

Report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# contigs (>= 1000 bp)	596	41	104	607
# contigs (>= 5000 bp)	94	7	4	70
# contigs (>= 10000 bp)	14	5	3	11
# contigs (>= 25000 bp)	0	3	2	1
# contigs (>= 50000 bp)	0	0	1	0
Total length (>= 1000 bp)	1881887	176440	378097	1765809
Total length (>= 5000 bp)	716891	131253	243772	570209
Total length (>= 10000 bp)	180425	119631	234879	185185
Total length (>= 25000 bp)	0	91281	217082	45693
Total length (>= 50000 bp)	0	0	169569	0
# contigs	804	409	643	820
Largest contig	22168	37555	169569	45693
Total length	2031046	409856	736177	1922386
Reference length	2932121	2932121	2932121	2932121
GC (%)	36.94	38.48	38.70	37.04
Reference GC (%)	36.59	36.59	36.59	36.59
N50	3715	825	1025	3336
NG50	2220	-	-	1721
N75	2049	610	674	1773
L50	164	74	95	168
LG50	322	-	-	381
L75	349	223	323	368
# misassemblies	29	4	4	29
# misassembled contigs	26	4	4	27
Misassembled contigs length	107992	5287	3141	111350
# local misassemblies	20	1	20	17
# structural variations	8	2	4	6
# unaligned contigs	0 + 256 part	0 + 37 part	0 + 167 part	0 + 243 part
Unaligned length	318206	133011	308733	245390
Genome fraction (%)	57.239	9.345	14.415	55.922
Duplication ratio	1.021	1.010	1.011	1.023
# N's per 100 kbp	0.00	0.00	1897.23	13.78
# mismatches per 100 kbp	2770.56	2249.93	2192.53	2727.37
# indels per 100 kbp	47.55	41.97	47.79	45.86
Largest alignment	15691	4967	4940	15072
NA50	2468	560	510	2290
NGA50	1110	-	-	995
NA75	952	-	-	1055
LA50	228	268	488	235
LGA50	494	-	-	563
LA75	550	-	-	539

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

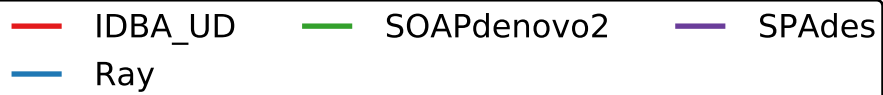
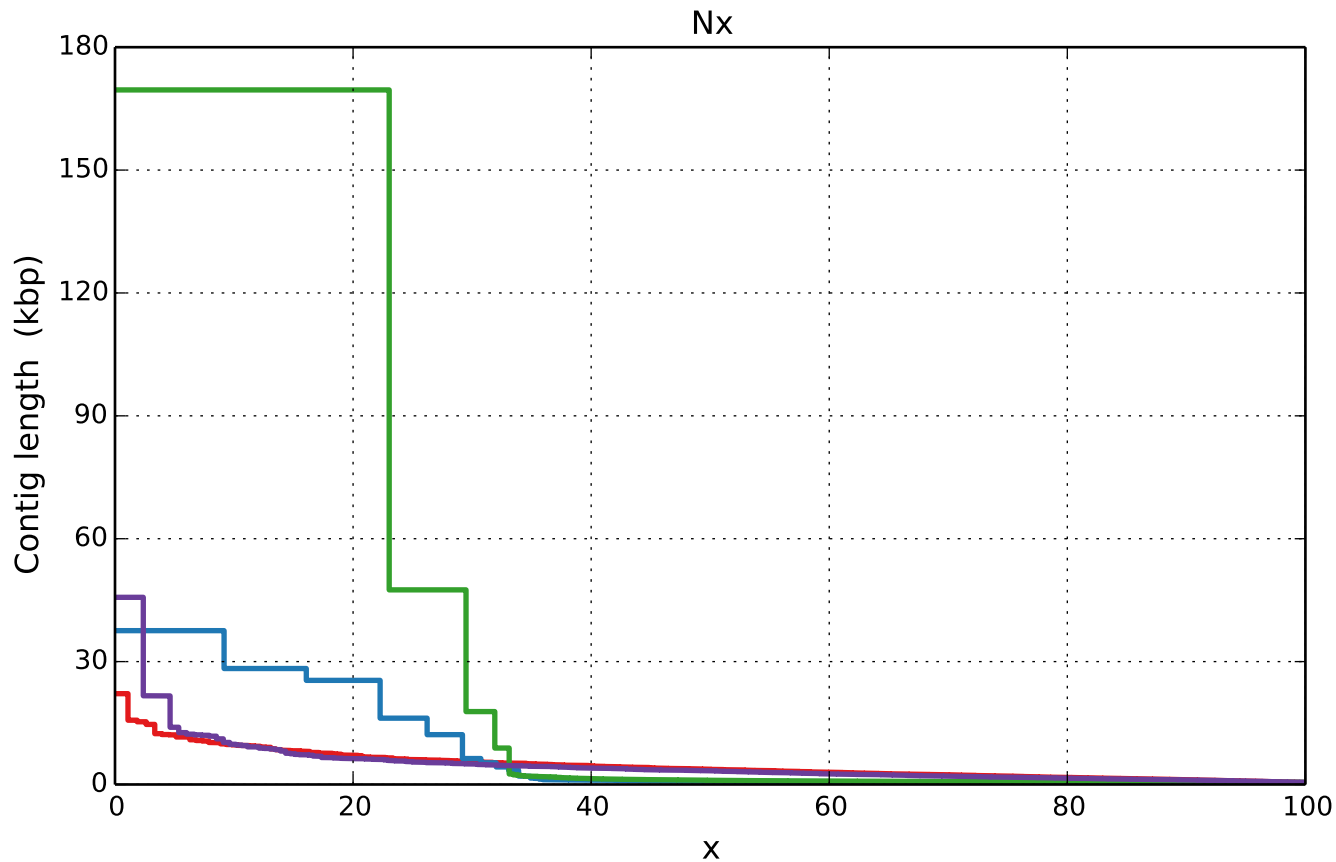
	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# misassemblies	29	4	4	29
# relocations	28	4	4	27
# translocations	0	0	0	0
# inversions	1	0	0	2
# possibly misassembled contigs	87	5	13	78
# misassembled contigs	26	4	4	27
Misassembled contigs length	107992	5287	3141	111350
# local misassemblies	20	1	20	17
# structural variations	8	2	4	6
# mismatches	46499	6165	9267	44721
# indels	798	115	202	752
# short indels	737	109	142	696
# long indels	61	6	60	56
Indels length	1859	262	1404	1748

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).

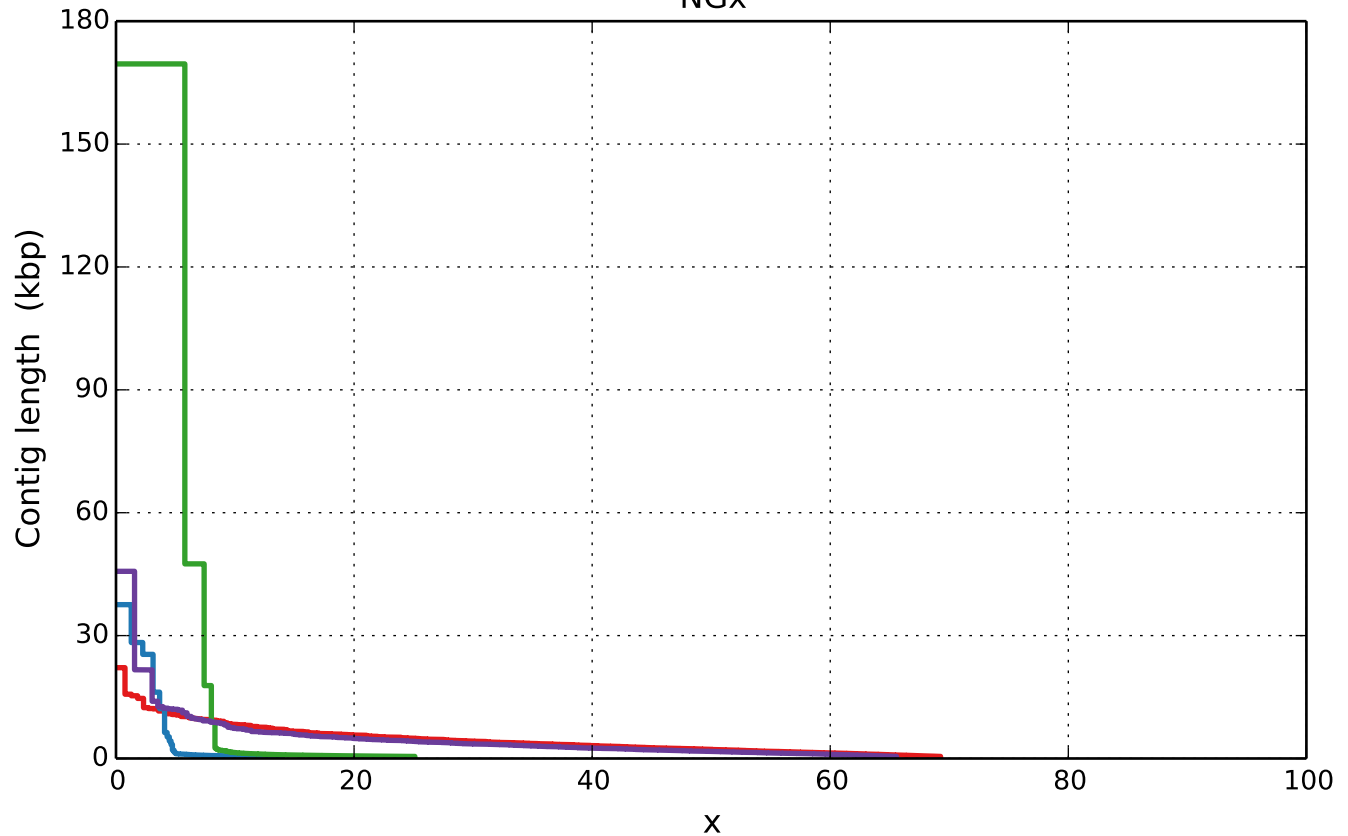
Unaligned report

	IDBA_UD	Ray	SOAPdenovo2	SPAdes
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	256	37	167	243
# with misassembly	5	0	7	5
# both parts are significant	76	5	13	66
Partially unaligned length	318206	133011	308733	245390
# N's	0	0	13967	265

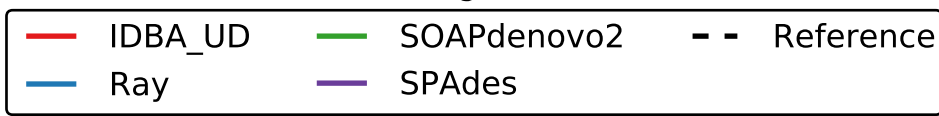
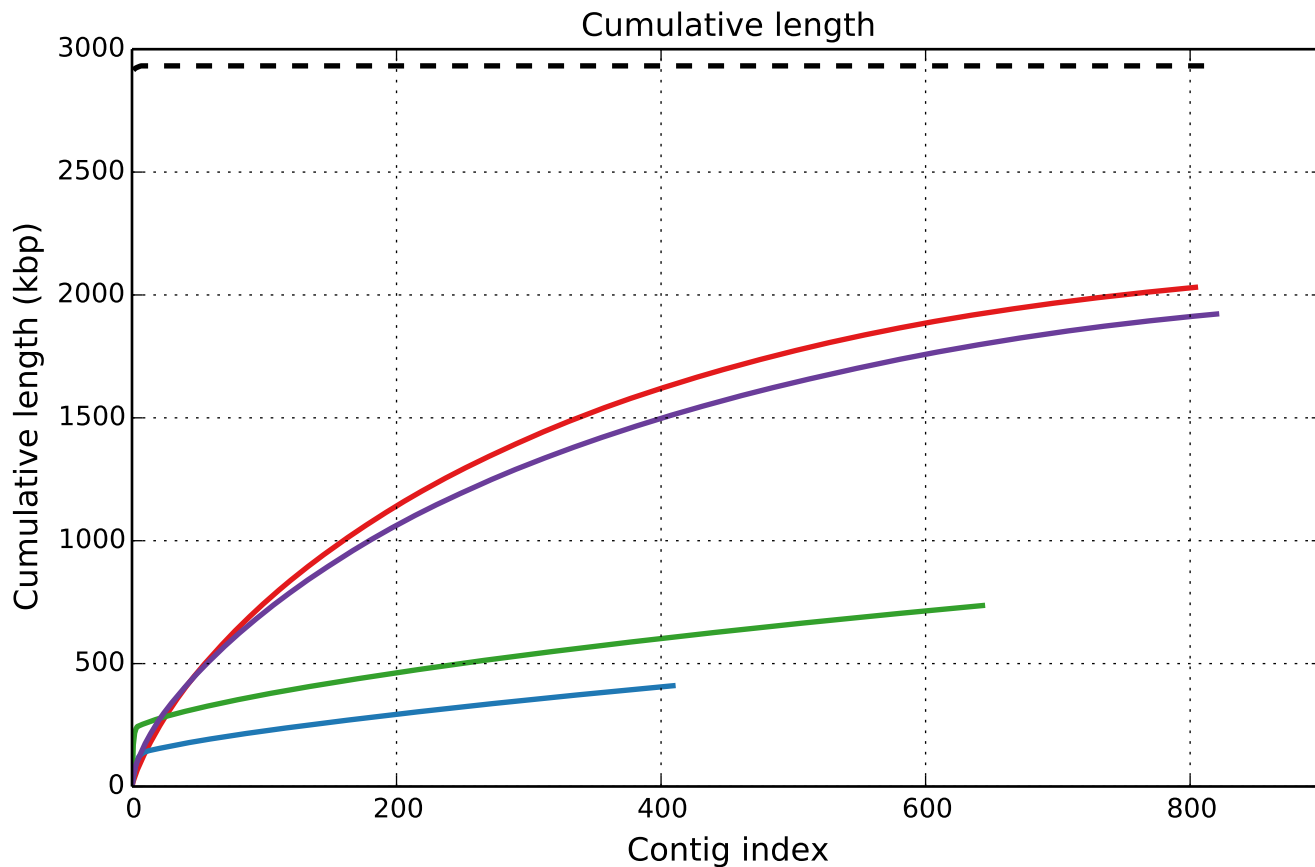
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



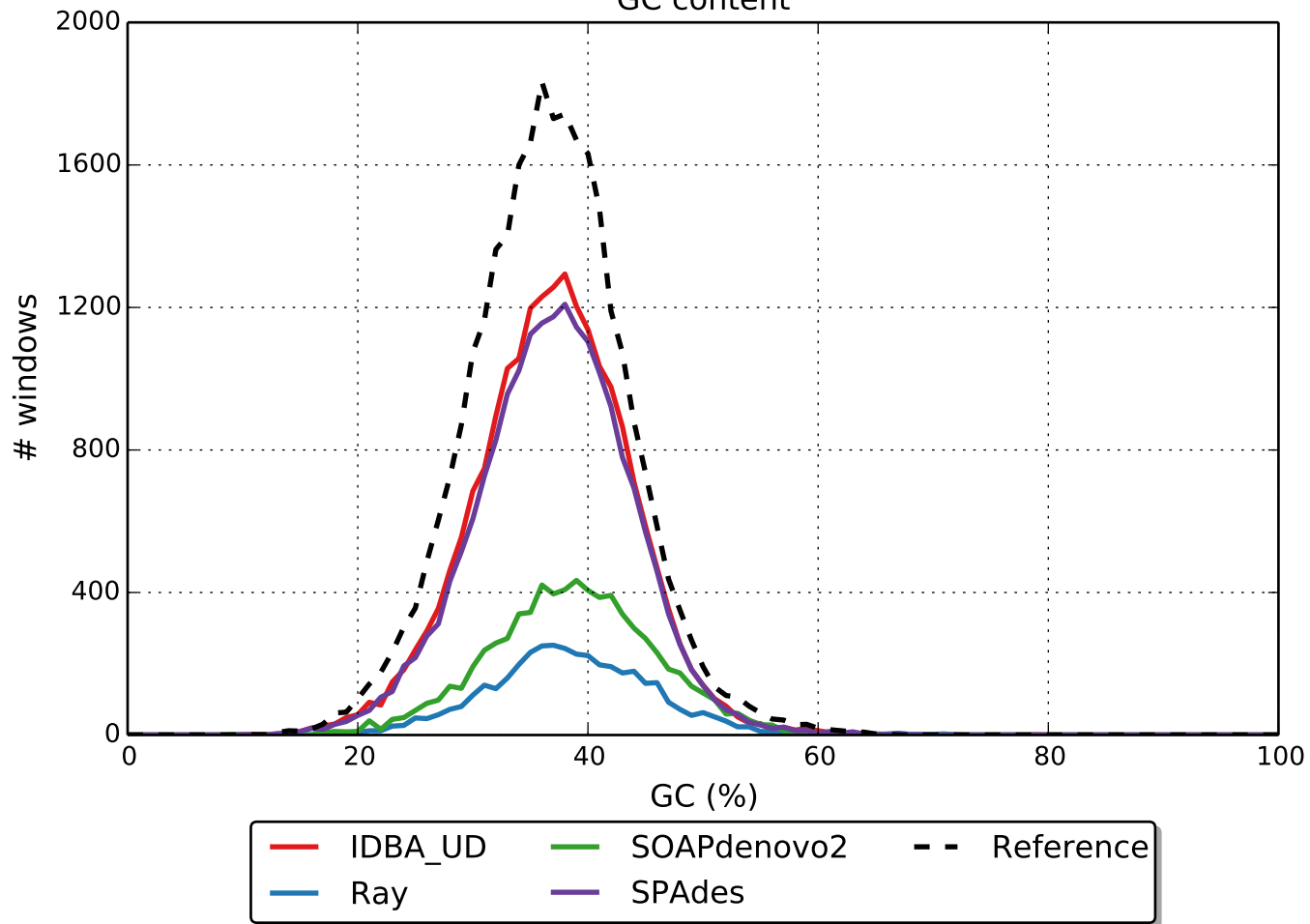
NGx



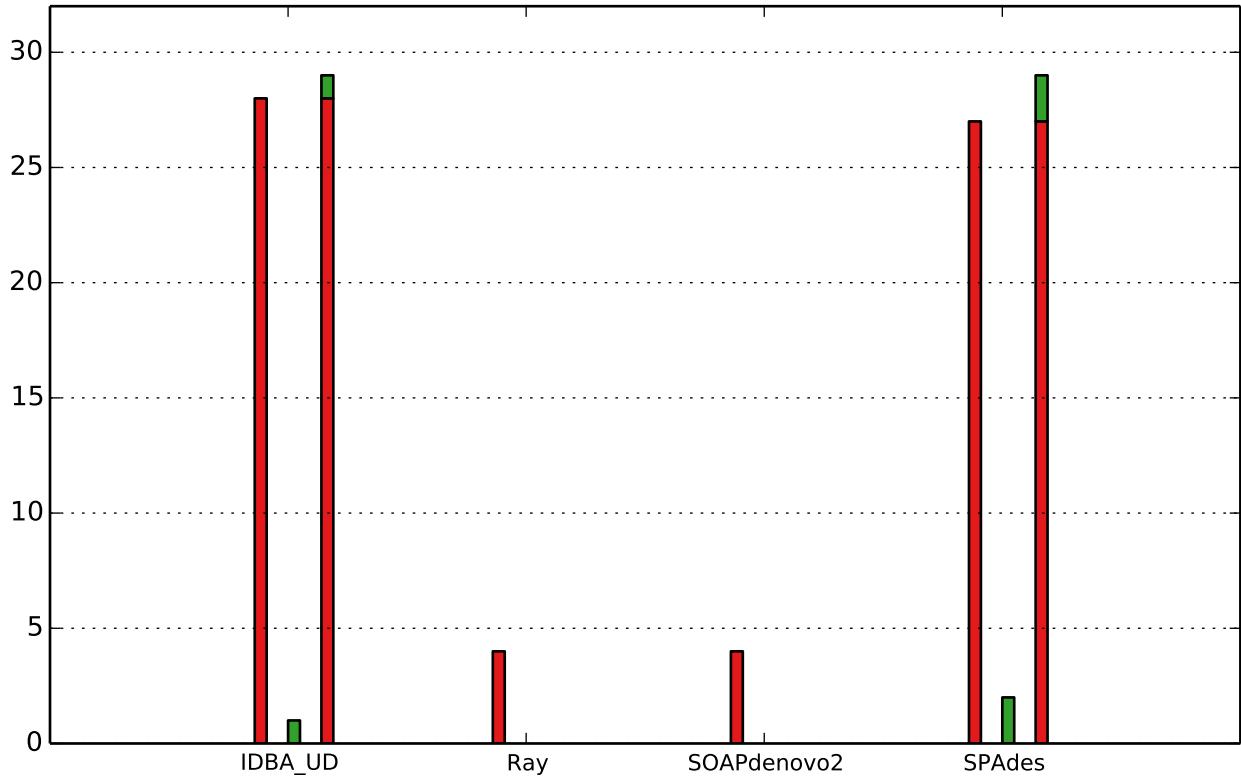
— IDBA_UD — SOAPdenovo2 — SPAdes
— Ray



GC content



Misassemblies

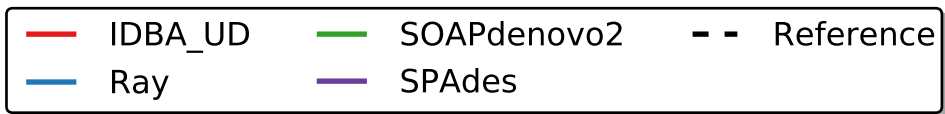
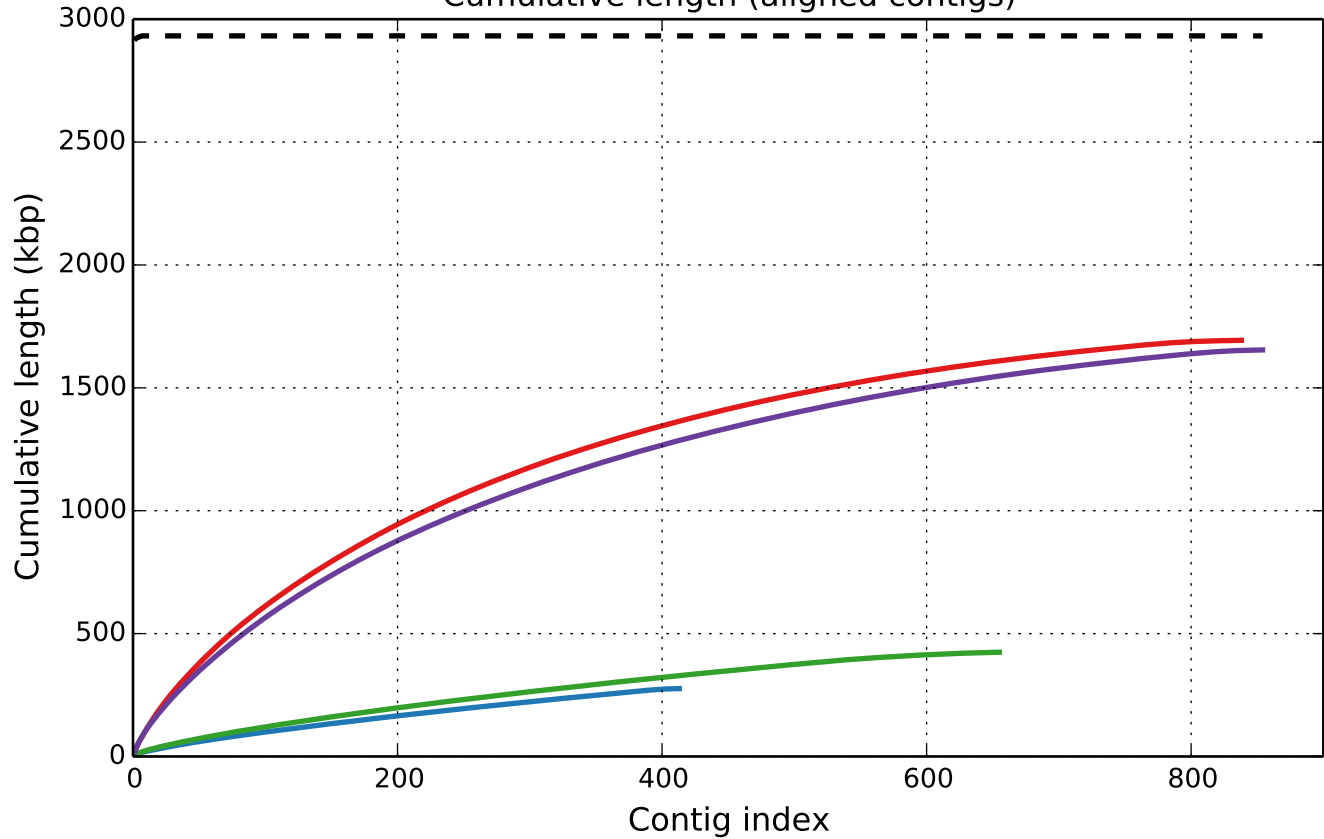


relocations

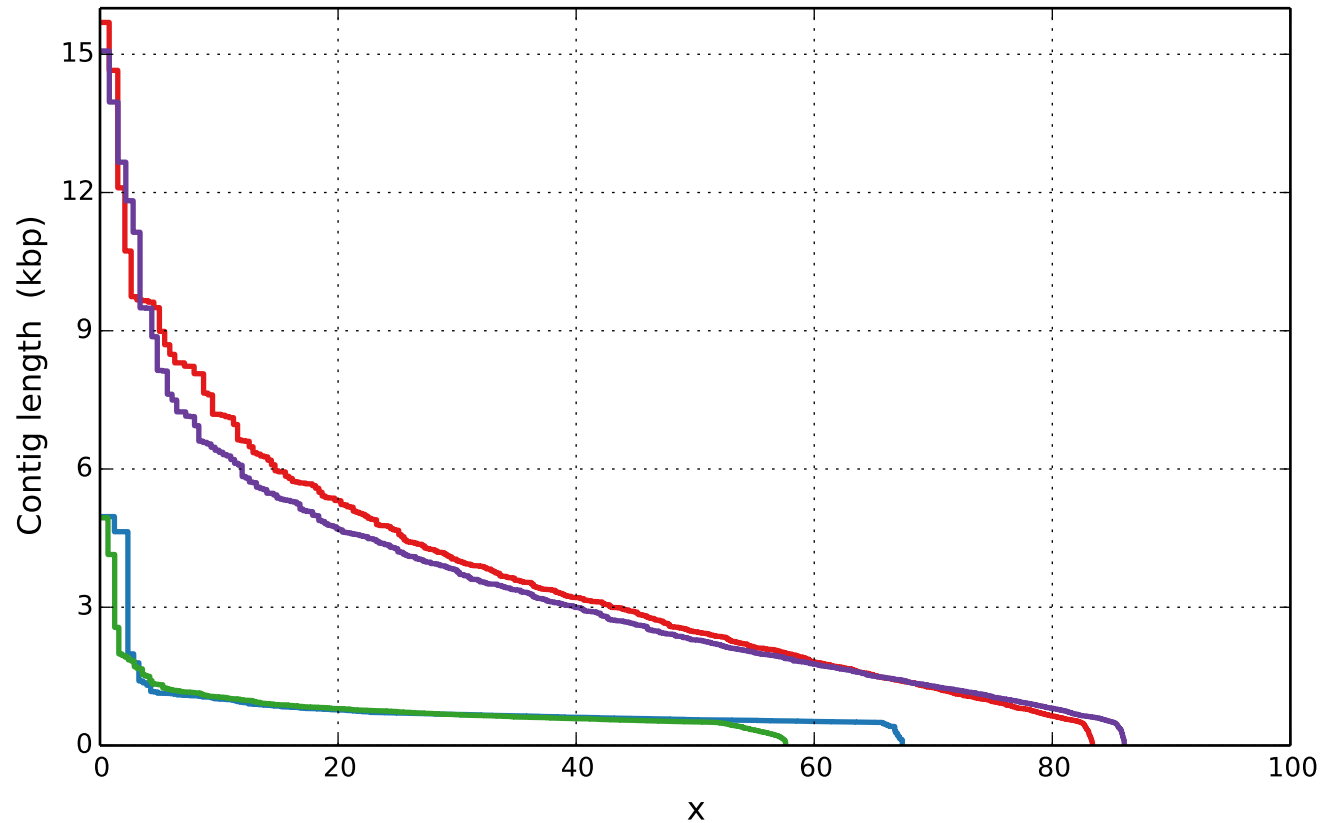


inversions

Cumulative length (aligned contigs)



NAx



NGAx

