

# Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	443	273	336	212
# contigs (>= 5000 bp)	93	92	15	84
# contigs (>= 10000 bp)	41	60	4	50
# contigs (>= 25000 bp)	8	32	1	14
# contigs (>= 50000 bp)	1	11	1	4
Total length (>= 1000 bp)	1863428	2600527	748362	1779766
Total length (>= 5000 bp)	1129526	2215365	170155	1533695
Total length (>= 10000 bp)	760484	1975707	102395	1281413
Total length (>= 25000 bp)	305612	1514353	55395	723405
Total length (>= 50000 bp)	79696	800120	55395	365623
# contigs	858	363	918	413
Largest contig	79696	118495	55395	163268
Total length	2146793	2668342	1143647	1922174
Reference length	1756105	1756105	1756105	1756105
GC (%)	29.74	29.84	29.75	29.71
Reference GC (%)	29.81	29.81	29.81	29.81
N50	5505	26948	1505	17911
NG50	8739	44409	784	19140
N75	1750	9686	813	6949
NG75	3707	28166	-	9612
L50	83	26	191	26
LG50	54	13	484	22
L75	253	63	458	69
LG75	137	25	-	54
# misassemblies	31	63	2	39
# misassembled contigs	28	43	2	30
Misassembled contigs length	153846	913838	2689	649316
# local misassemblies	49	62	33	35
# structural variations	15	26	5	14
# unaligned contigs	0 + 172 part	0 + 63 part	0 + 196 part	0 + 81 part
Unaligned length	463379	417509	301121	234170
Genome fraction (%)	82.201	89.535	45.476	87.002
Duplication ratio	1.166	1.432	1.055	1.105
# N's per 100 kbp	0.51	289.62	2573.17	559.57
# mismatches per 100 kbp	1817.69	2269.24	1268.84	2043.14
# indels per 100 kbp	68.93	76.57	43.33	64.67
Largest alignment	29768	69026	11298	73172
NA50	2184	10628	743	9455
NGA50	3675	23234	-	11128
NA75	514	856	-	1162
NGA75	1114	10925	-	2409
LA50	174	51	392	48
LGA50	106	23	-	40
LA75	738	308	-	194
LGA75	335	50	-	115

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

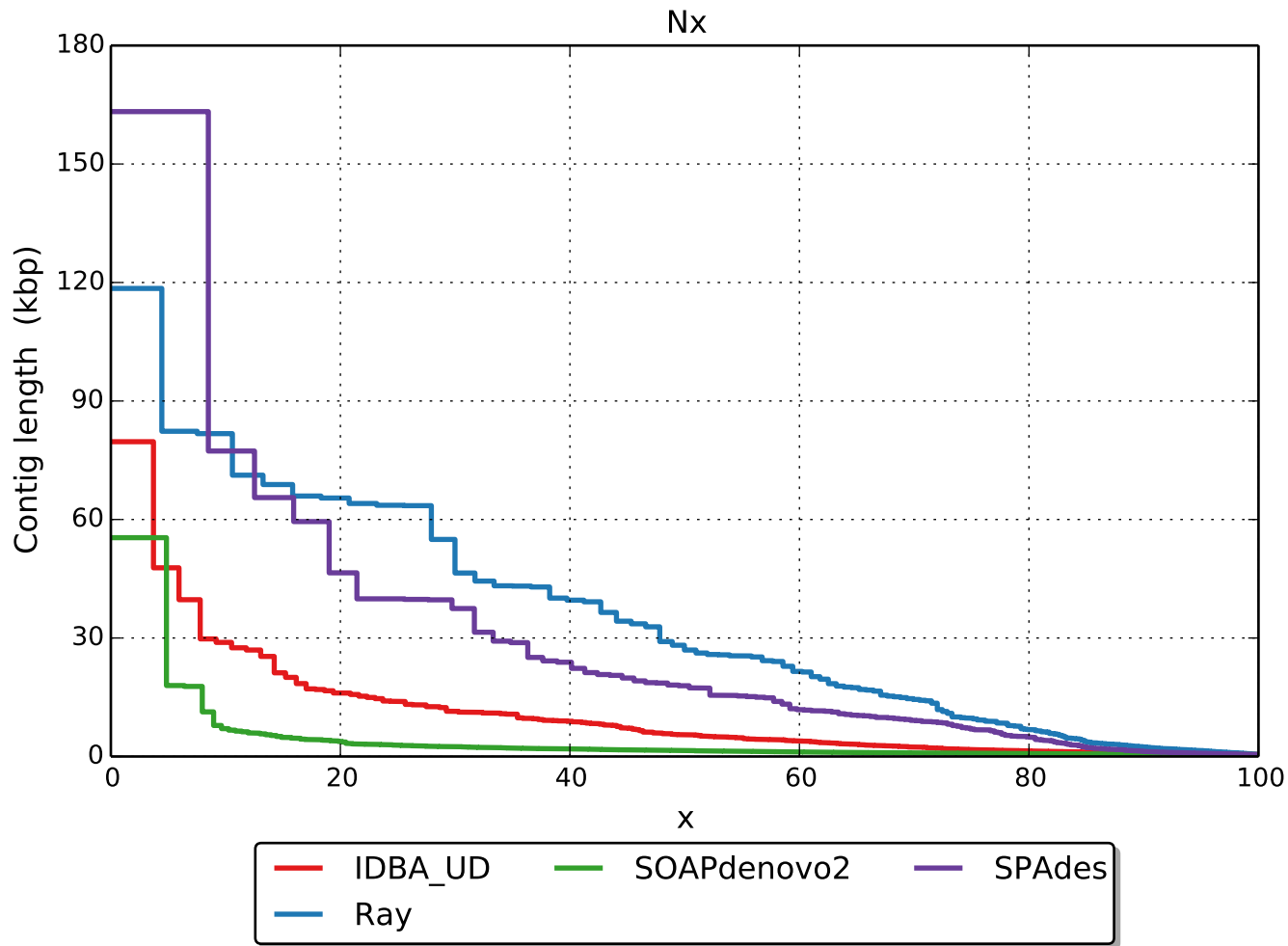
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	31	63	2	39
# relocations	13	39	2	35
# translocations	18	24	0	4
# inversions	0	0	0	0
# possibly misassembled contigs	55	51	36	50
# misassembled contigs	28	43	2	30
Misassembled contigs length	153846	913838	2689	649316
# local misassemblies	49	62	33	35
# structural variations	15	26	5	14
# mismatches	26239	35680	10133	31216
# indels	995	1204	346	988
# short indels	805	1115	284	917
# long indels	190	89	62	71
Indels length	6138	2541	2198	3075

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).

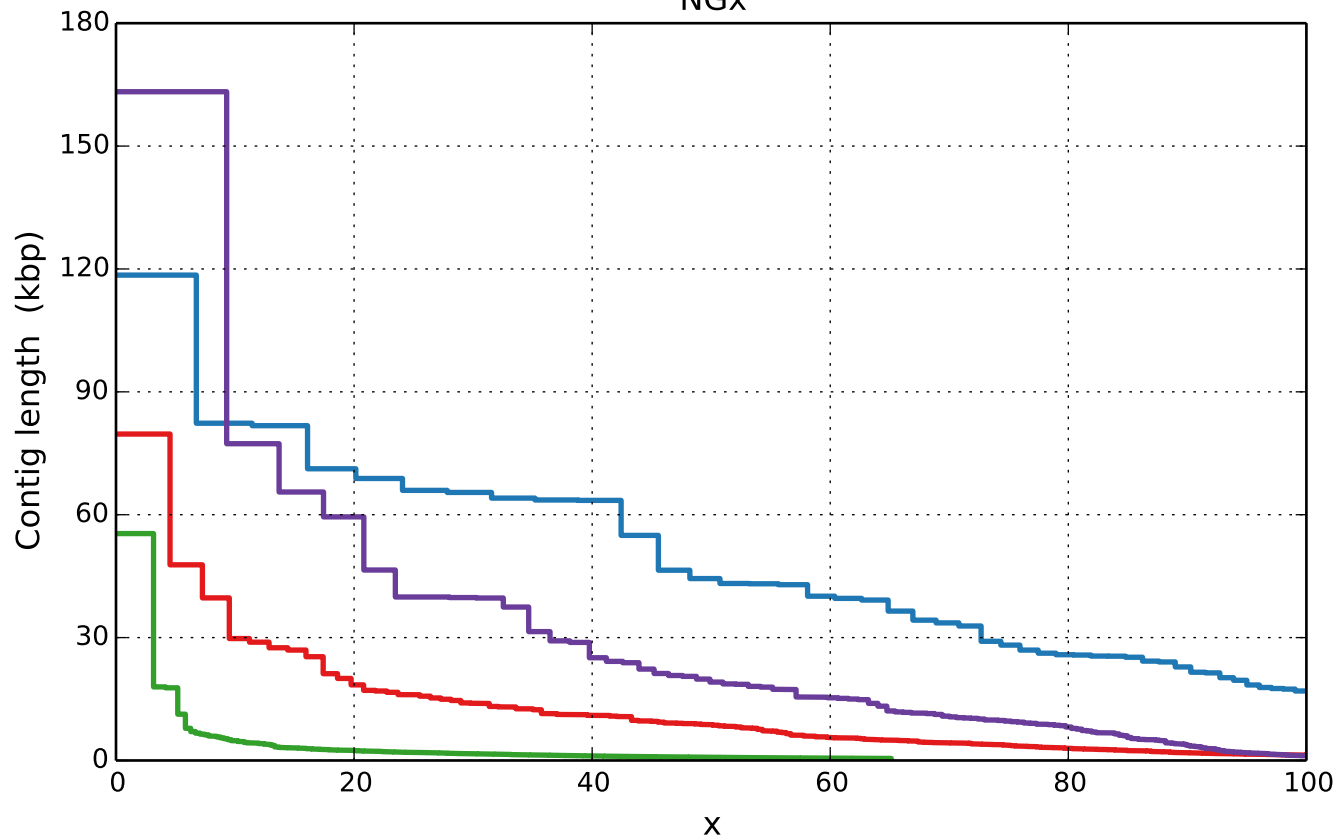
## Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	172	63	196	81
# with misassembly	16	13	30	8
# both parts are significant	38	27	28	21
Partially unaligned length	463379	417509	301121	234170
# N's	11	7728	29428	10756

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).

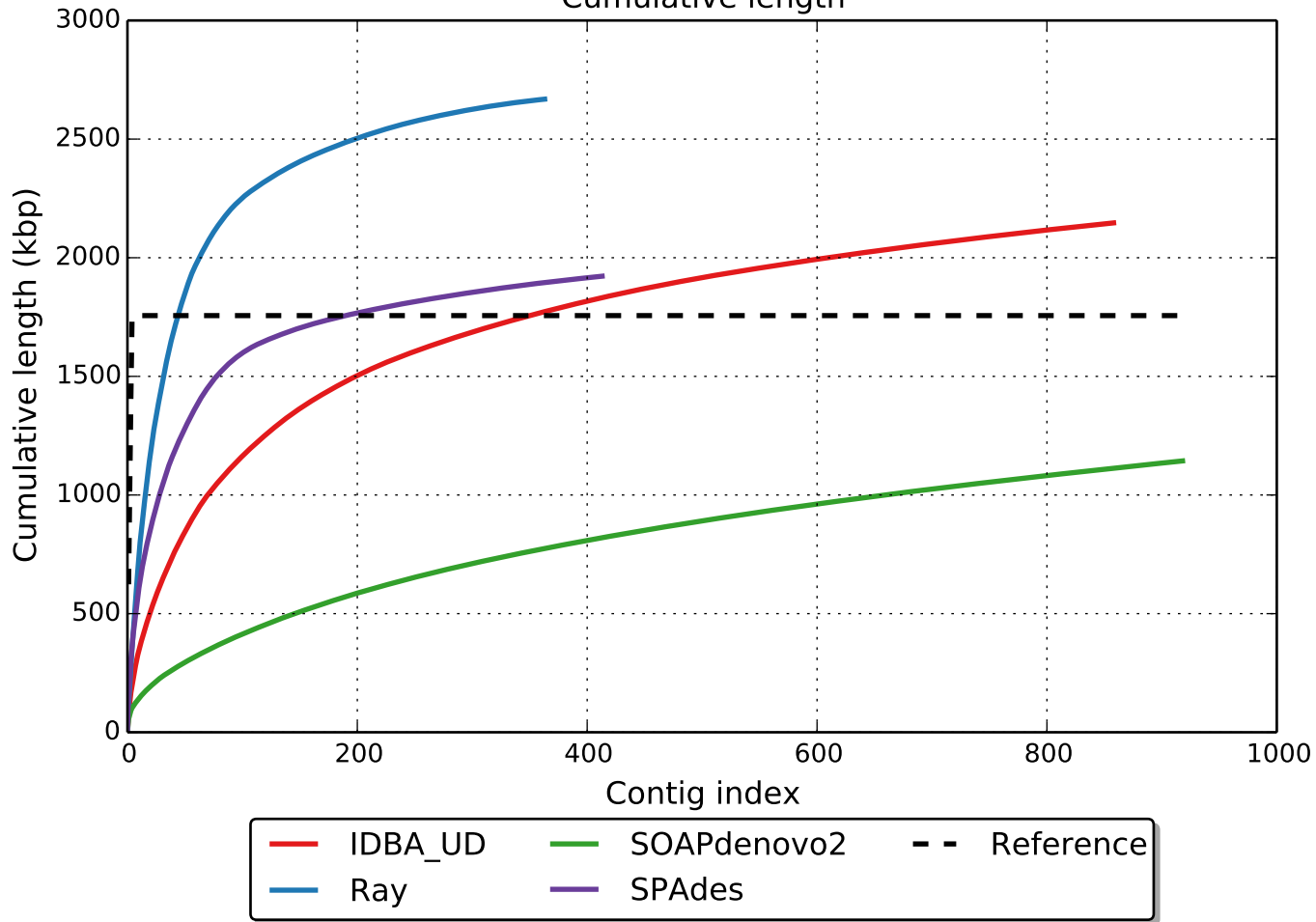


NGx

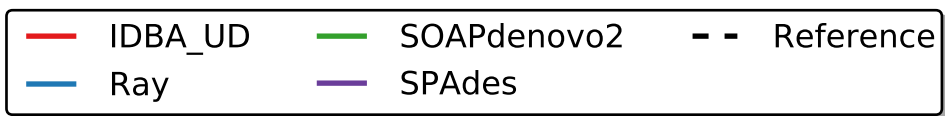
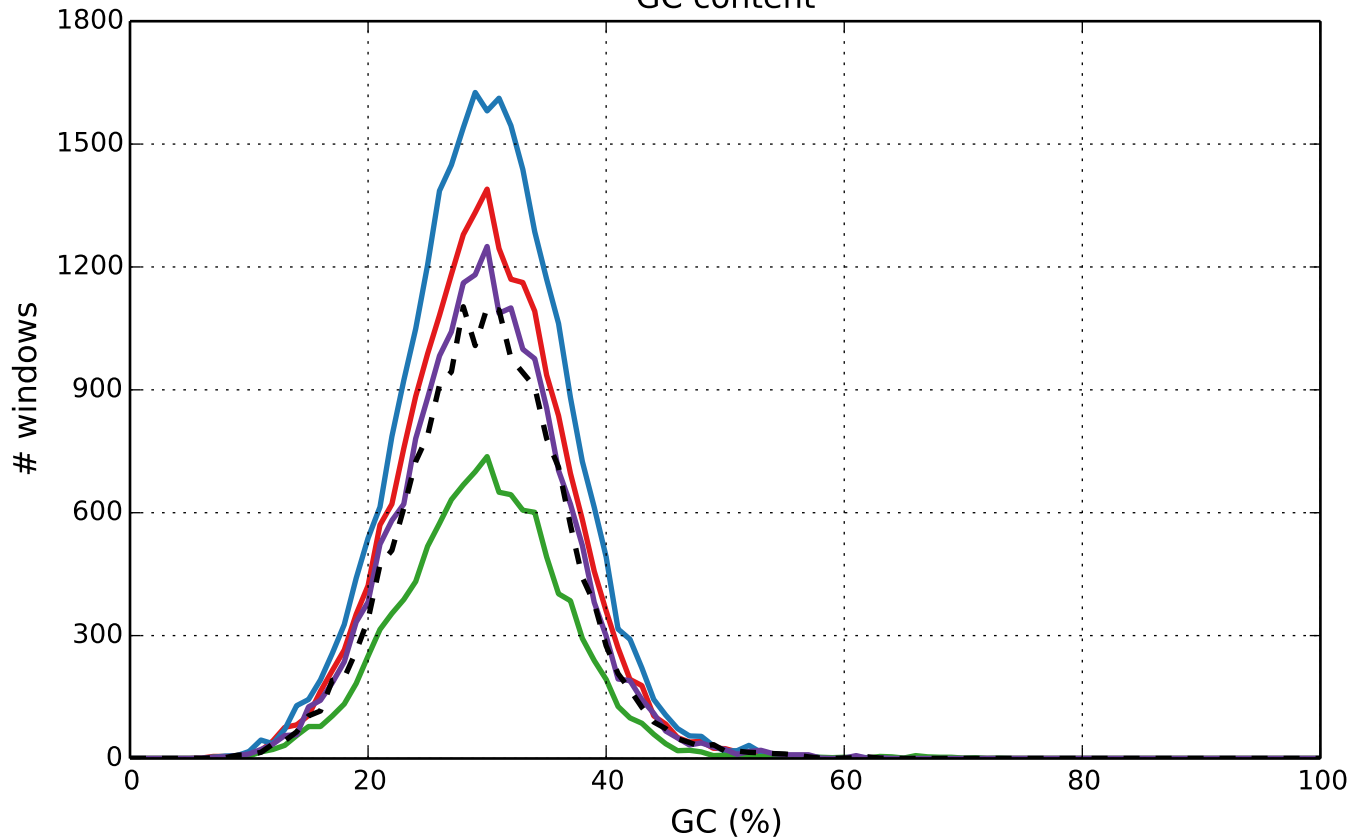


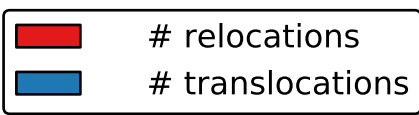
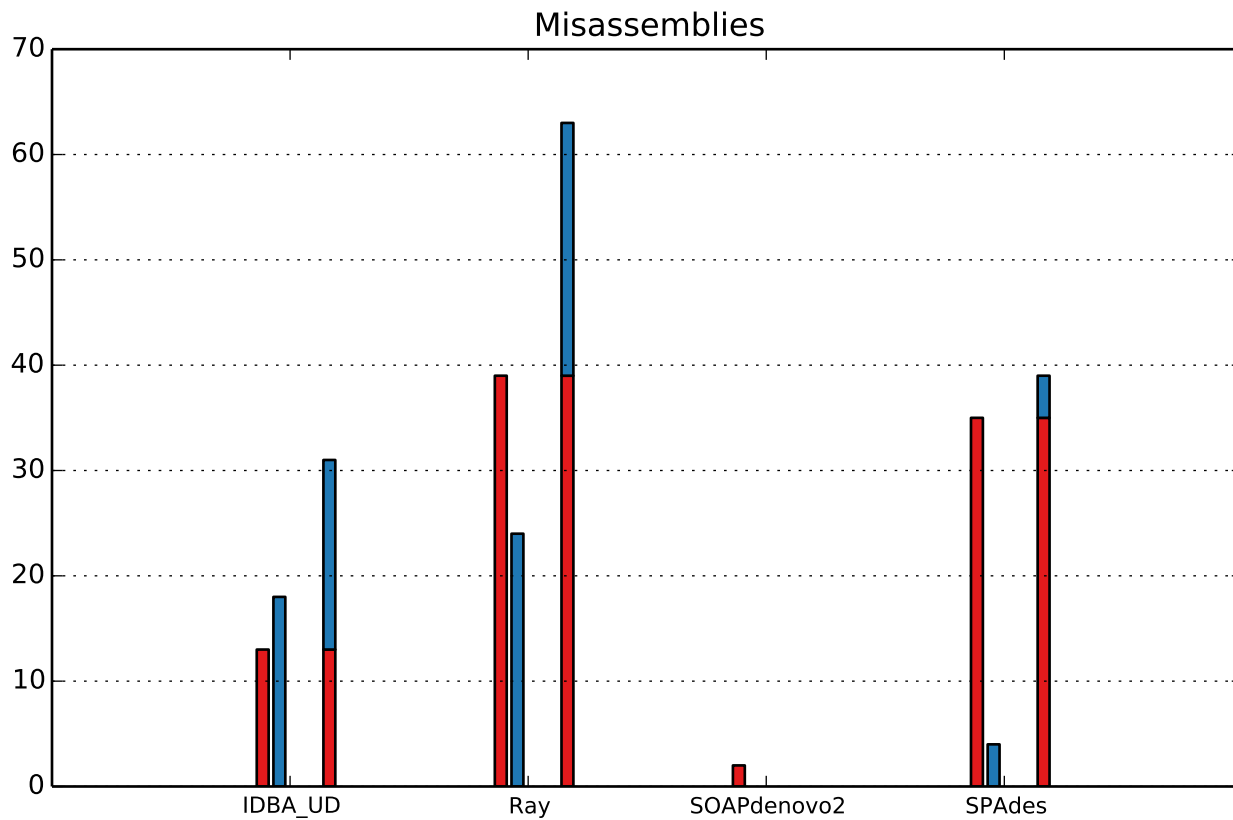
— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray

Cumulative length



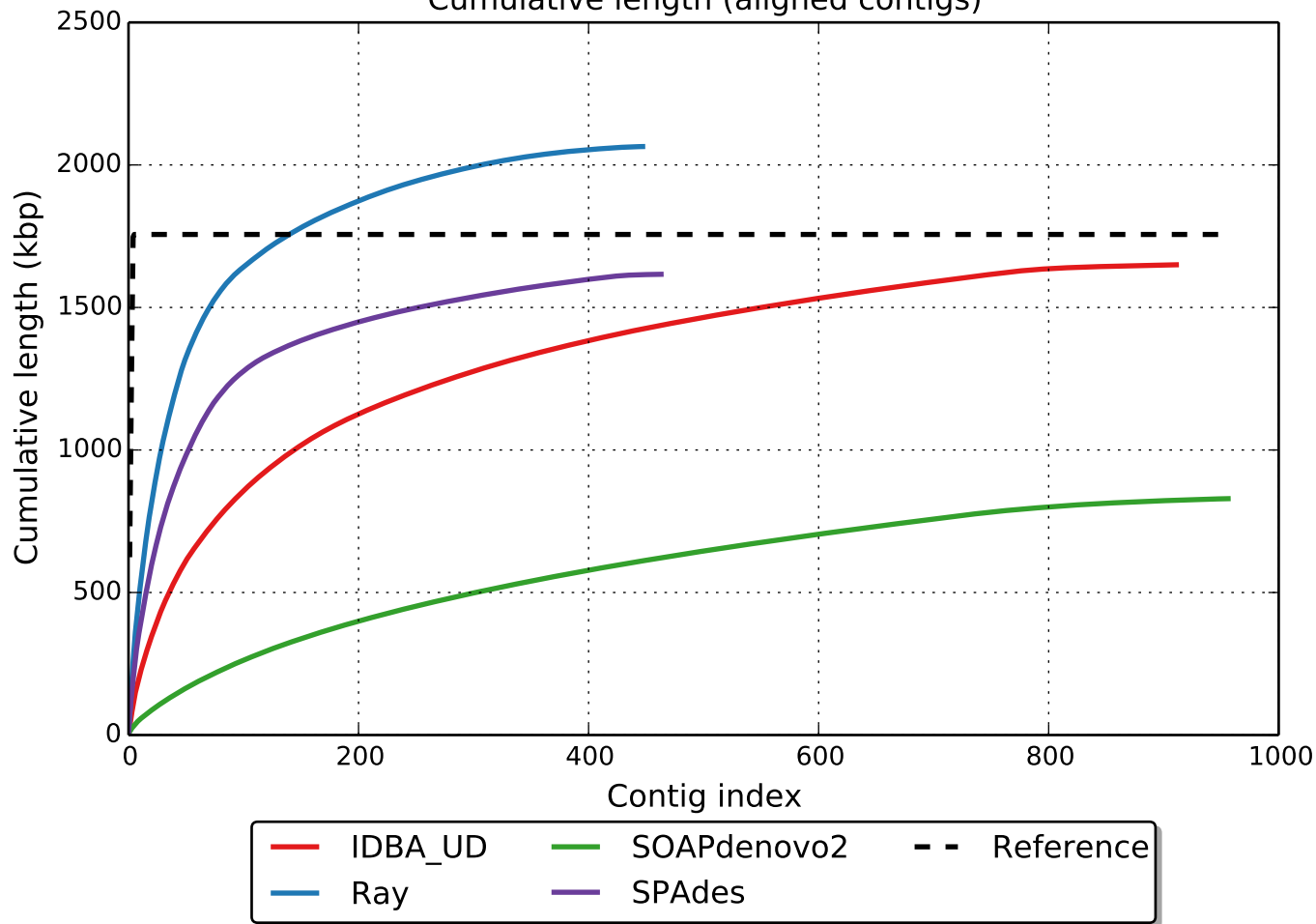
GC content

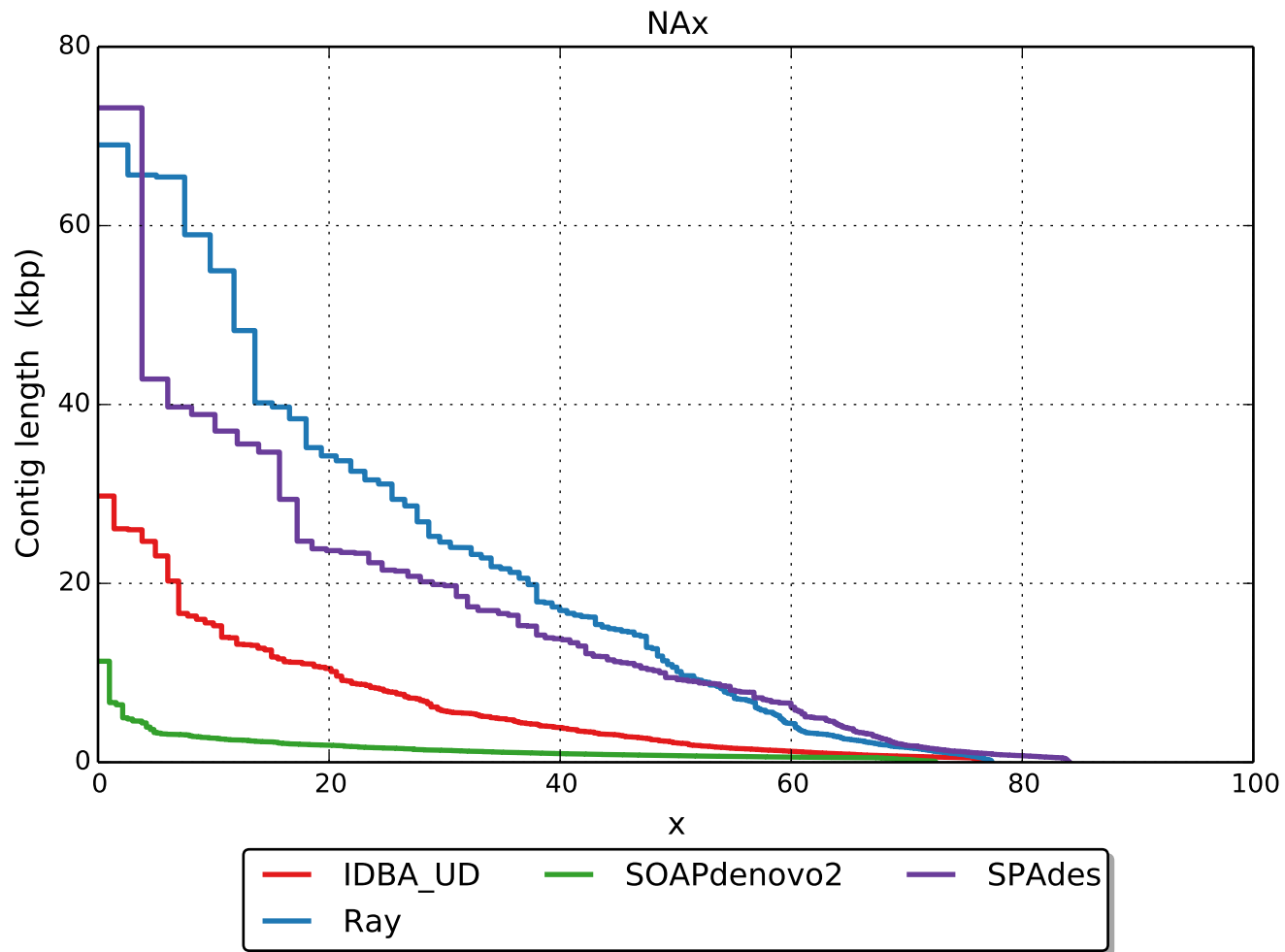






Cumulative length (aligned contigs)





# NGAx

