

## Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	98	201	882	137
# contigs (>= 5000 bp)	71	160	116	107
# contigs (>= 10000 bp)	67	127	26	97
# contigs (>= 25000 bp)	50	58	1	71
# contigs (>= 50000 bp)	34	23	0	36
Total length (>= 1000 bp)	4368578	4203370	2615939	4786572
Total length (>= 5000 bp)	4304727	4112099	945448	4715631
Total length (>= 10000 bp)	4278420	3871981	356370	4642158
Total length (>= 25000 bp)	3983656	2754486	26206	4177861
Total length (>= 50000 bp)	3380416	1518927	0	2992612
# contigs	112	211	1510	147
Largest contig	246677	99107	26206	189063
Total length	4378740	4211304	3066458	4794148
Reference length	4835507	4835507	4835507	4835507
GC (%)	46.30	46.62	47.01	46.32
Reference GC (%)	46.49	46.49	46.49	46.49
N50	92168	37090	3089	57361
NG50	75257	30088	1292	57278
N75	50466	18095	1497	34281
NG75	40689	13710	-	34221
L50	16	37	267	25
LG50	19	46	709	26
L75	33	78	624	52
LG75	40	107	-	53
# misassemblies	50	47	8	44
# misassembled contigs	33	37	8	30
Misassembled contigs length	2773515	1439079	66749	1869799
# local misassemblies	42	218	23	38
# structural variations	47	42	32	42
# unaligned contigs	0 + 39 part	0 + 59 part	0 + 138 part	0 + 57 part
Unaligned length	397322	444817	262975	956477
Genome fraction (%)	69.266	67.241	56.949	68.969
Duplication ratio	1.189	1.158	1.018	1.151
# N's per 100 kbp	7.86	832.09	38.42	28.97
# mismatches per 100 kbp	1479.65	1409.96	1199.33	1508.10
# indels per 100 kbp	42.28	35.34	23.93	39.13
Largest alignment	118704	72570	21339	108559
NA50	32189	15126	2377	22673
NGA50	26880	12965	868	22673
NA75	3450	3528	1007	-
LA50	41	70	352	61
LGA50	48	92	975	61
LA75	116	187	849	-

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

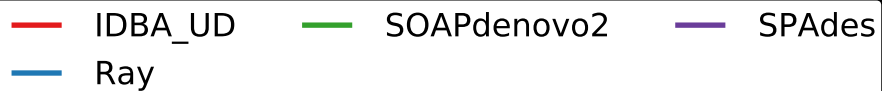
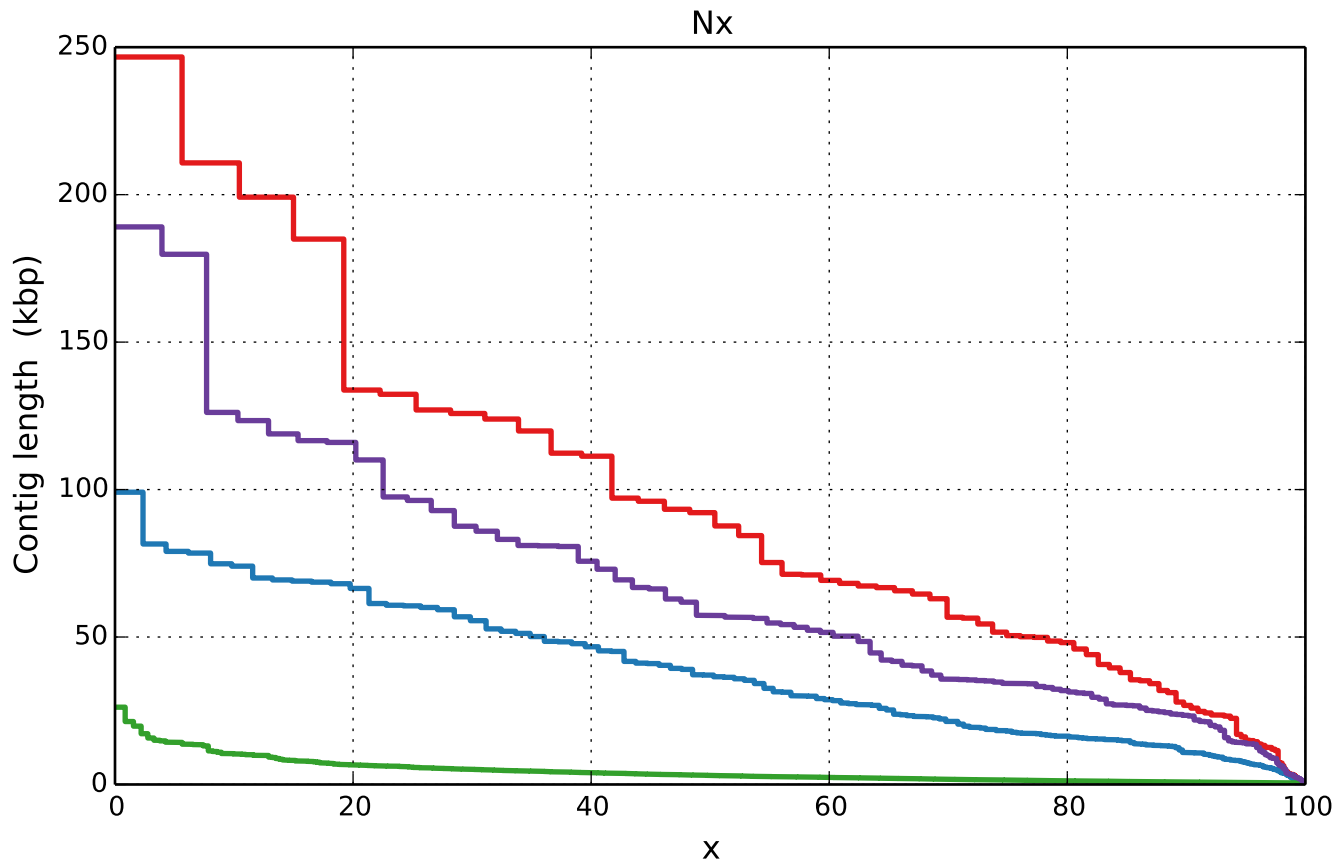
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	50	47	8	44
# relocations	41	37	6	34
# translocations	8	9	2	9
# inversions	1	1	0	1
# possibly misassembled contigs	60	112	65	86
# misassembled contigs	33	37	8	30
Misassembled contigs length	2773515	1439079	66749	1869799
# local misassemblies	42	218	23	38
# structural variations	47	42	32	42
# mismatches	49559	45844	33027	50295
# indels	1416	1149	659	1305
# short indels	1197	985	562	1096
# long indels	219	164	97	209
Indels length	4736	3495	1868	4438

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).

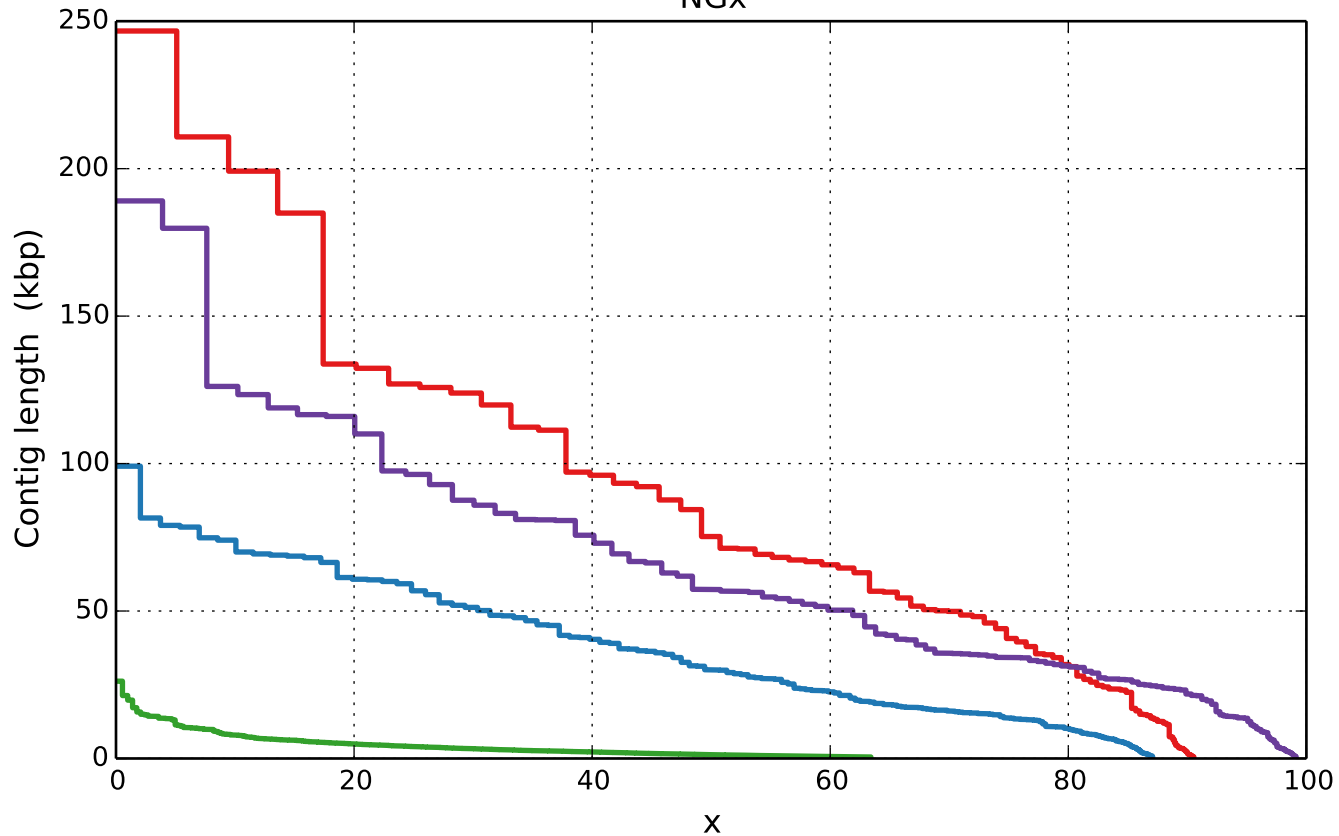
## Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	39	59	138	57
# with misassembly	8	13	7	13
# both parts are significant	19	43	52	44
Partially unaligned length	397322	444817	262975	956477
# N's	344	35042	1178	1389

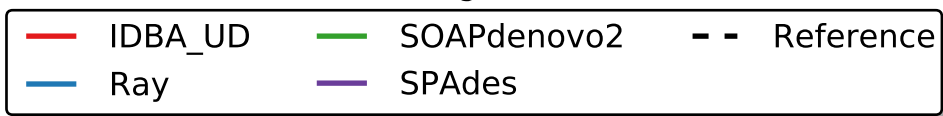
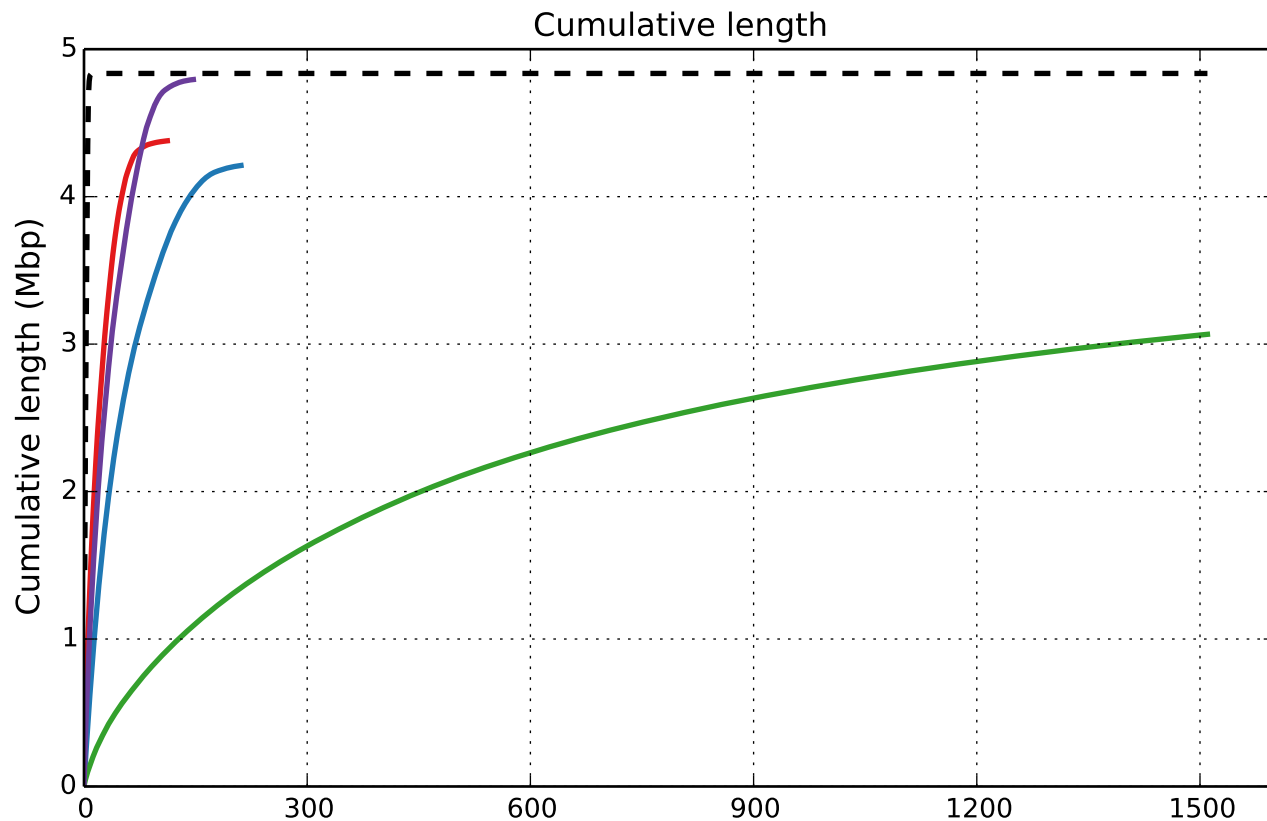
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



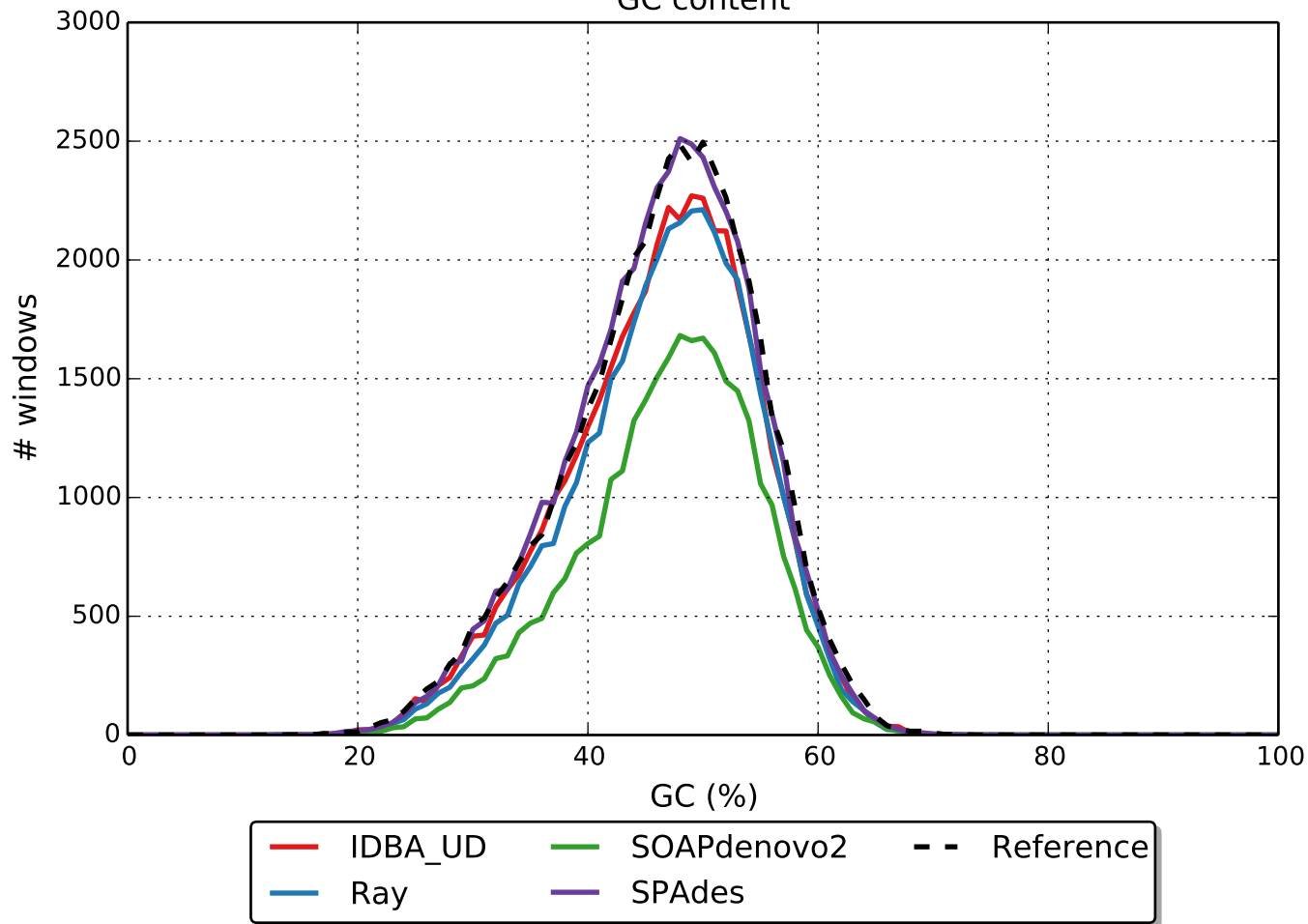
NGx



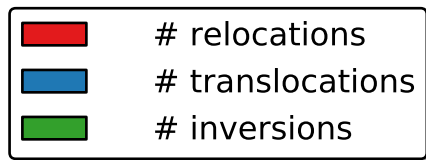
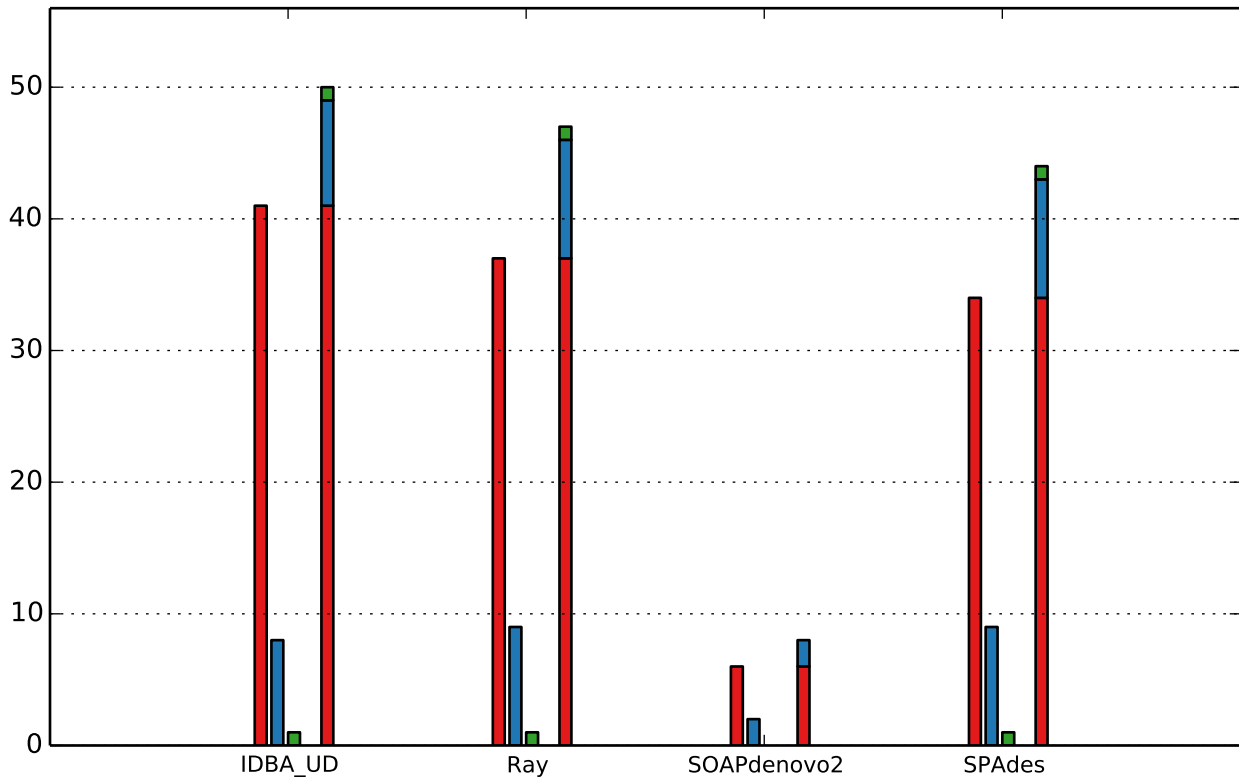
— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray



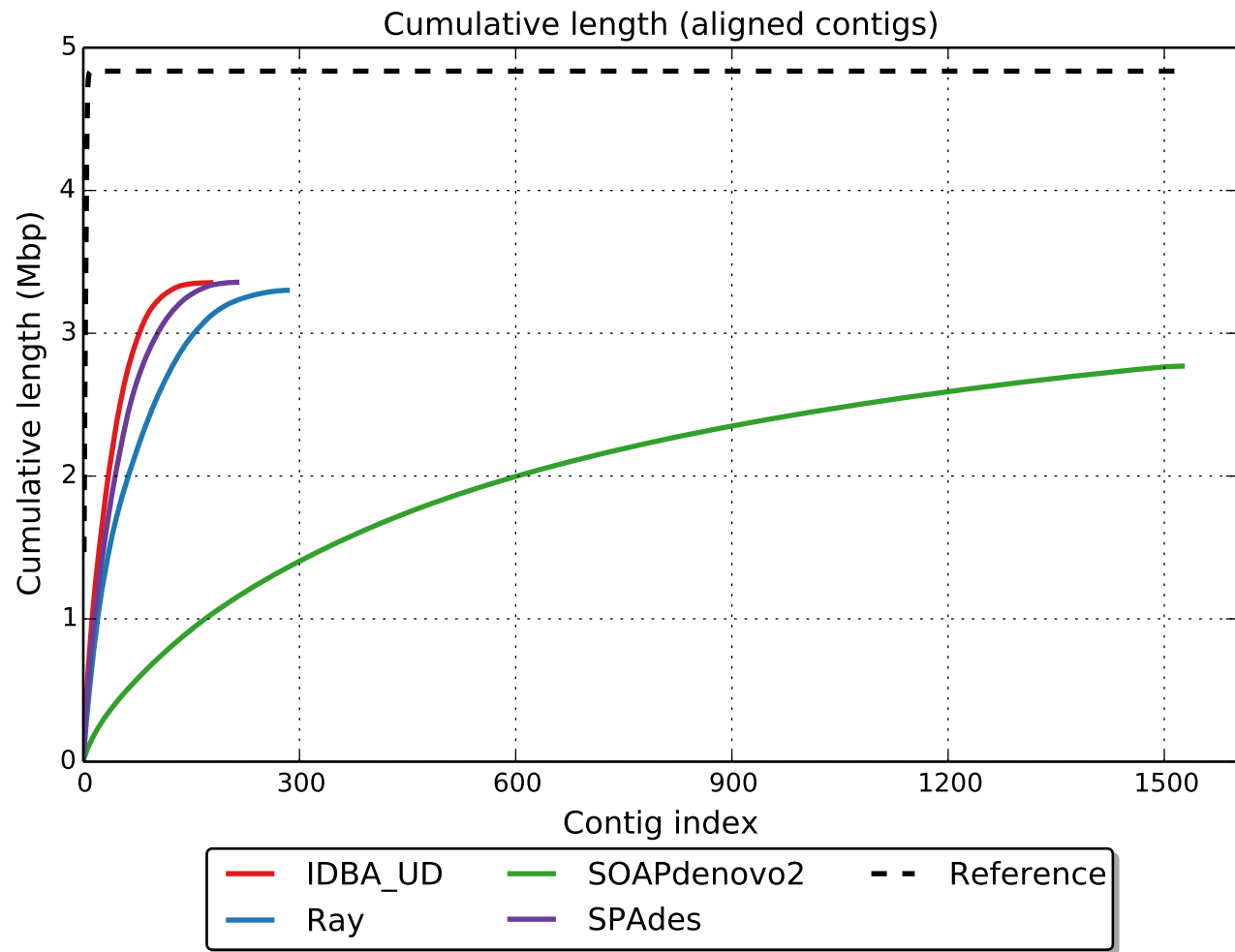
GC content



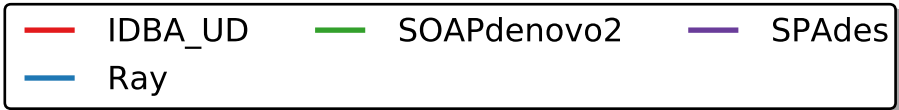
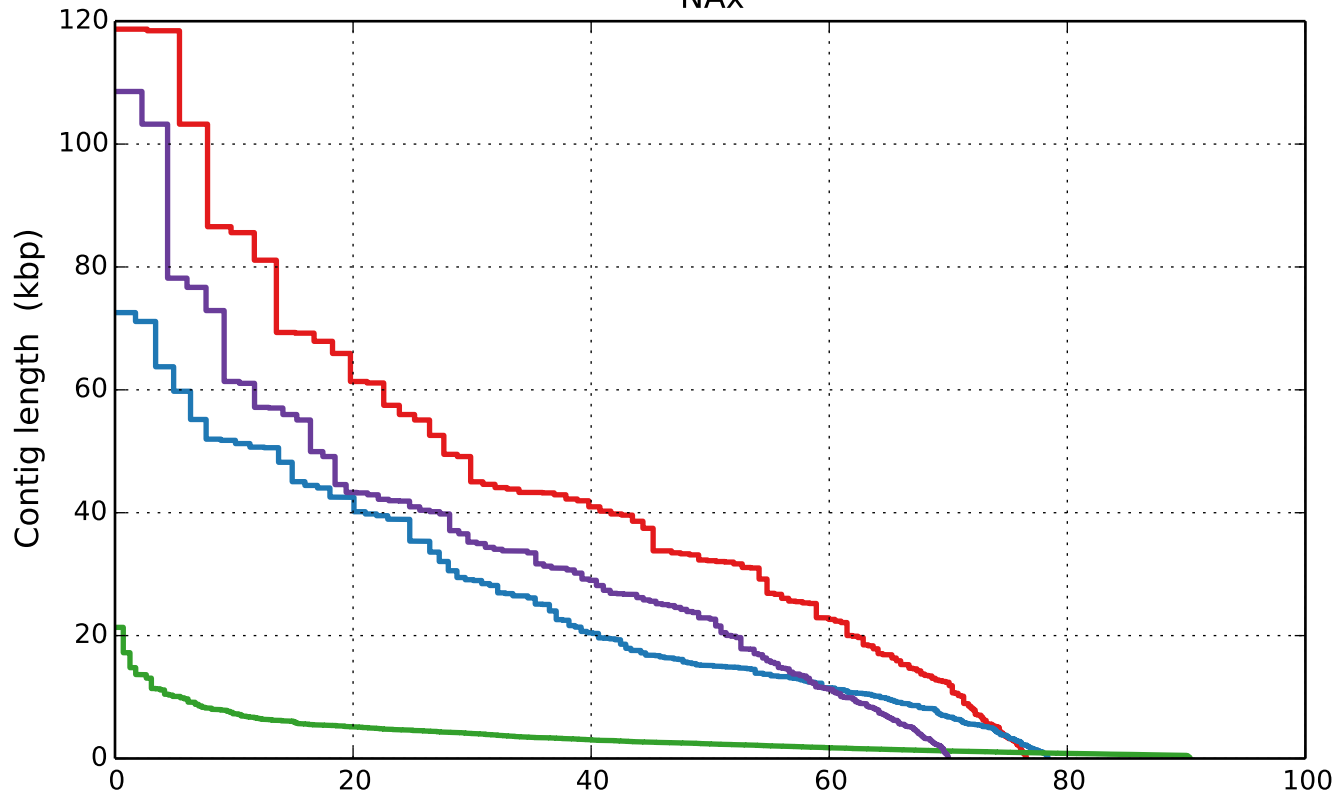
# Misassemblies



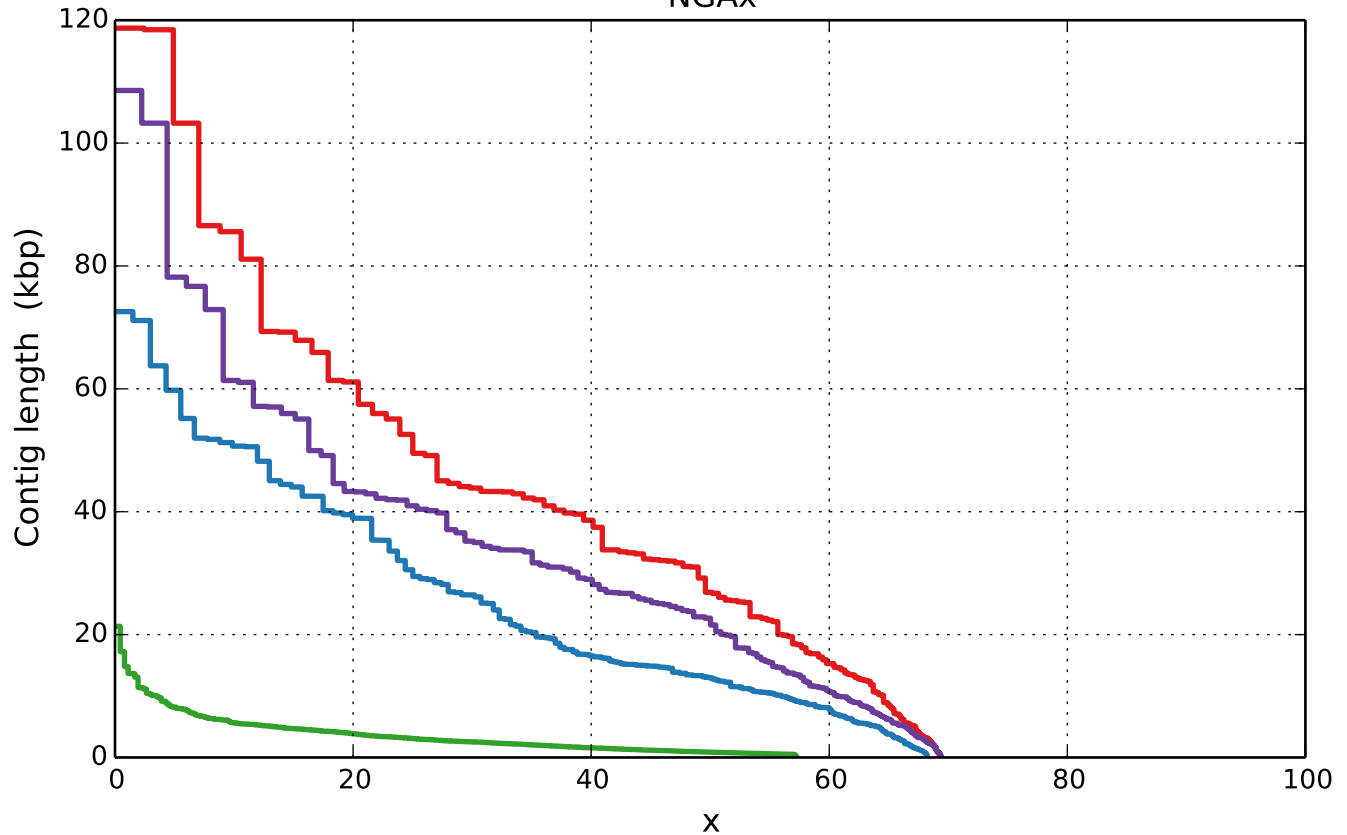




NAx



# NGAx



— IDBA\_UD    — SOAPdenovo2    — SPAdes  
— Ray

