

# Report

	Gold_Assembly	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	25	35	40	5	31
# contigs (>= 5000 bp)	22	29	34	0	27
# contigs (>= 10000 bp)	22	28	32	0	26
# contigs (>= 25000 bp)	21	24	27	0	23
# contigs (>= 50000 bp)	16	18	20	0	15
Total length (>= 1000 bp)	3576049	3570739	3824040	5892	3573507
Total length (>= 5000 bp)	3567651	3557551	3809811	0	3563778
Total length (>= 10000 bp)	3567651	3549830	3790502	0	3556121
Total length (>= 25000 bp)	3552232	3477145	3705059	0	3505100
Total length (>= 50000 bp)	3359881	3241115	3436700	0	3172226
# contigs	25	37	42	445	31
Largest contig	465765	315244	315243	1240	453618
Total length	3576049	3572113	3825616	272363	3573507
Reference length	3576081	3576081	3576081	3576081	3576081
GC (%)	51.82	51.82	51.86	51.61	51.82
Reference GC (%)	51.82	51.82	51.82	51.82	51.82
N50	274230	230838	198137	584	262399
NG50	274230	230838	220459	-	262399
N75	159550	131675	122244	536	159550
NG75	159550	131675	131674	-	159550
L50	6	7	8	192	6
LG50	6	7	7	-	6
L75	10	12	14	314	10
LG75	10	12	12	-	10
# misassemblies	0	1	1	0	1
# misassembled contigs	0	1	1	0	1
Misassembled contigs length	0	74142	74243	0	309681
# local misassemblies	0	4	2	0	2
# structural variations	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 2 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	5467	0	0
Genome fraction (%)	99.999	99.877	99.901	7.615	99.879
Duplication ratio	1.000	1.000	1.069	1.000	1.000
# N's per 100 kbp	0.00	0.00	4.42	0.00	0.00
# mismatches per 100 kbp	0.00	2.02	0.03	76.01	1.79
# indels per 100 kbp	0.00	0.39	0.48	0.00	0.48
Largest alignment	465765	315244	315243	1240	453618
NA50	274230	230838	198137	584	262399
NGA50	274230	230838	220459	-	262399
NA75	159550	131675	120573	536	159550
NGA75	159550	131675	131674	-	159550
LA50	6	7	8	192	6
LGA50	6	7	7	-	6
LA75	10	12	14	314	10
LGA75	10	12	12	-	10

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	1	1	0	1
# relocations	0	0	0	0	0
# translocations	0	1	1	0	1
# inversions	0	0	0	0	0
# possibly misassembled contigs	0	0	2	0	0
# misassembled contigs	0	1	1	0	1
Misassembled contigs length	0	74142	74243	0	309681
# local misassemblies	0	4	2	0	2
# structural variations	0	0	0	0	0
# mismatches	0	72	1	207	64
# indels	0	14	17	0	17
# short indels	0	5	5	0	5
# long indels	0	9	12	0	12
Indels length	0	103	158	0	205

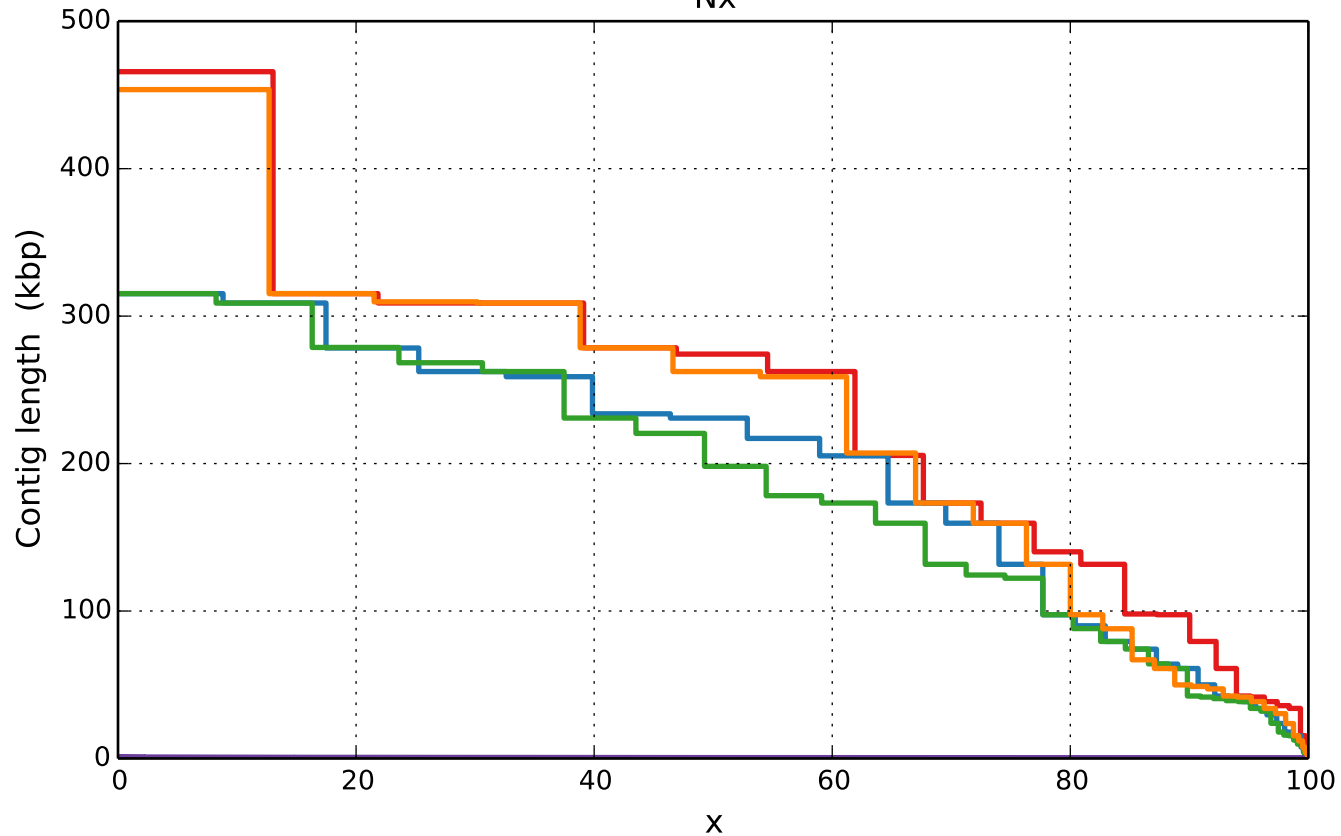
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	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	0	2	0	0
# with misassembly	0	0	0	0	0
# both parts are significant	0	0	2	0	0
Partially unaligned length	0	0	5467	0	0
# N's	0	0	169	0	0

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



Gold\_Assembly

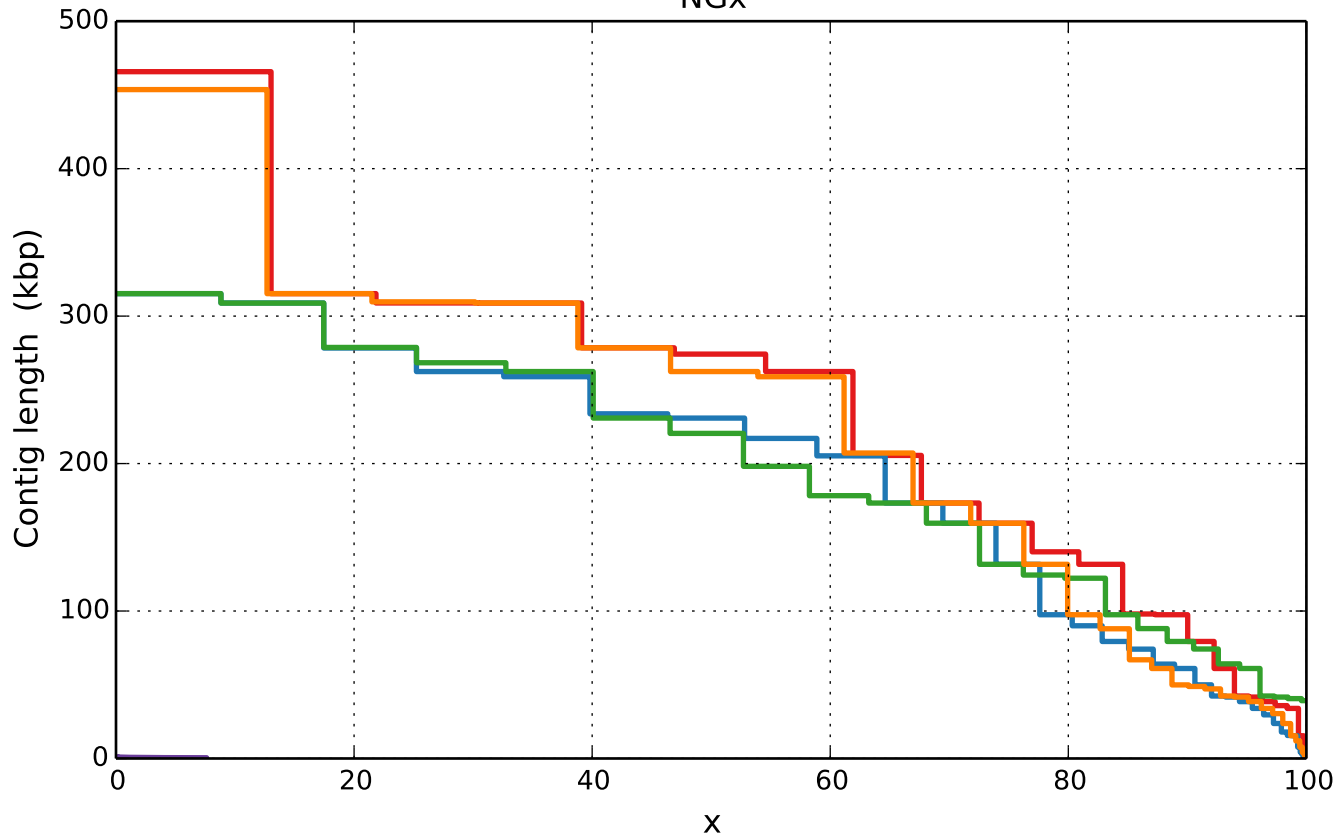
Ray

SPAdes

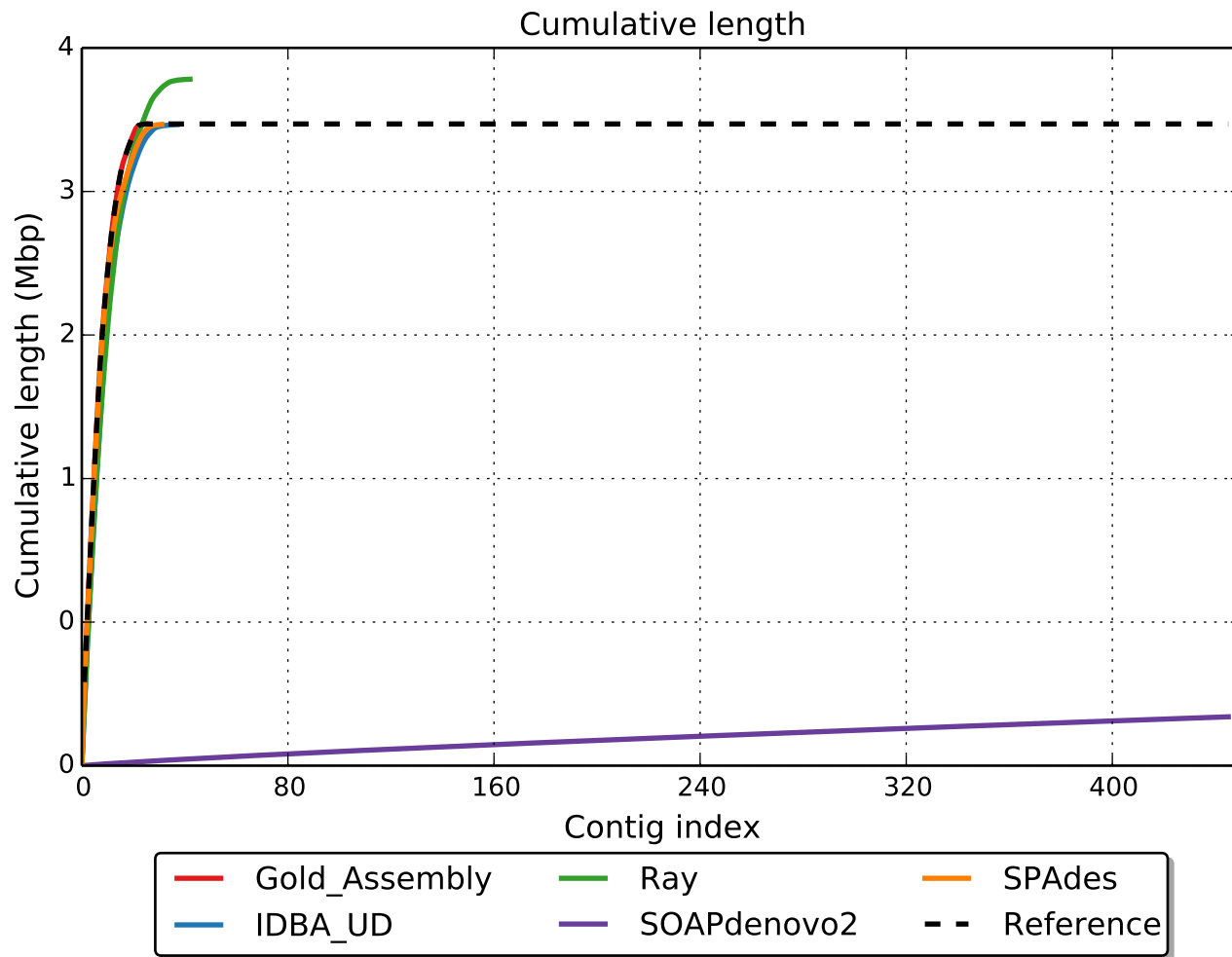
IDBA\_UD

SOAPdenovo2

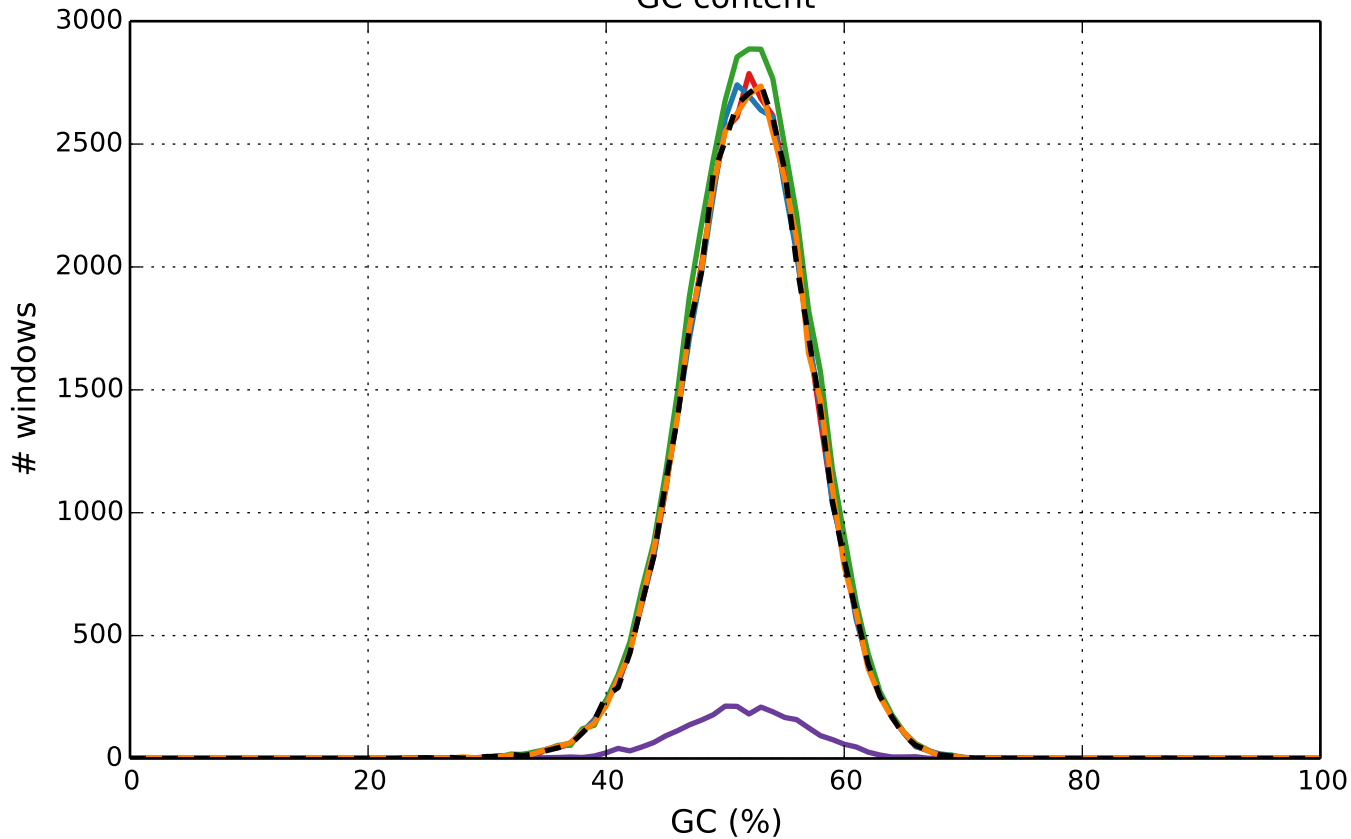
NGx



Gold\_Assembly IDBA\_UD Ray SOAPdenovo2 SPAdes



GC content



Gold\_Assembly

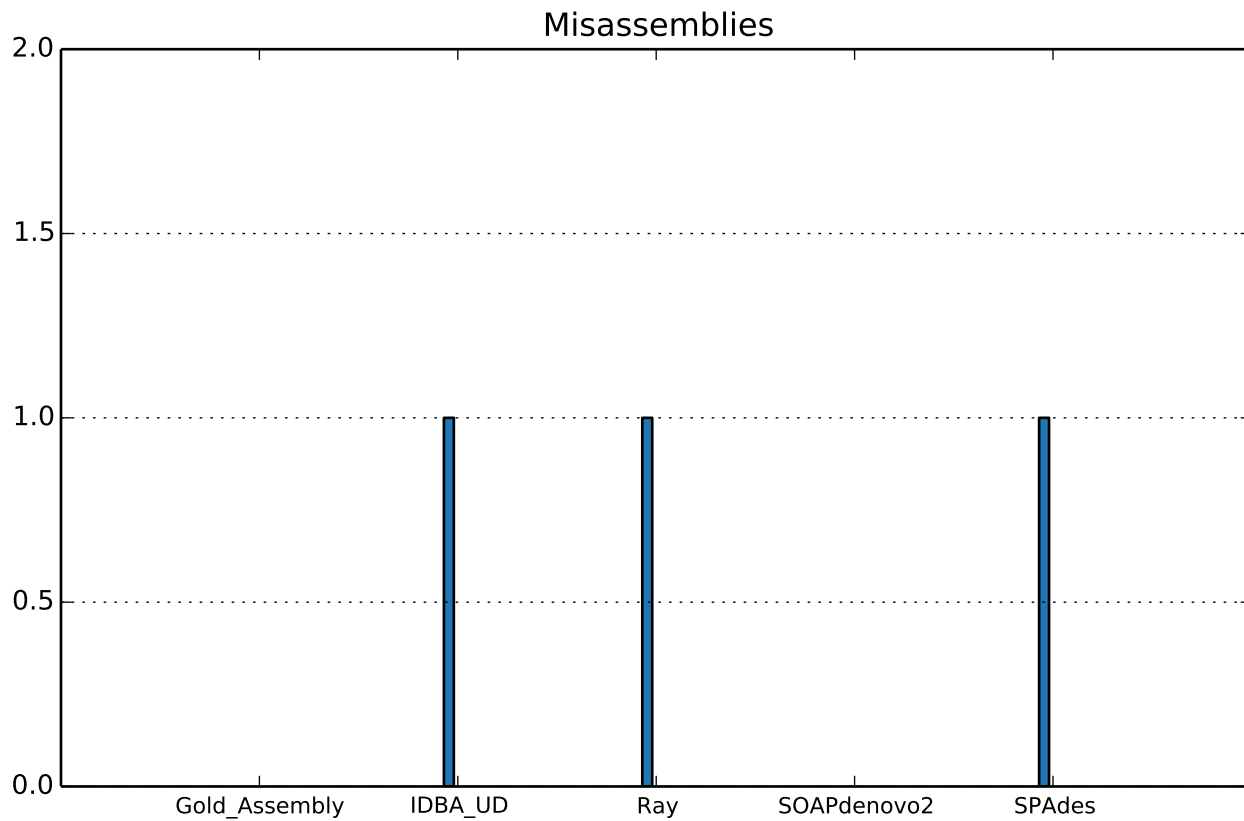
Ray

SPAdes

IDBA\_UD

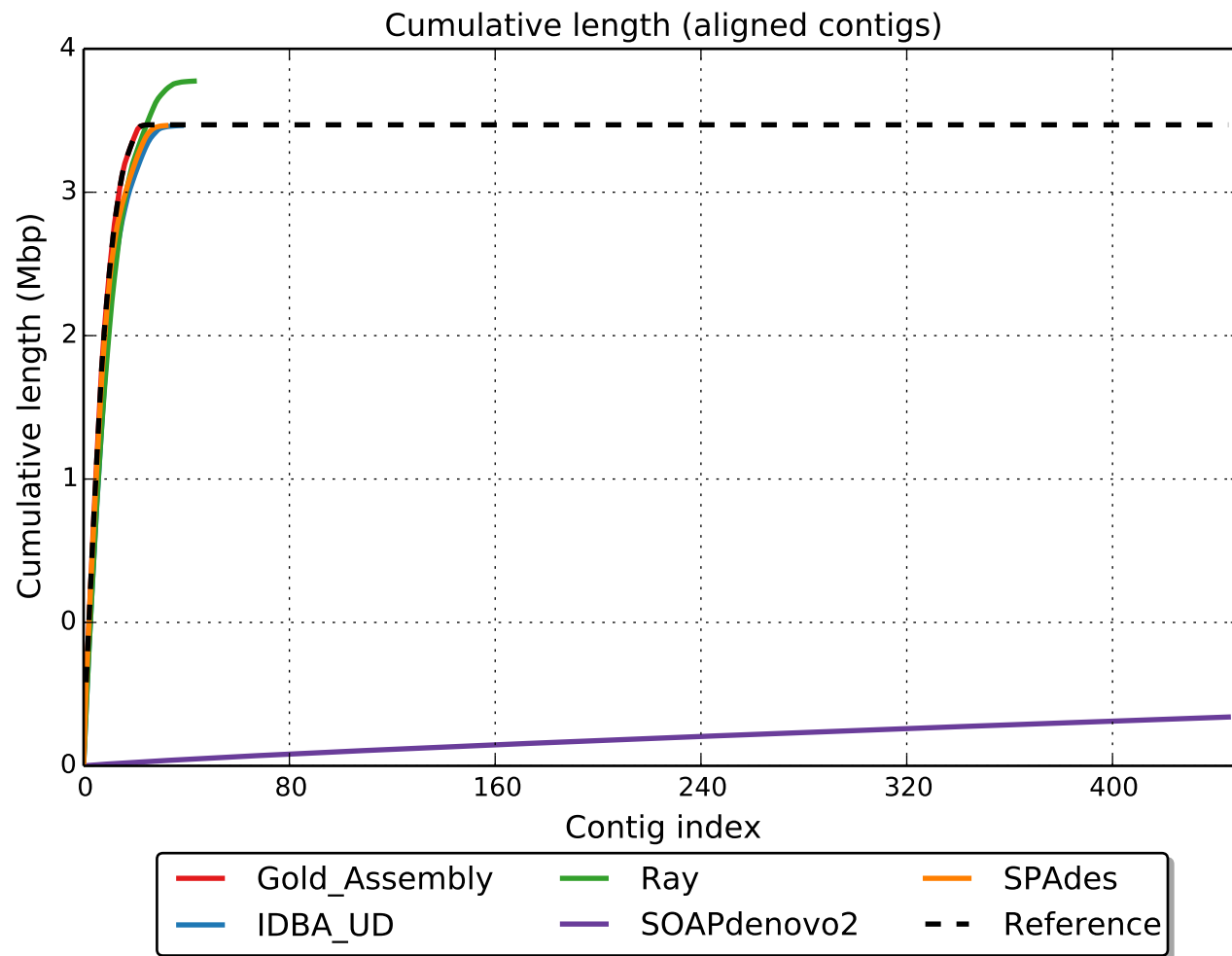
SOAPdenovo2

Reference

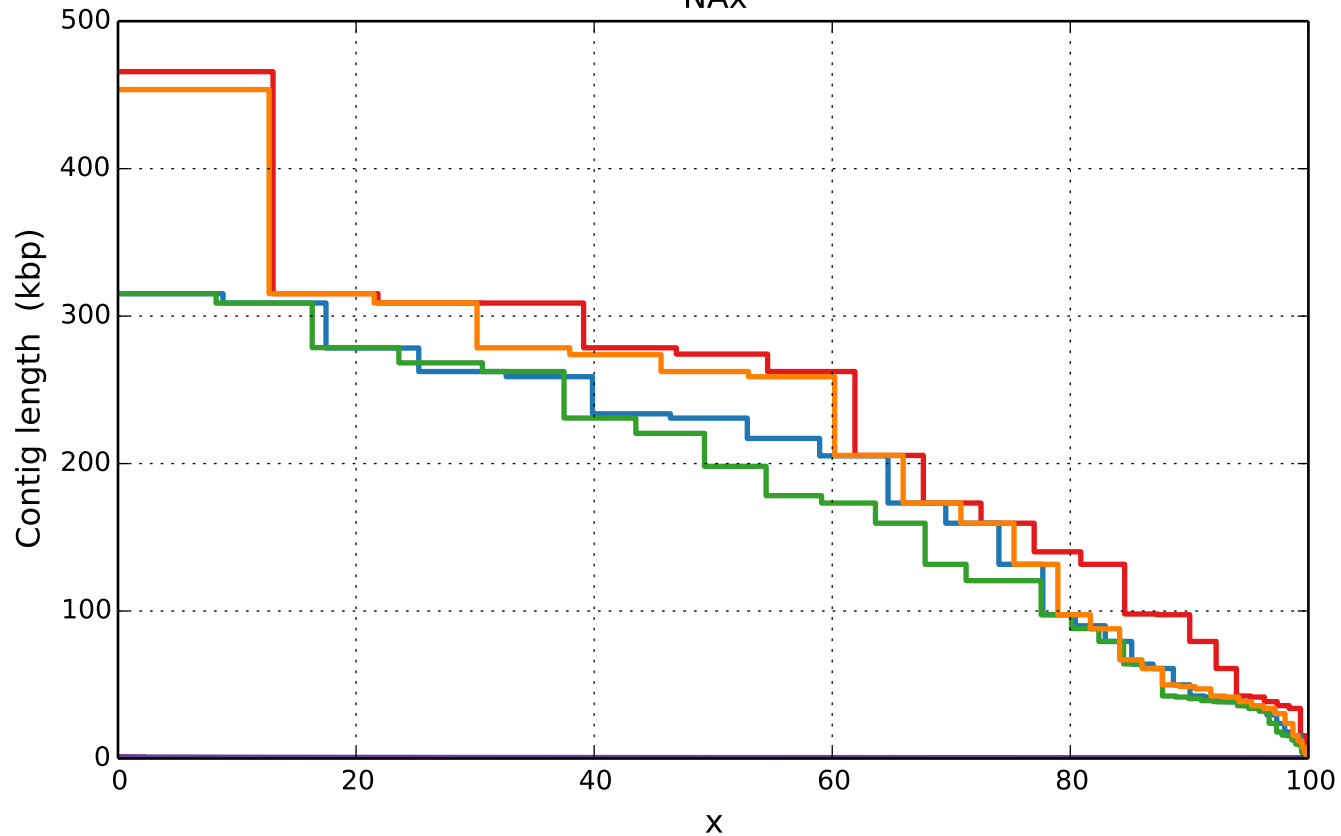


 # translocations





NAx



Gold\_Assembly

Ray

SPAdes

IDBA\_UD

SOAPdenovo2

# NGAx

