

Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	71	67	64	103	66
# contigs (>= 5000 bp)	35	34	34	47	36
# contigs (>= 10000 bp)	21	21	25	19	22
# contigs (>= 25000 bp)	11	13	12	9	12
# contigs (>= 50000 bp)	3	3	4	2	4
Total length (>= 1000 bp)	840043	837243	891484	828966	860918
Total length (>= 5000 bp)	764949	759112	824384	702141	793124
Total length (>= 10000 bp)	661293	669938	761610	504905	699234
Total length (>= 25000 bp)	503236	546414	560651	360036	556113
Total length (>= 50000 bp)	221971	221319	285468	125218	299828
# contigs	72	71	68	108	69
Largest contig	82622	82584	82616	68949	97305
Total length	841036	840021	894776	832457	863608
Reference length	842801	842801	842801	842801	842801
GC (%)	41.39	41.46	41.40	41.37	41.41
Reference GC (%)	41.39	41.39	41.39	41.39	41.39
N50	36580	28824	36864	15225	31363
NG50	36580	28824	36864	15225	31363
N75	11788	15084	15331	7130	13917
NG75	11788	15084	17750	6855	14694
L50	8	9	8	13	8
LG50	8	9	8	13	8
L75	19	18	19	34	18
LG75	19	18	16	35	17
# misassemblies	0	12	19	8	24
# misassembled contigs	0	9	12	8	14
Misassembled contigs length	0	157090	226327	108350	308240
# local misassemblies	0	0	0	0	0
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 1 part	0 + 0 part	0 + 0 part	0 + 2 part
Unaligned length	0	2194	0	0	1468
Genome fraction (%)	99.791	99.357	97.843	98.686	99.005
Duplication ratio	1.000	1.001	1.085	1.001	1.033
# N's per 100 kbp	0.00	0.00	0.00	1.32	0.00
# mismatches per 100 kbp	0.00	0.72	0.00	2.52	6.71
# indels per 100 kbp	0.00	0.12	0.12	1.32	0.36
Largest alignment	82622	82584	82616	68949	77436
NA50	36580	26973	30484	15225	25372
NGA50	36580	26973	30484	14997	25372
NA75	11788	9834	10285	5696	7788
NGA75	11788	9834	15080	5663	8445
LA50	8	9	9	13	10
LGA50	8	9	9	14	10
LA75	19	21	22	37	26
LGA75	19	21	19	38	25

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

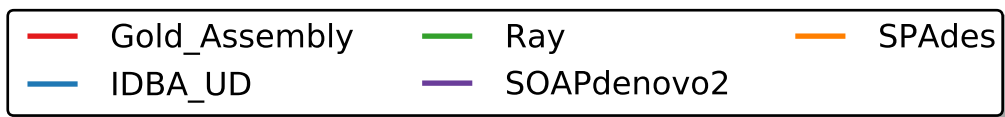
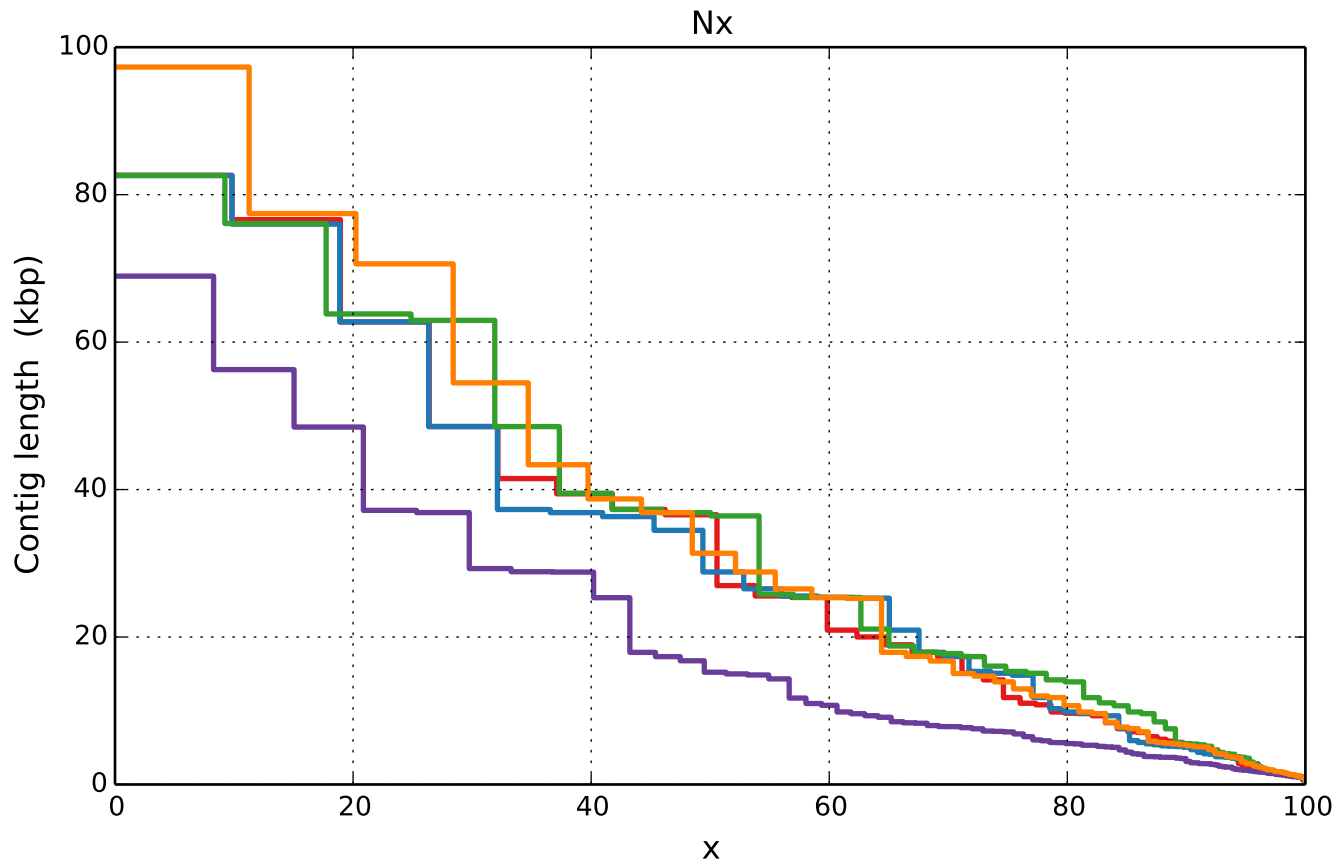
	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	0	12	19	8	24
# relocations	0	2	6	3	6
# translocations	0	9	9	4	13
# inversions	0	1	4	1	5
# possibly misassembled contigs	0	1	0	0	1
# misassembled contigs	0	9	12	8	14
Misassembled contigs length	0	157090	226327	108350	308240
# local misassemblies	0	0	0	0	0
# structural variations	0	0	0	0	0
# mismatches	0	6	0	21	56
# indels	0	1	1	11	3
# short indels	0	0	0	9	2
# long indels	0	1	1	2	1
Indels length	0	33	33	53	35

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).

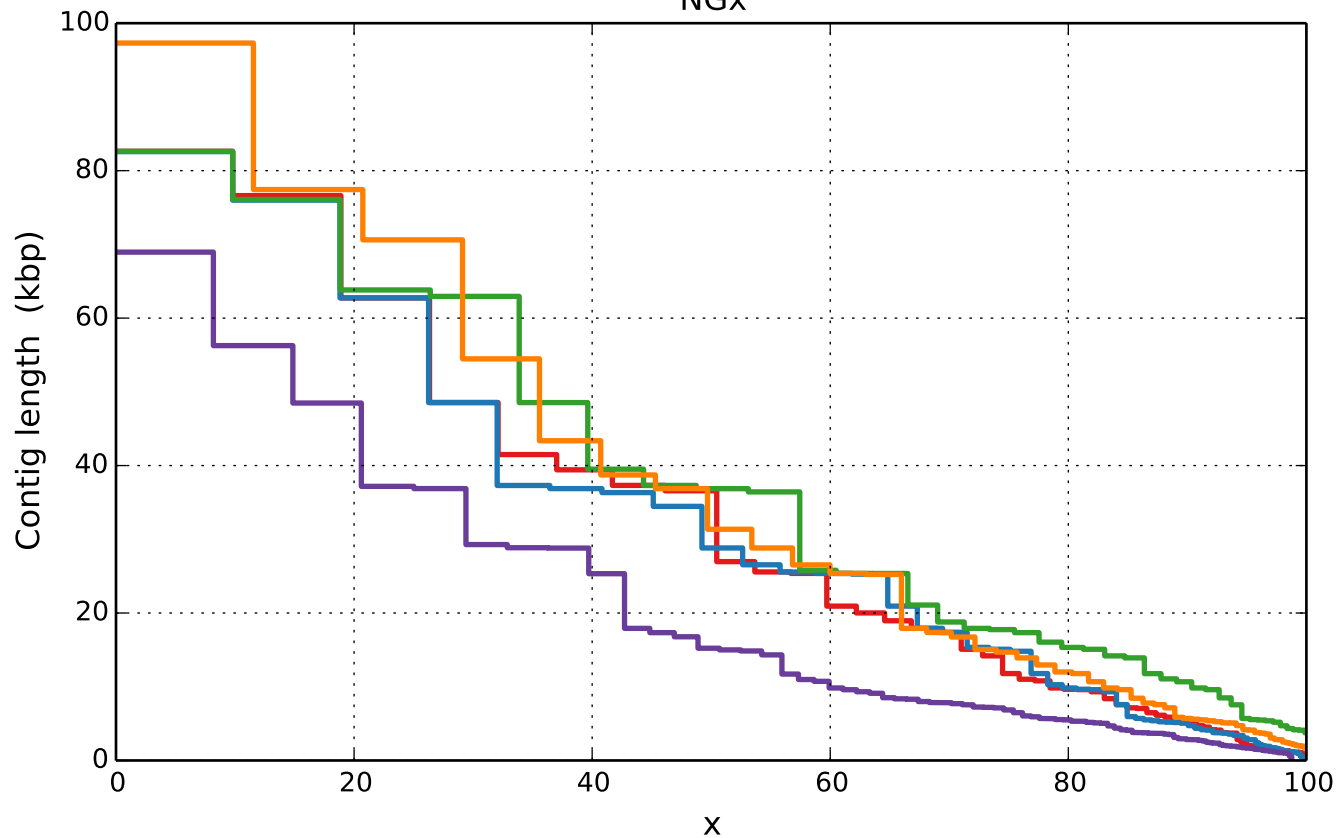
Unaligned report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	1	0	0	2
# with misassembly	0	0	0	0	0
# both parts are significant	0	1	0	0	1
Partially unaligned length	0	2194	0	0	1468
# N's	0	0	0	11	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).



NGx



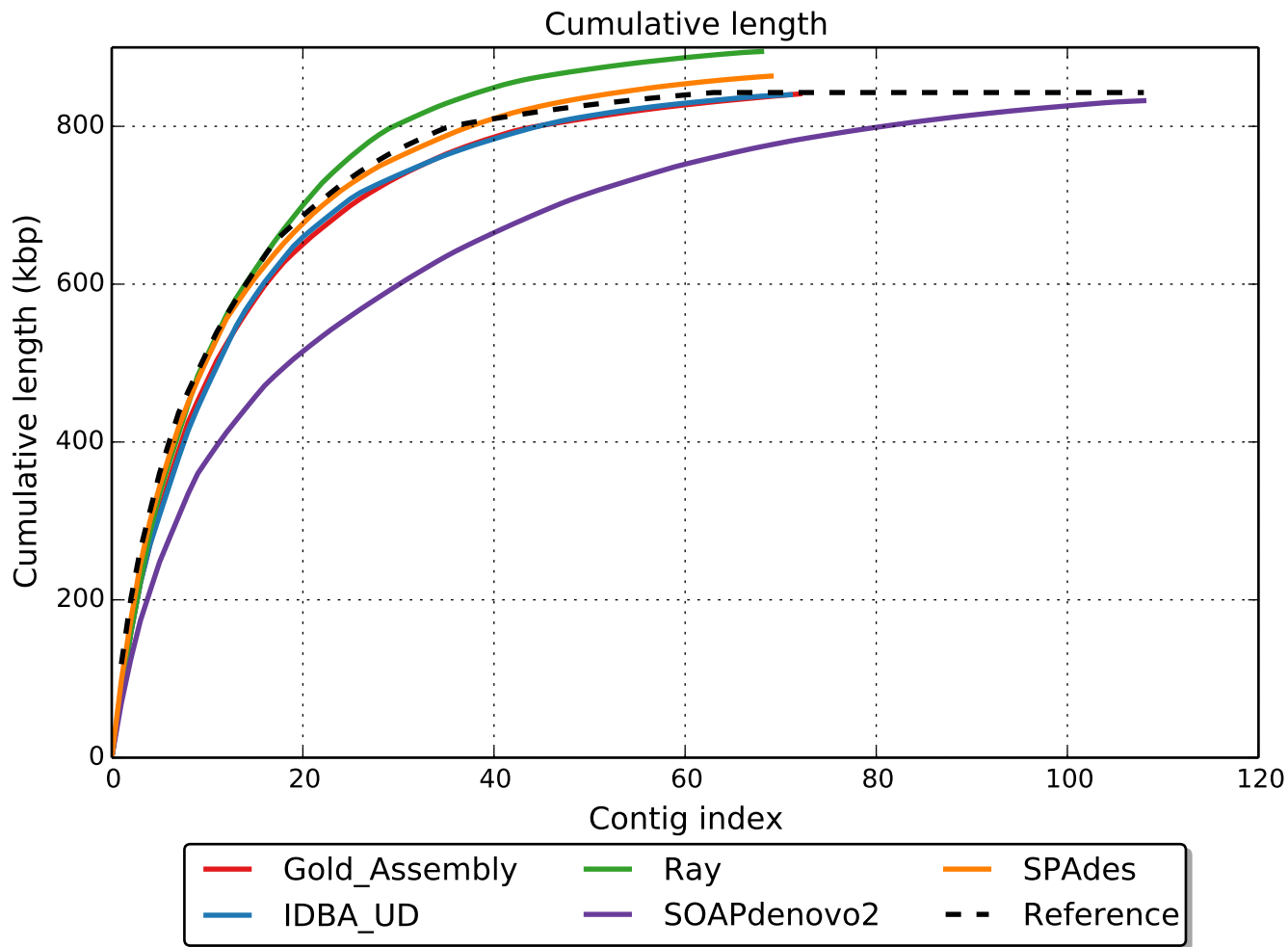
Gold_Assembly

Ray

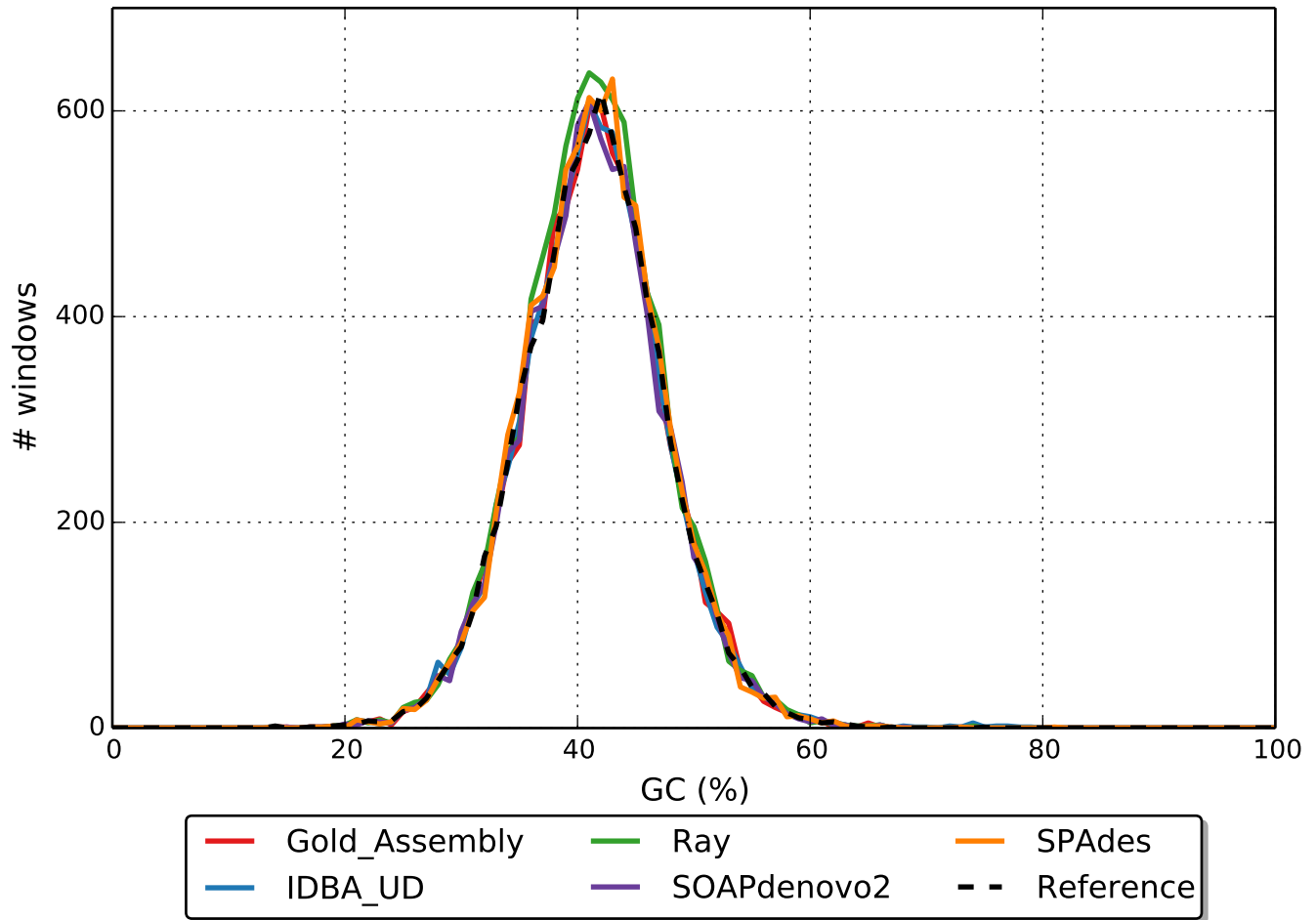
SPAdes

IDBA_UD

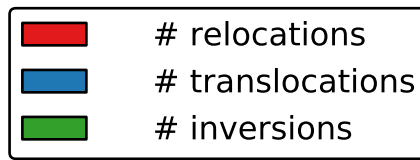
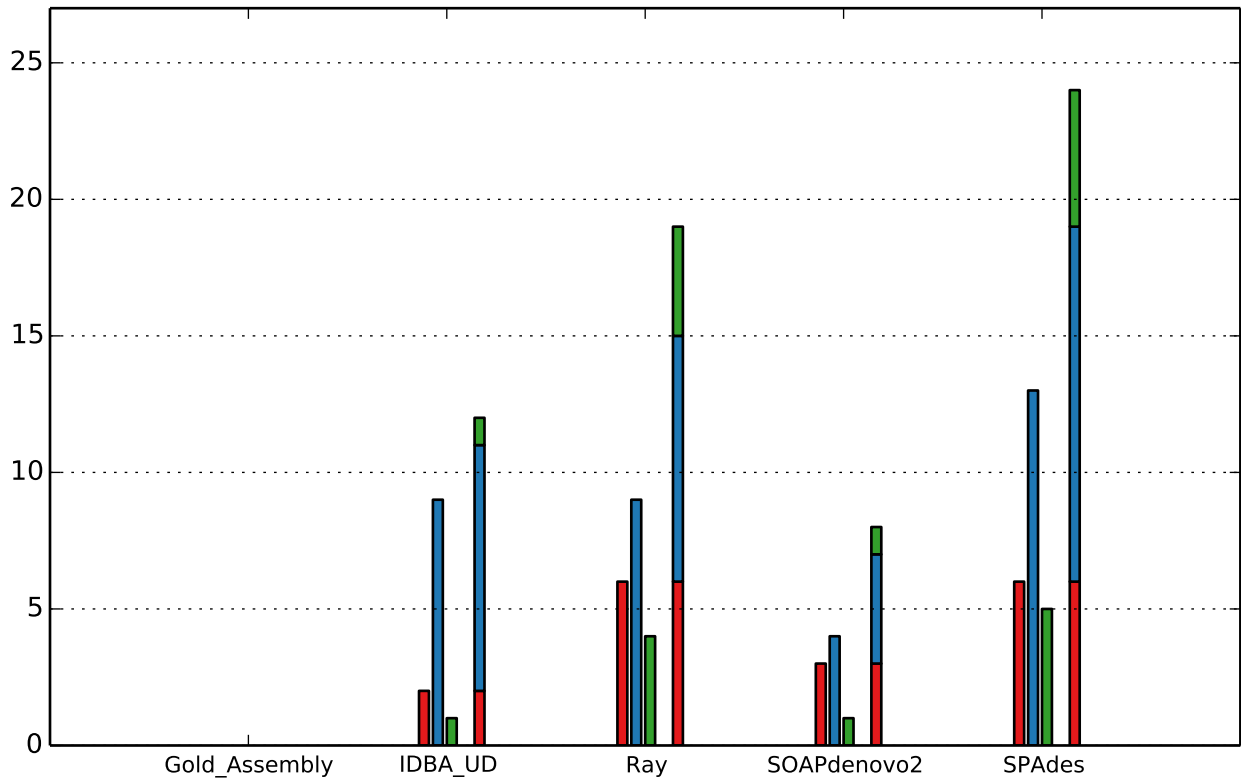
SOAPdenovo2

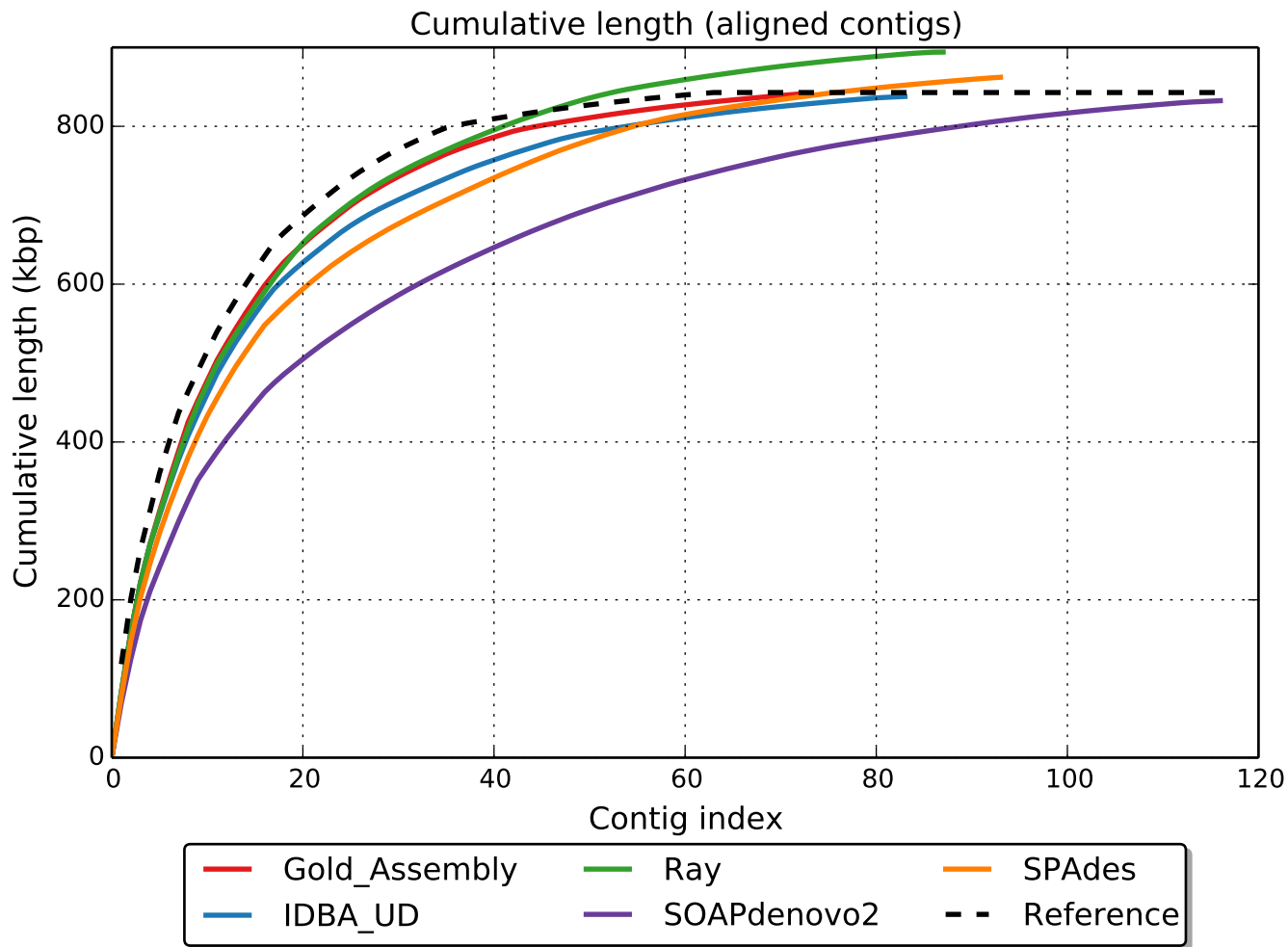


GC content

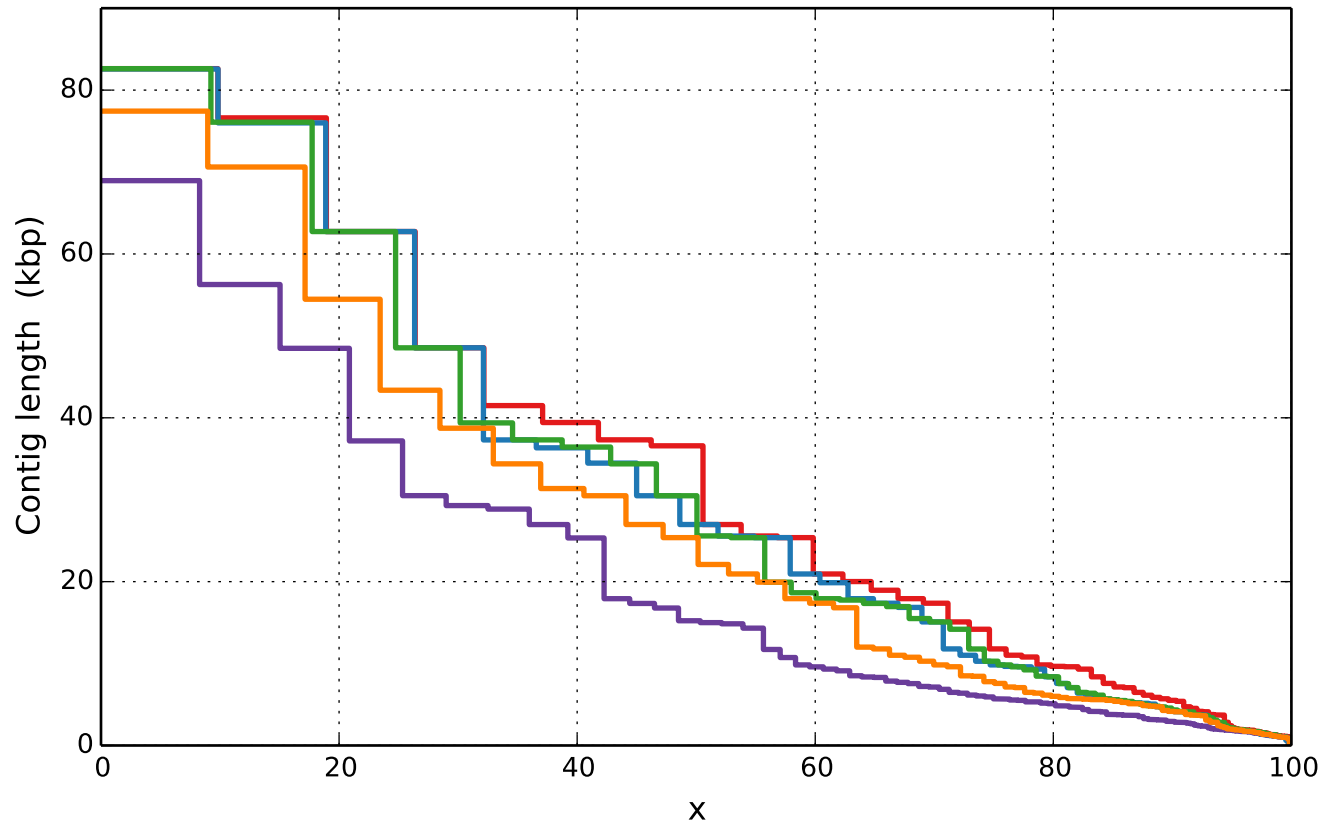


Misassemblies





NAx



Gold_Assembly Ray SPAdes
IDBA_UD SOAPdenovo2

NGAx

