

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (≥ 1000 bp)	574	414	340	499
# contigs (≥ 5000 bp)	64	159	24	79
# contigs (≥ 10000 bp)	13	101	6	23
# contigs (≥ 25000 bp)	3	42	2	1
# contigs (≥ 50000 bp)	0	6	0	0
Total length (≥ 1000 bp)	1573576	3727188	813549	1588764
Total length (≥ 5000 bp)	590814	3124709	237941	719197
Total length (≥ 10000 bp)	233112	2720379	117995	340859
Total length (≥ 25000 bp)	93234	1802621	67530	43808
Total length (≥ 50000 bp)	0	509315	0	0
# contigs	1254	521	953	941
Largest contig	38590	133326	39722	43808
Total length	2046301	3809572	1233247	1902589
Reference length	2176752	2176752	2176752	2176752
GC (%)	38.56	39.14	38.89	38.49
Reference GC (%)	38.95	38.95	38.95	38.95
N50	2239	22583	1497	3454
NG50	2047	37789	625	2683
N75	1066	7831	821	1333
NG75	939	28131	-	917
L50	196	47	178	135
LG50	227	20	692	180
L75	537	117	463	361
LG75	635	36	-	545
# misassemblies	28	80	3	18
# misassembled contigs	27	61	3	17
Misassembled contigs length	79377	1095179	33947	83280
# local misassemblies	113	114	47	29
# structural variations	5	14	3	10
# unaligned contigs	0 + 320 part	0 + 171 part	0 + 321 part	0 + 206 part
Unaligned length	524947	1257260	458302	346079
Genome fraction (%)	59.468	77.657	32.606	66.798
Duplication ratio	1.175	1.510	1.092	1.070
# N's per 100 kbp	0.78	443.12	4052.55	227.69
# mismatches per 100 kbp	2155.17	2659.19	1892.32	2319.91
# indels per 100 kbp	62.50	80.75	45.51	58.32
Largest alignment	23706	39467	20883	20883
NA50	965	2669	545	1772
NGA50	858	12868	-	1295
NA75	-	-	-	613
NGA75	-	5034	-	-
LA50	443	192	573	230
LGA50	515	50	-	323
LA75	-	-	-	709
LGA75	-	116	-	-

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	28	80	3	18
# relocations	8	30	0	8
# translocations	20	49	3	10
# inversions	0	1	0	0
# possibly misassembled contigs	75	150	54	62
# misassembled contigs	27	61	3	17
Misassembled contigs length	79377	1095179	33947	83280
# local misassemblies	113	114	47	29
# structural variations	5	14	3	10
# mismatches	27898	44951	13431	33732
# indels	809	1365	323	848
# short indels	657	1223	261	783
# long indels	152	142	62	65
Indels length	4918	3639	2765	2151

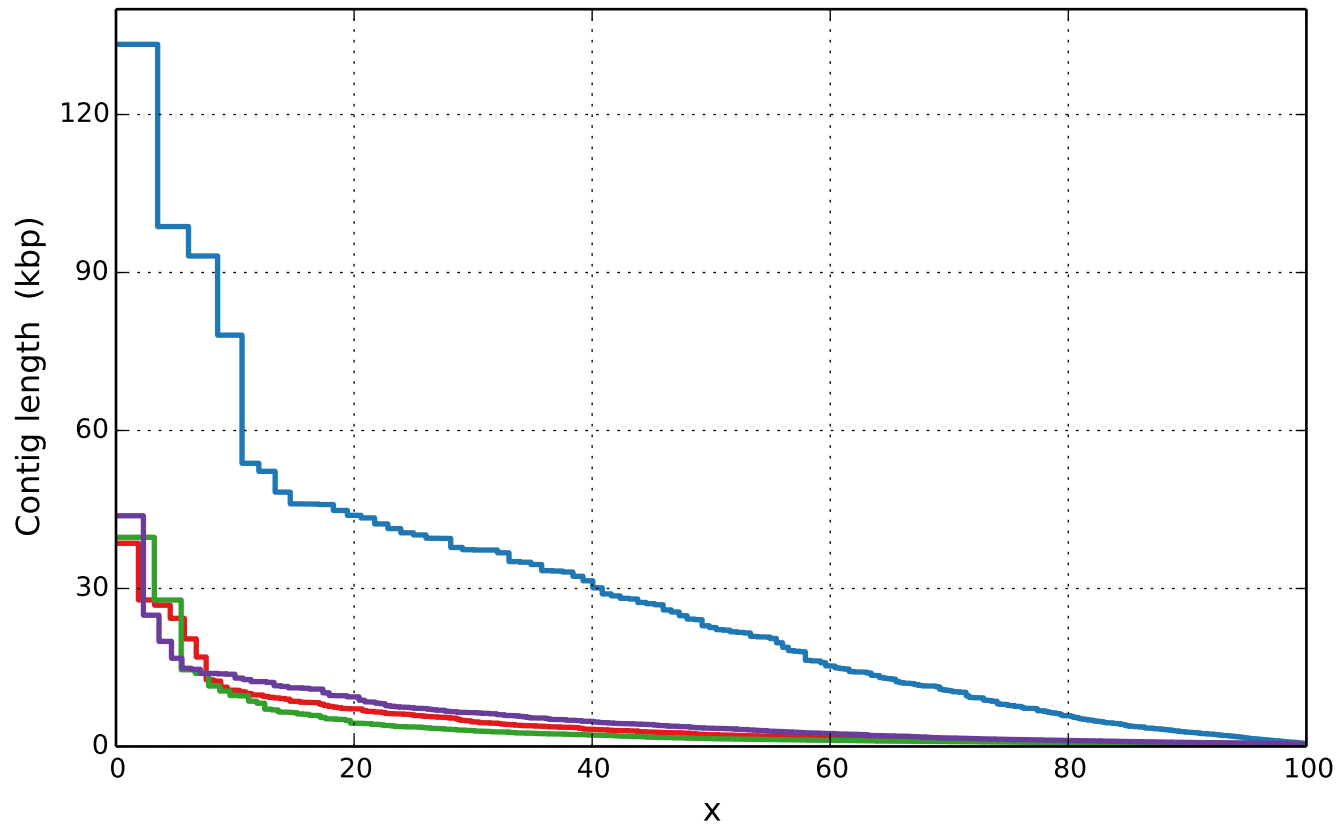
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

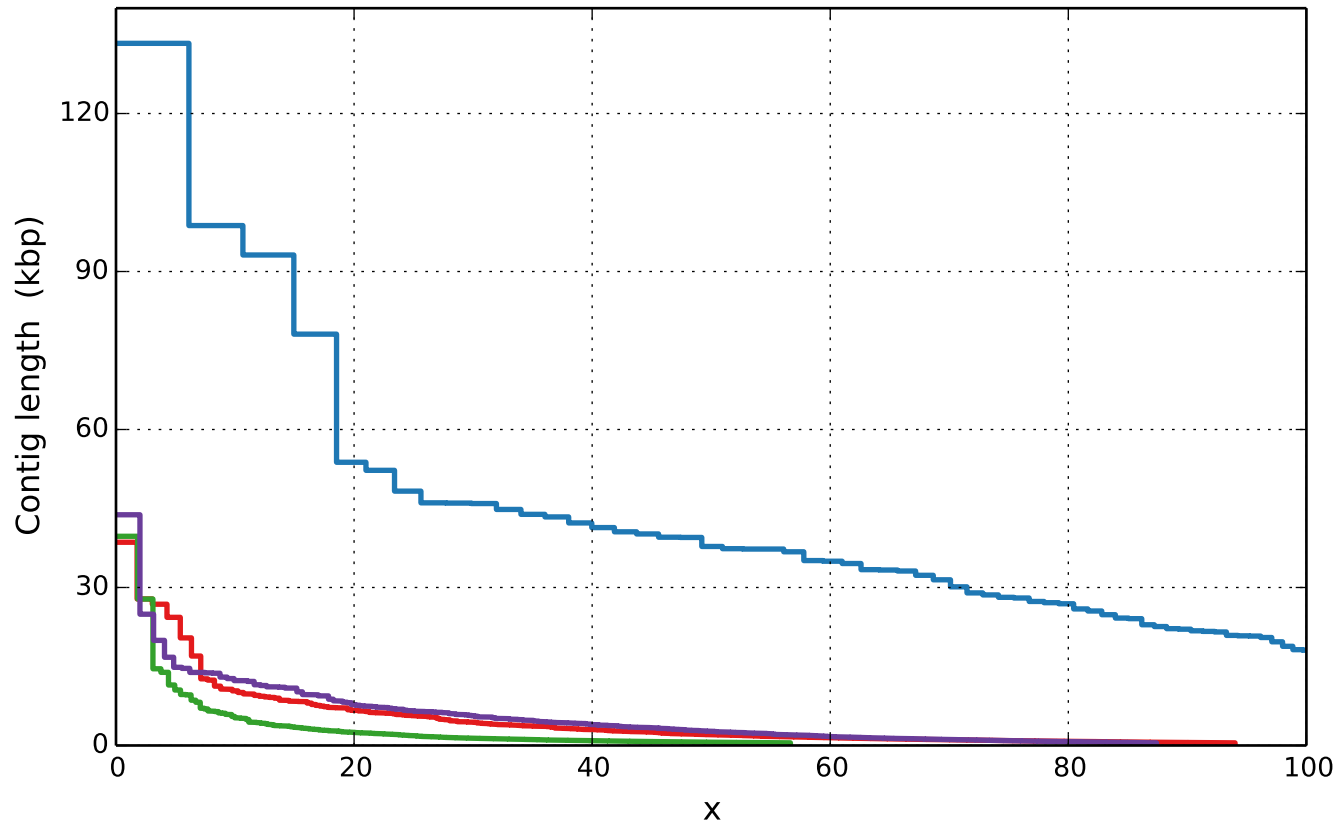
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	320	171	321	206
# with misassembly	27	41	51	13
# both parts are significant	64	94	41	53
Partially unaligned length	524947	1257260	458302	346079
# N's	16	16881	49978	4332

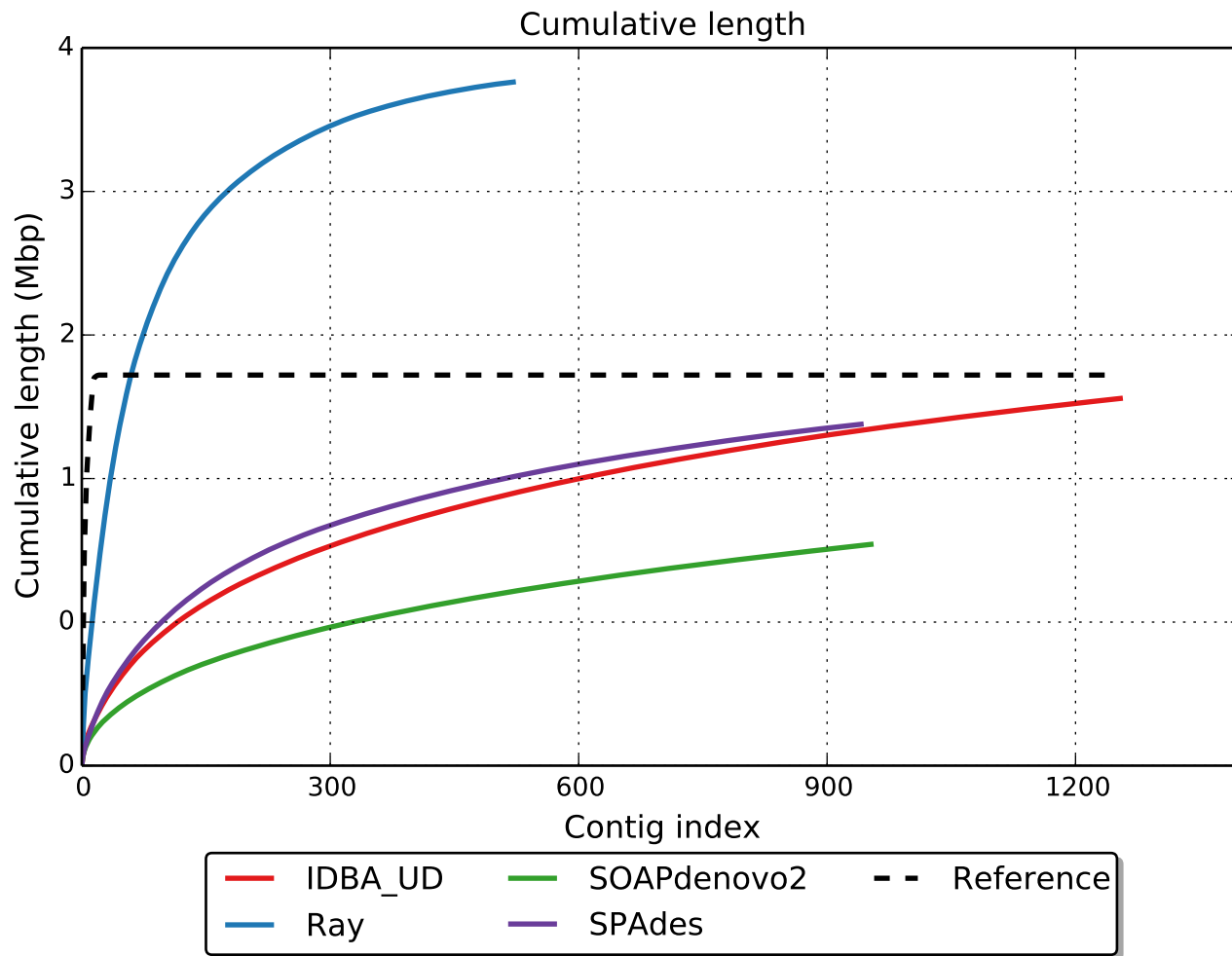
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

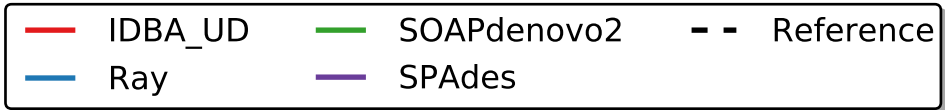
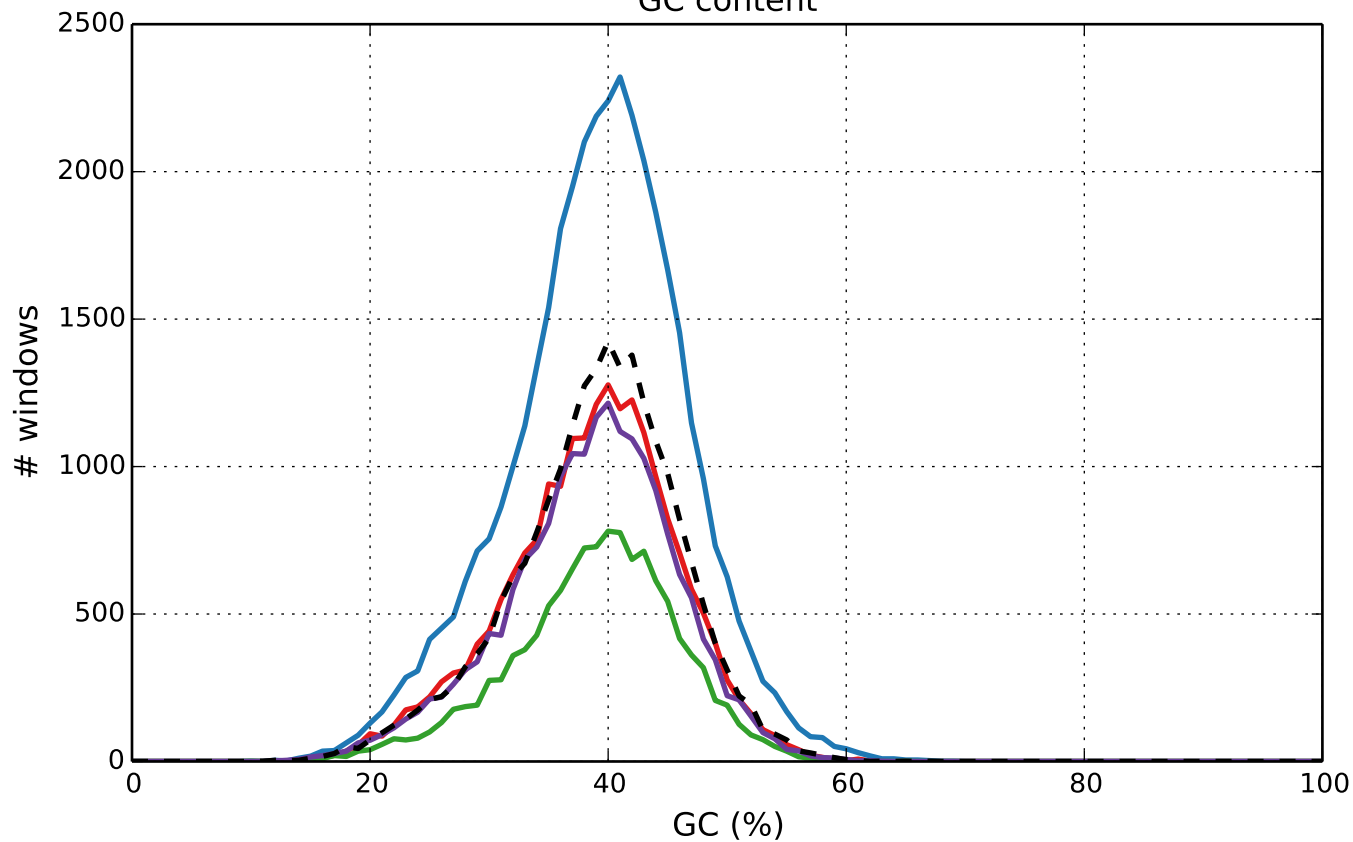


NGx

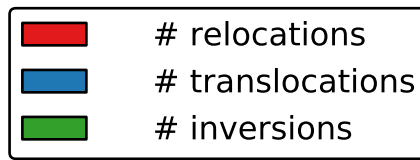
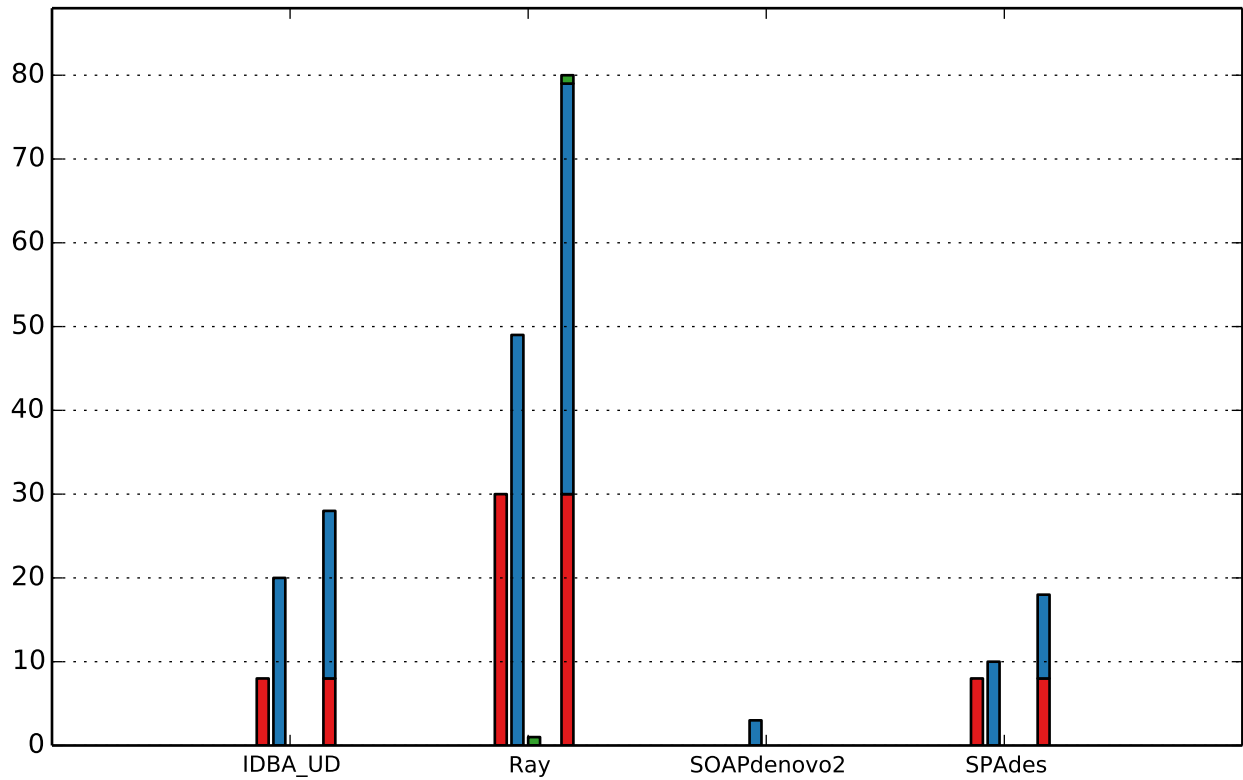




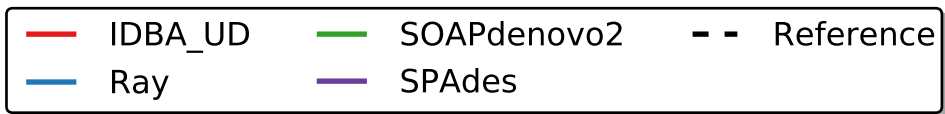
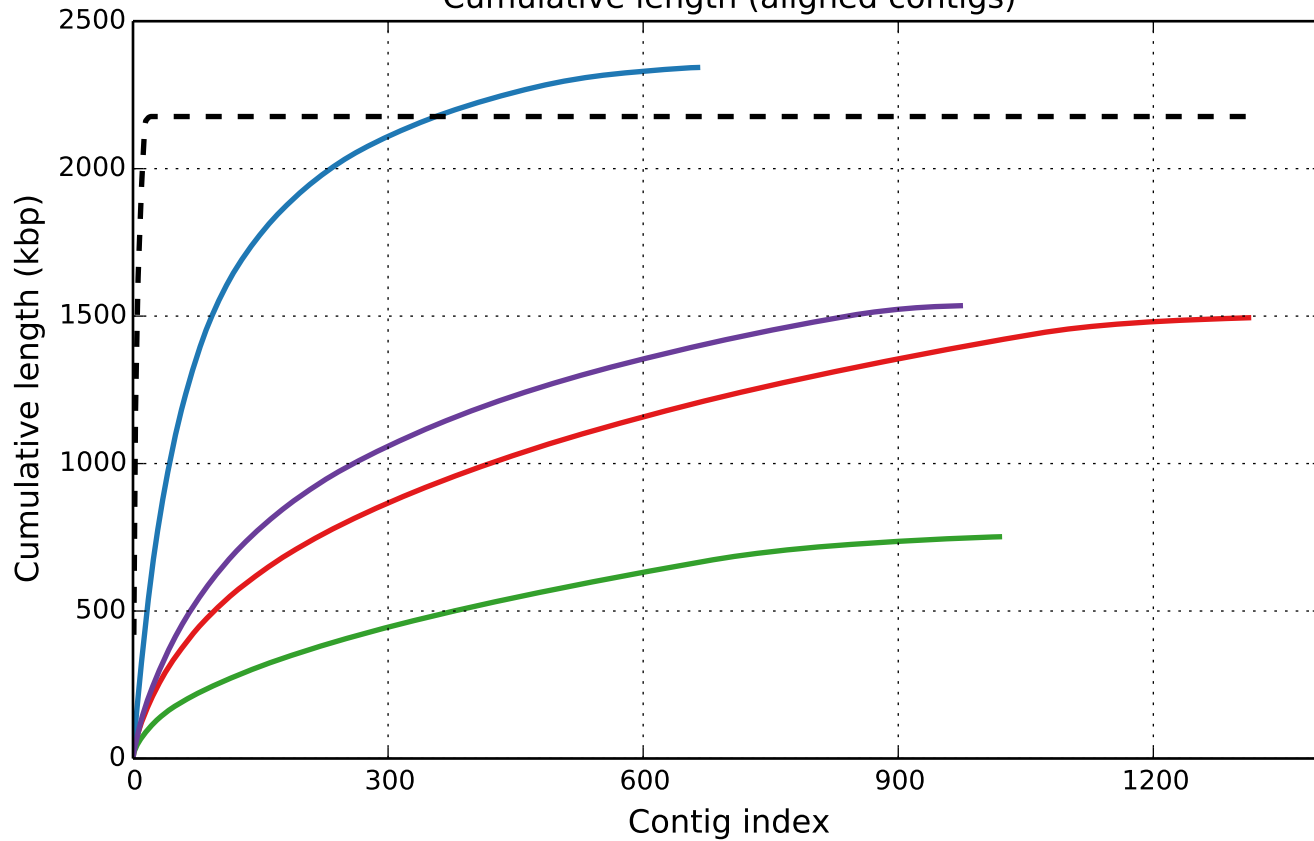
GC content

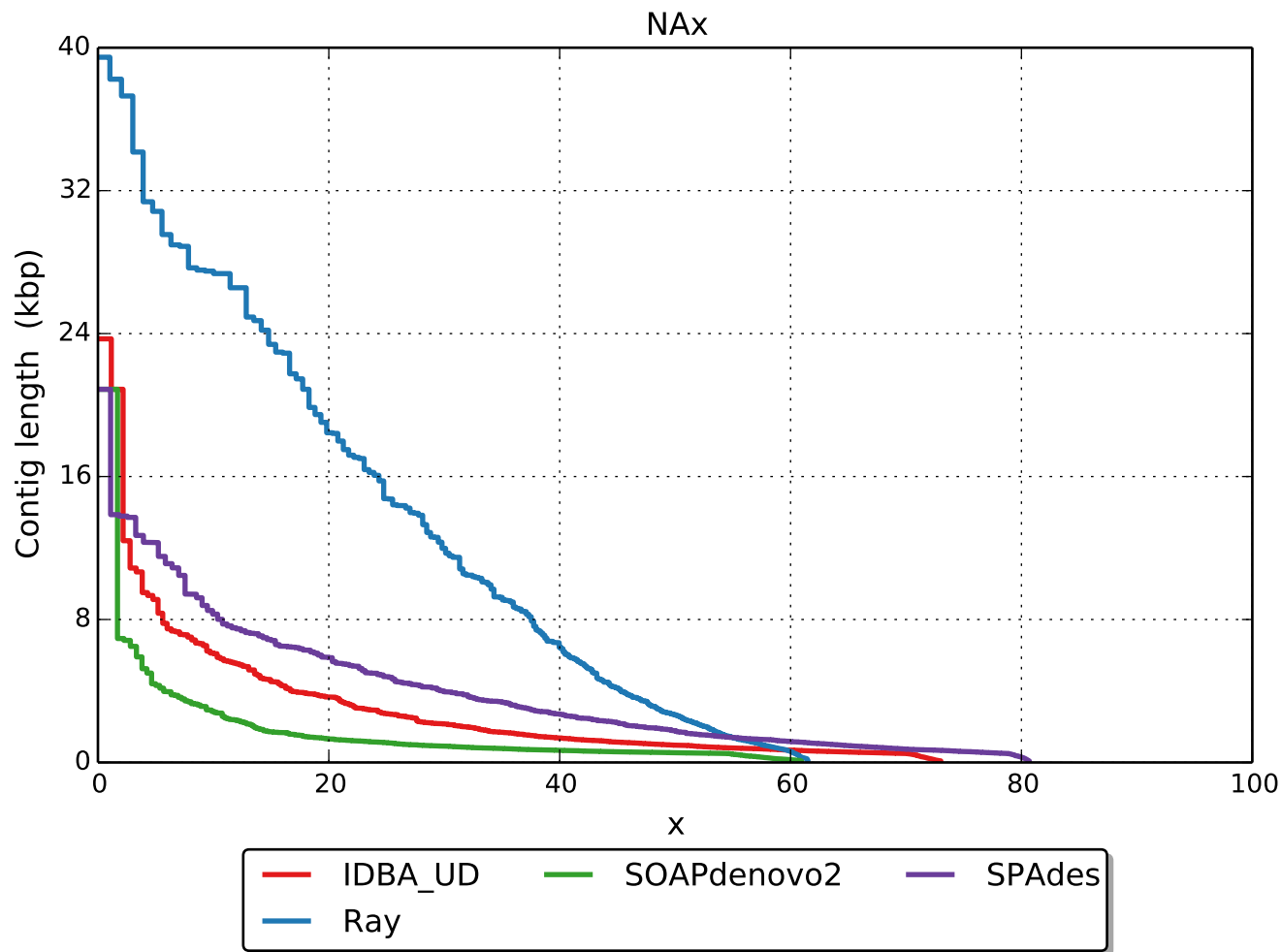


Misassemblies



Cumulative length (aligned contigs)





NGAx

