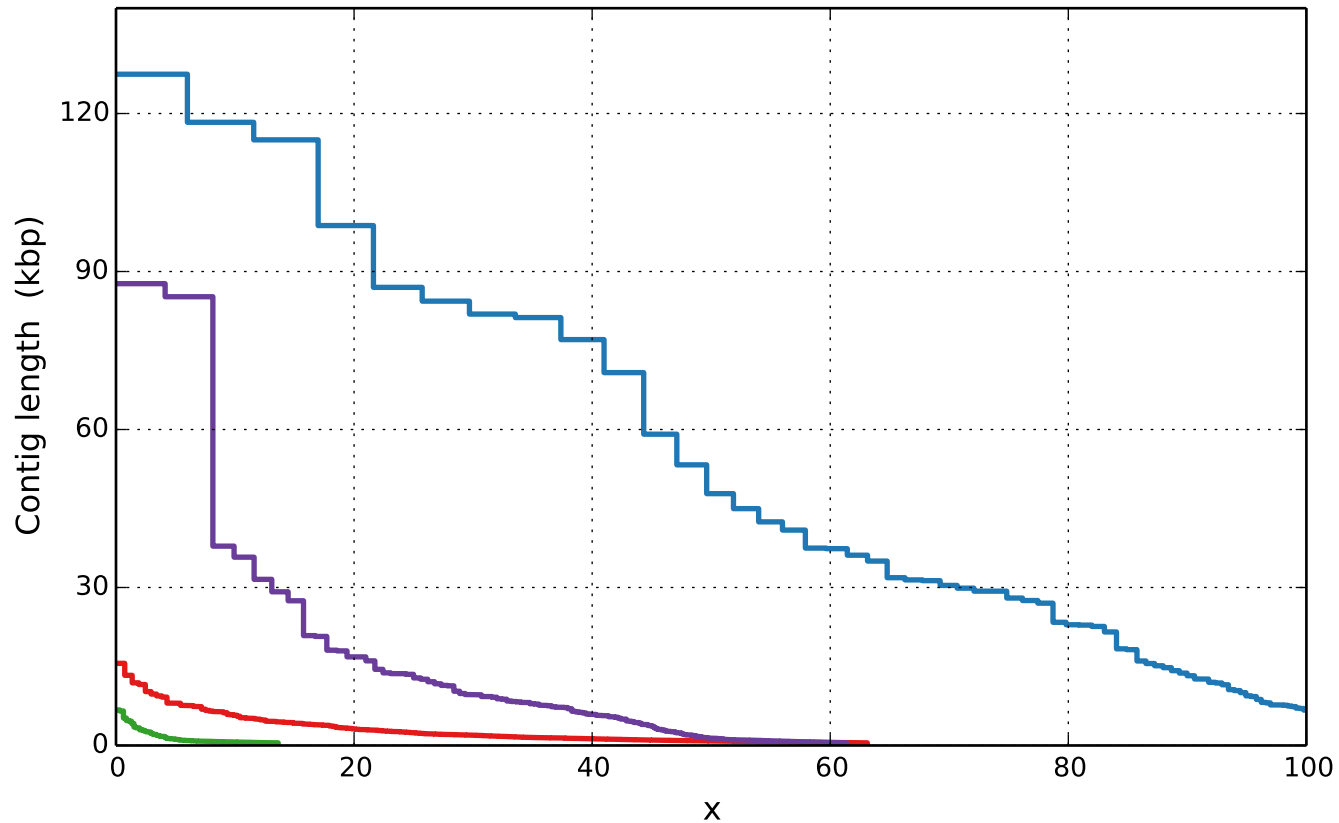
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



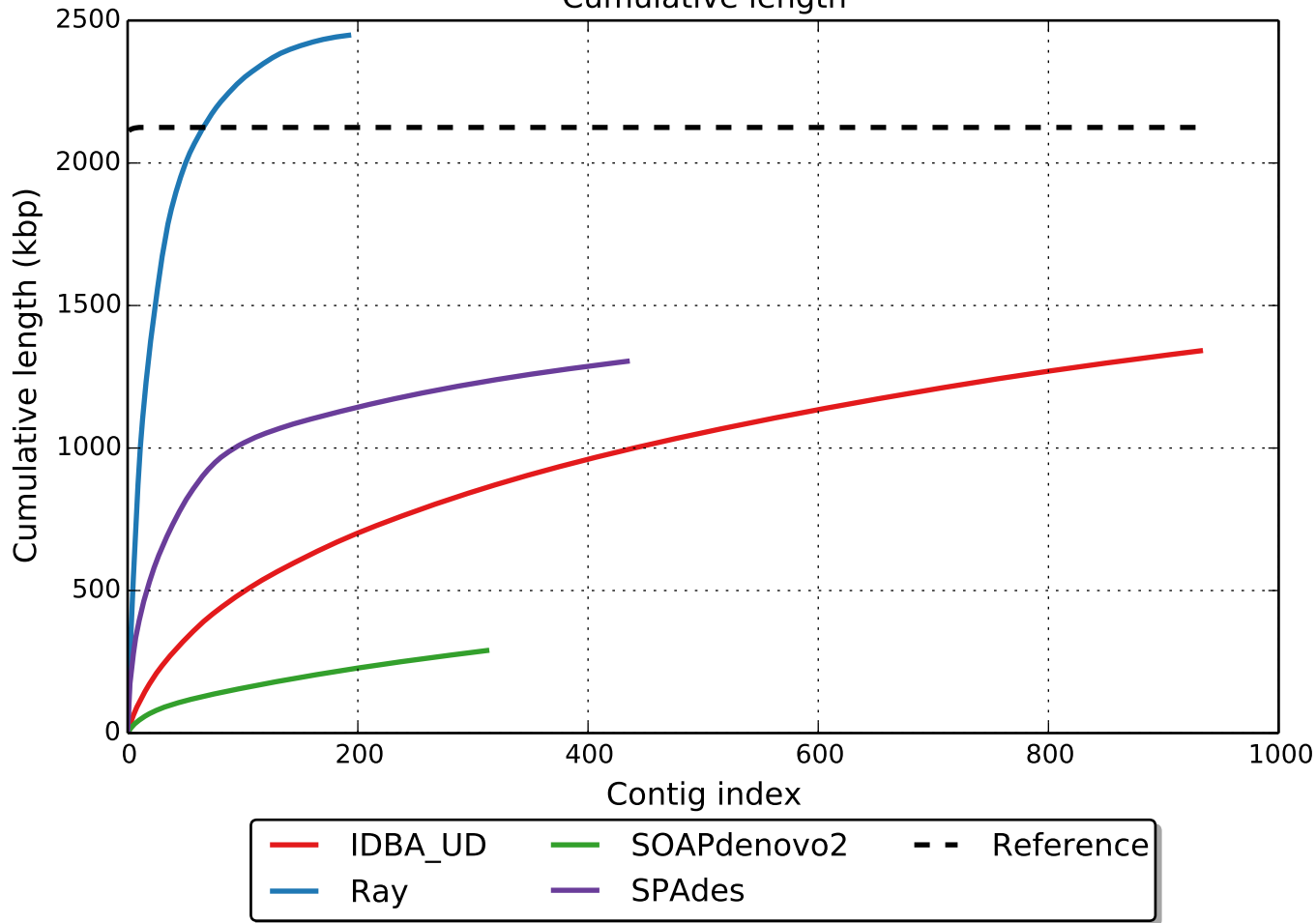
— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray

NGx

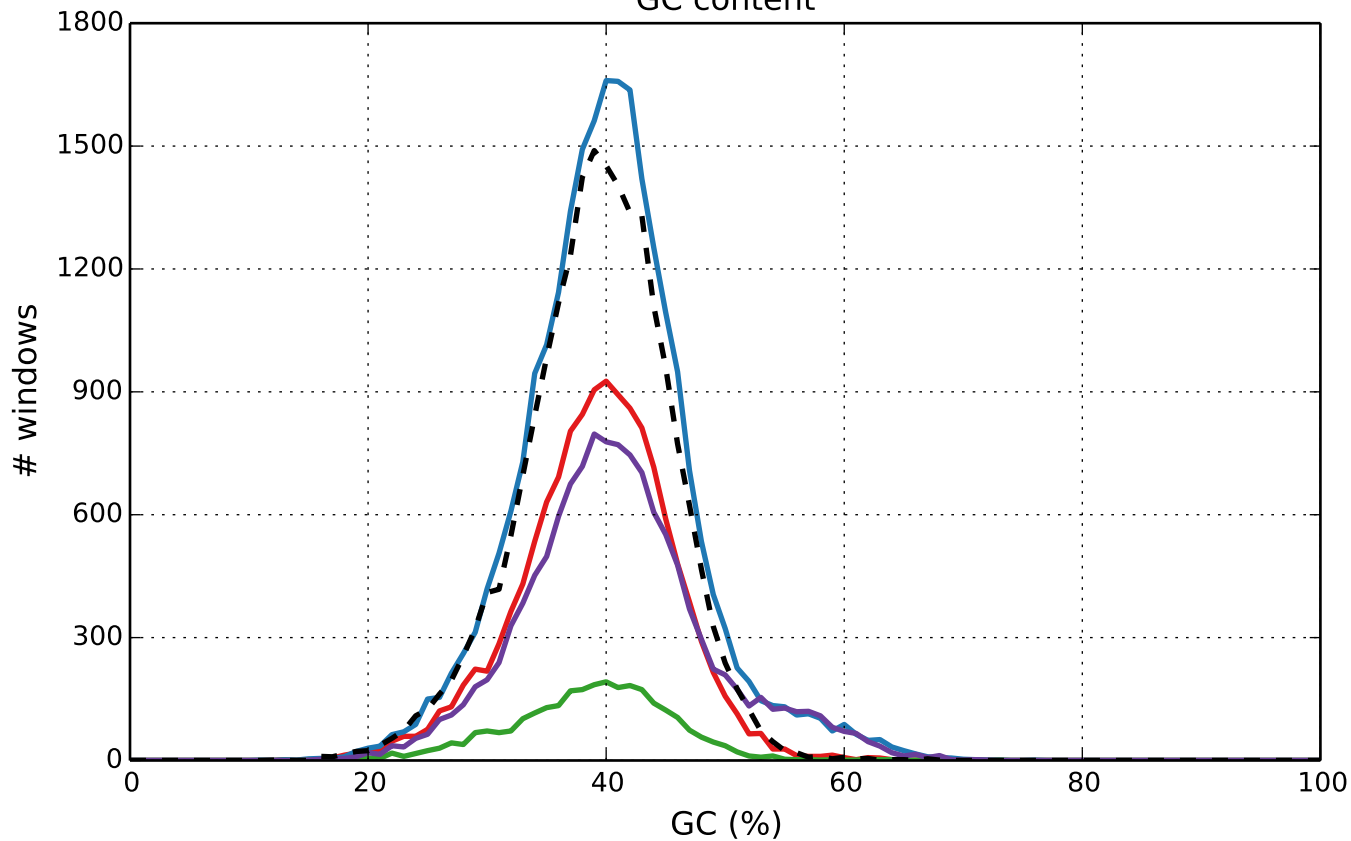


— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray

Cumulative length

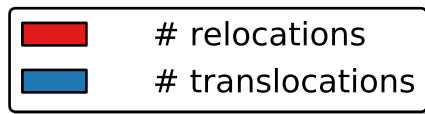
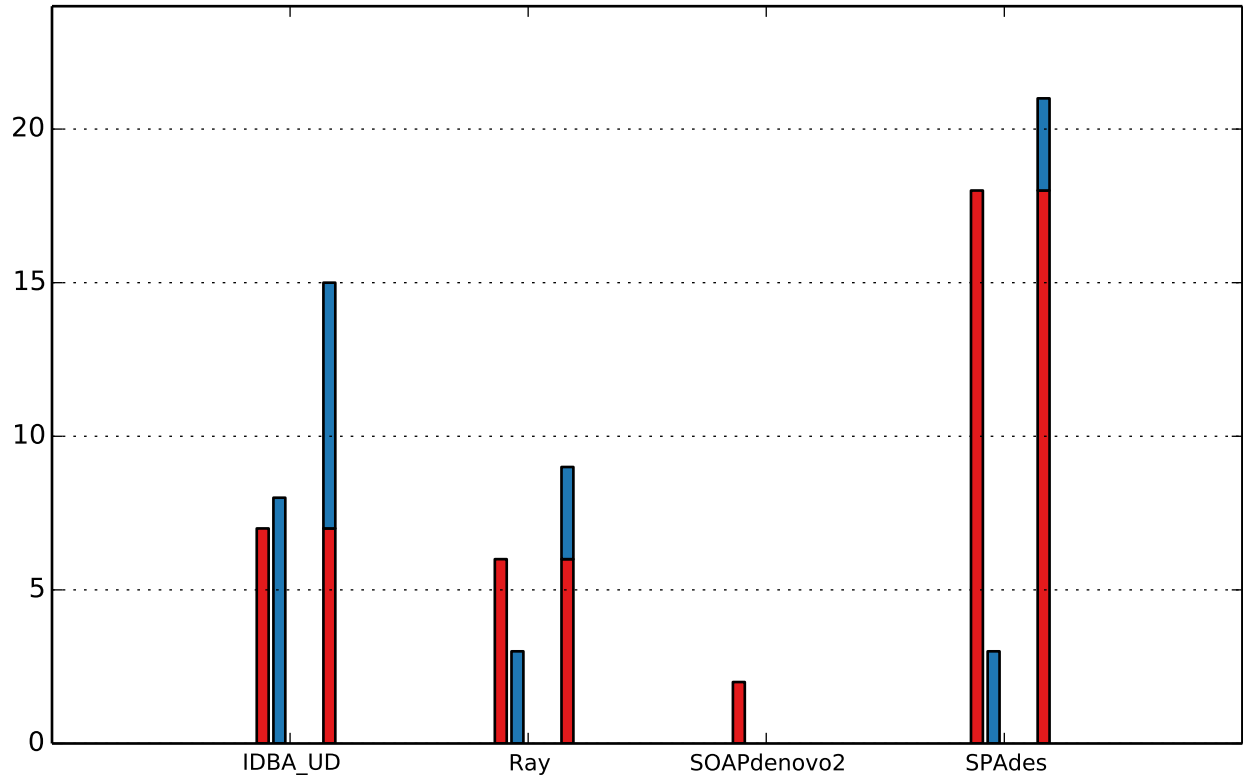


GC content



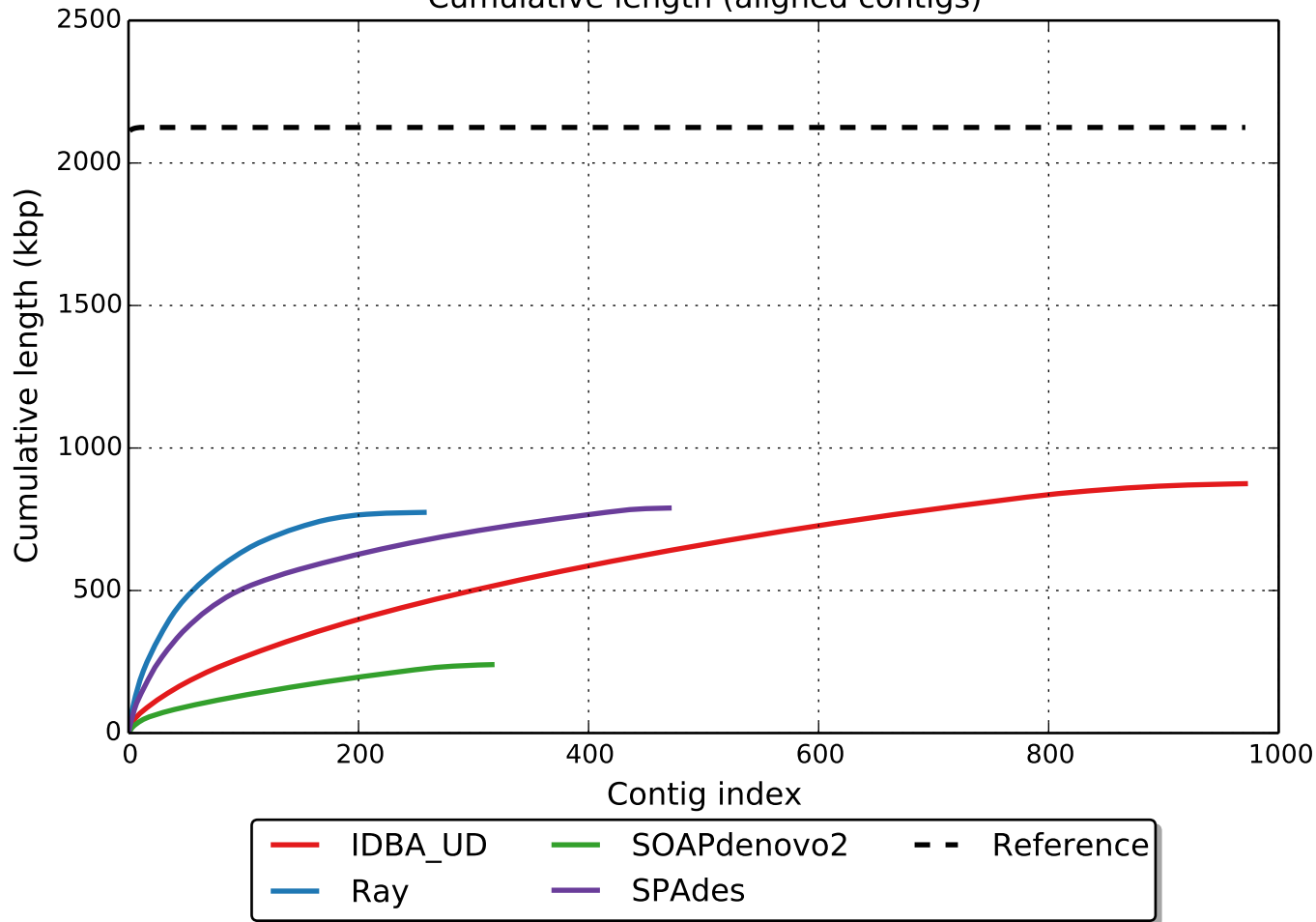
— IDBA\_UD — SOAPdenovo2 - - Reference  
— Ray — SPAdes

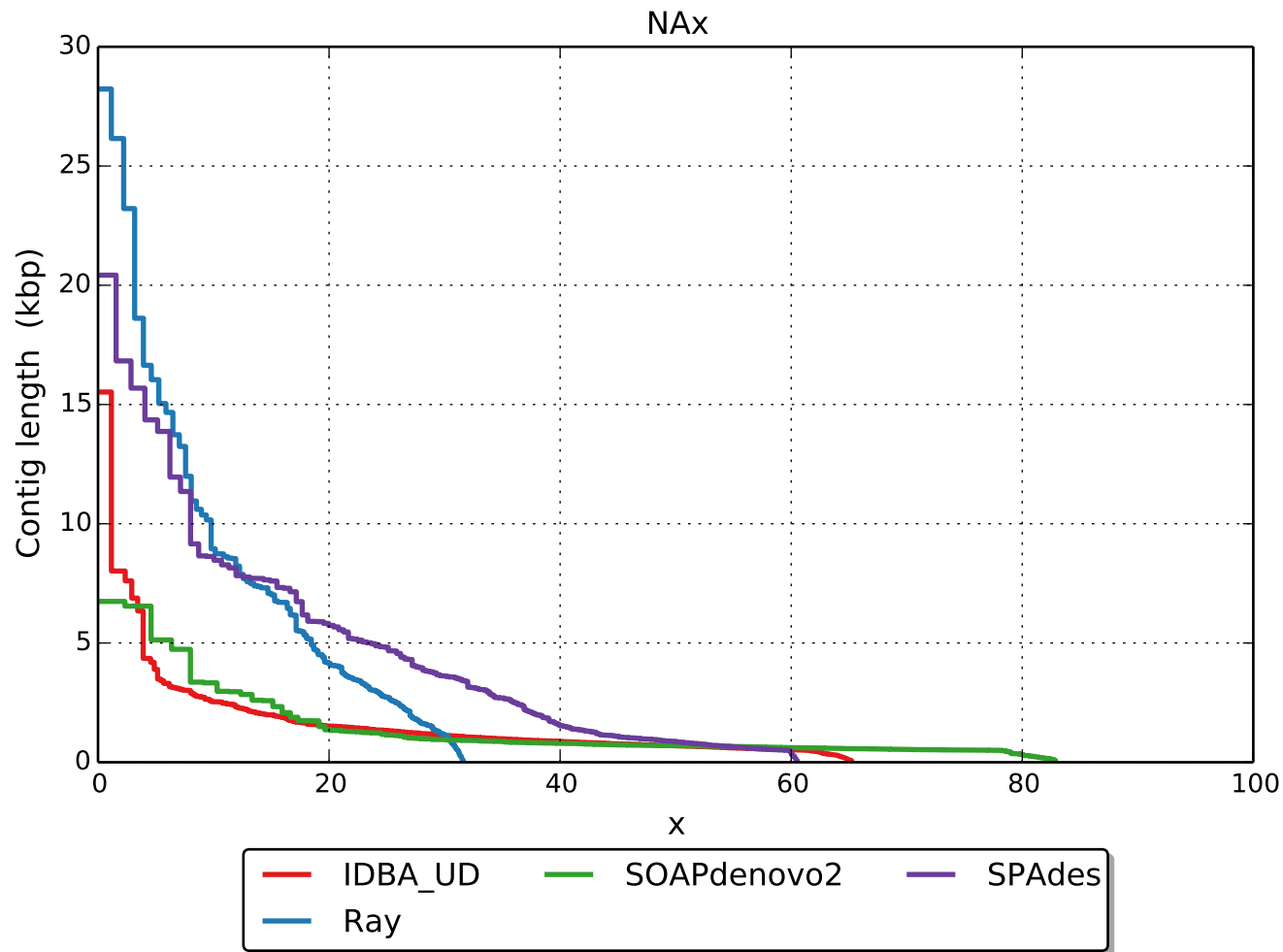
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

