

Report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# contigs (>= 0 bp)	42	56	18	7028
# contigs (>= 1000 bp)	14	36	11	621
# contigs (>= 5000 bp)	11	22	8	3
# contigs (>= 10000 bp)	10	18	8	0
# contigs (>= 25000 bp)	10	14	7	0
# contigs (>= 50000 bp)	8	12	4	0
Total length (>= 0 bp)	1831657	1965102	1811331	3320808
Total length (>= 1000 bp)	1821194	1955209	1808761	1071265
Total length (>= 5000 bp)	1816377	1924256	1802504	16099
Total length (>= 10000 bp)	1810330	1897645	1802504	0
Total length (>= 25000 bp)	1810330	1840422	1792310	0
Total length (>= 50000 bp)	1739635	1787121	1700270	0
# contigs	19	45	12	1590
Largest contig	545971	305868	1150911	5936
Total length	1824603	1961709	1809438	1738815
Reference length	1819370	1819370	1819370	1819370
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.02	38.02	38.02	38.02
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1164
N75	179754	79547	311459	786
NG75	179754	112073	311459	728
L50	2	4	1	437
LG50	2	4	1	471
L75	4	8	2	884
LG75	4	7	2	964
# misassemblies	23	32	29	7
# misassembled contigs	7	12	4	7
Misassembled contigs length	1489261	1685479	588604	14284
# local misassemblies	42	65	14	11
# unaligned contigs	1 + 1 part	18 + 5 part	0 + 5 part	367 + 103 part
Unaligned length	3376	100281	633661	457904
Genome fraction (%)	93.068	87.973	50.478	65.013
Duplication ratio	1.076	1.163	1.280	1.083
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	1980.27	2309.20	3502.32	2061.43
# indels per 100 kbp	56.75	61.79	87.44	45.91
Largest alignment	300479	255057	67913	5147
NA50	98146	50394	1514	845
NGA50	98146	51885	1171	804
NA75	38878	20822	-	-
NGA75	38878	25638	-	-
LA50	5	11	80	572
LGA50	5	10	84	621
LA75	14	27	-	-
LGA75	14	23	-	-

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

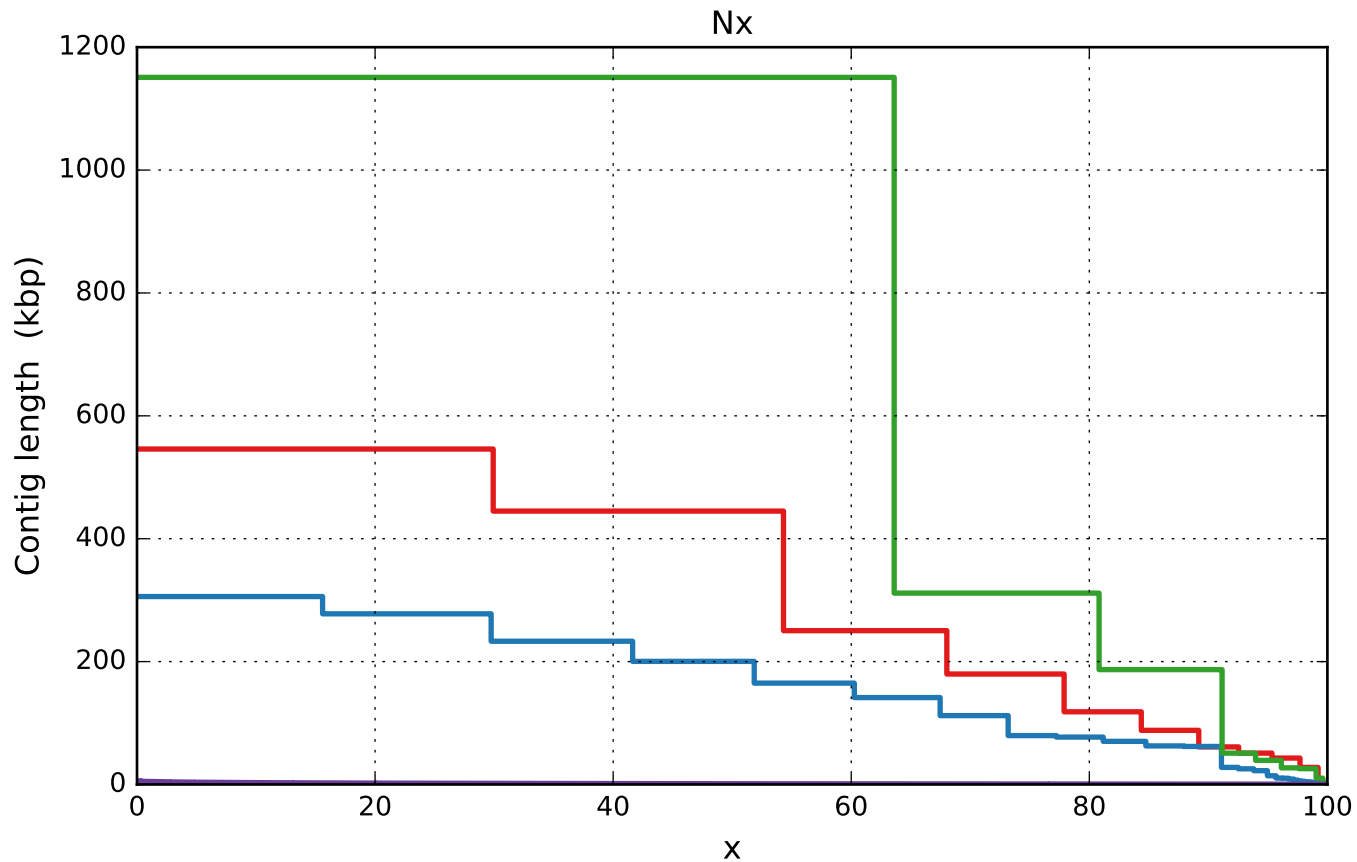
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	23	32	29	7
# relocations	22	32	29	7
# translocations	0	0	0	0
# inversions	1	0	0	0
# misassembled contigs	7	12	4	7
Misassembled contigs length	1489261	1685479	588604	14284
# local misassemblies	42	65	14	11
# mismatches	33531	36960	32165	24383
# indels	961	989	803	543
# short indels	842	868	725	490
# long indels	119	121	78	53
Indels length	3374	3384	1960	1601

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).

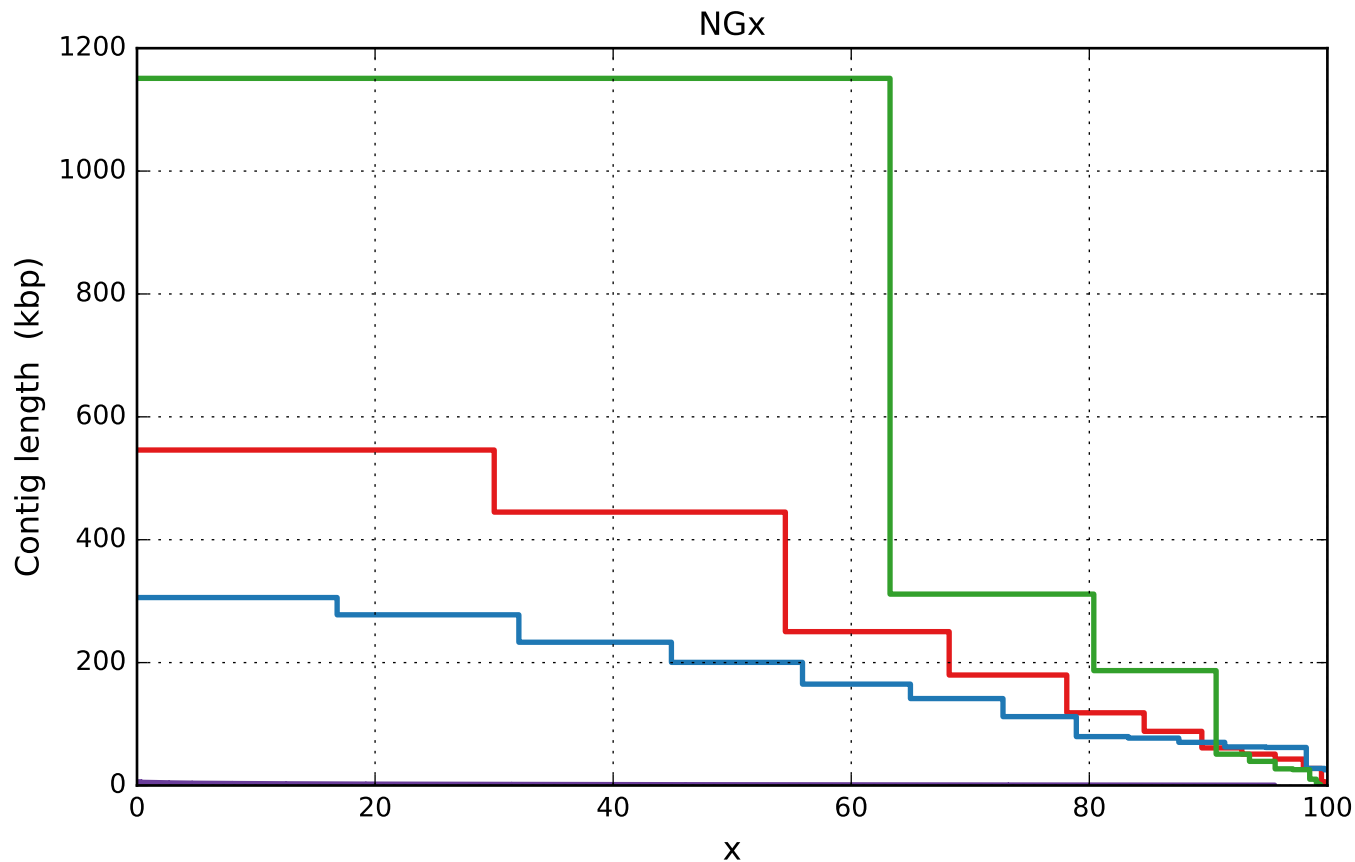
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	1	18	0	367
Fully unaligned length	2293	75280	0	404099
# partially unaligned contigs	1	5	5	103
# with misassembly	0	0	3	3
# both parts are significant	1	1	2	18
Partially unaligned length	1083	25001	633661	53805
# N's	1086	1127	693	1471

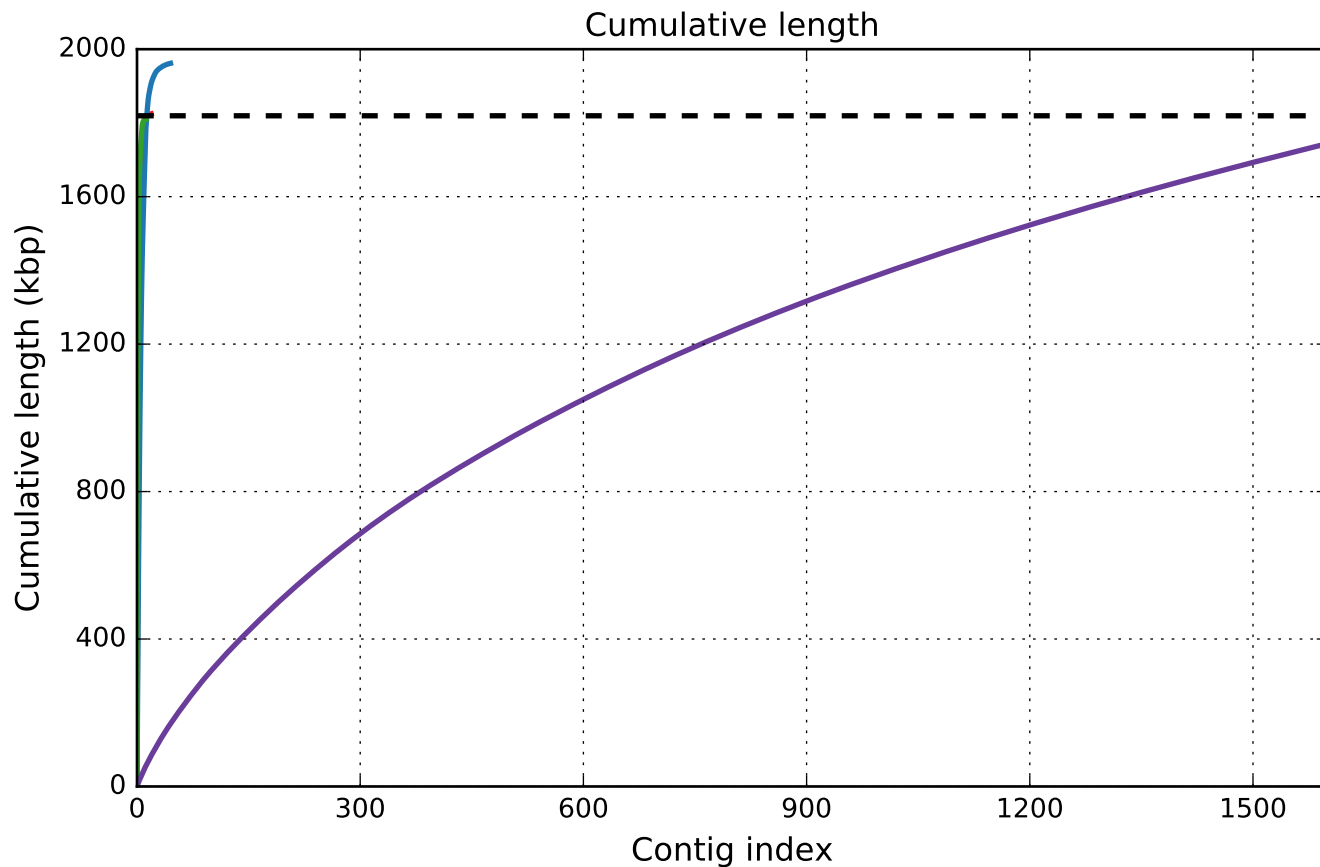
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



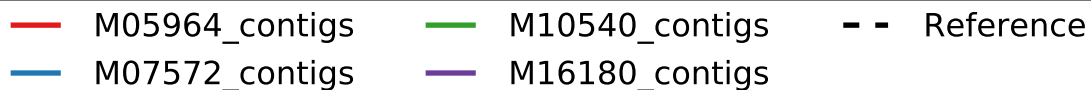
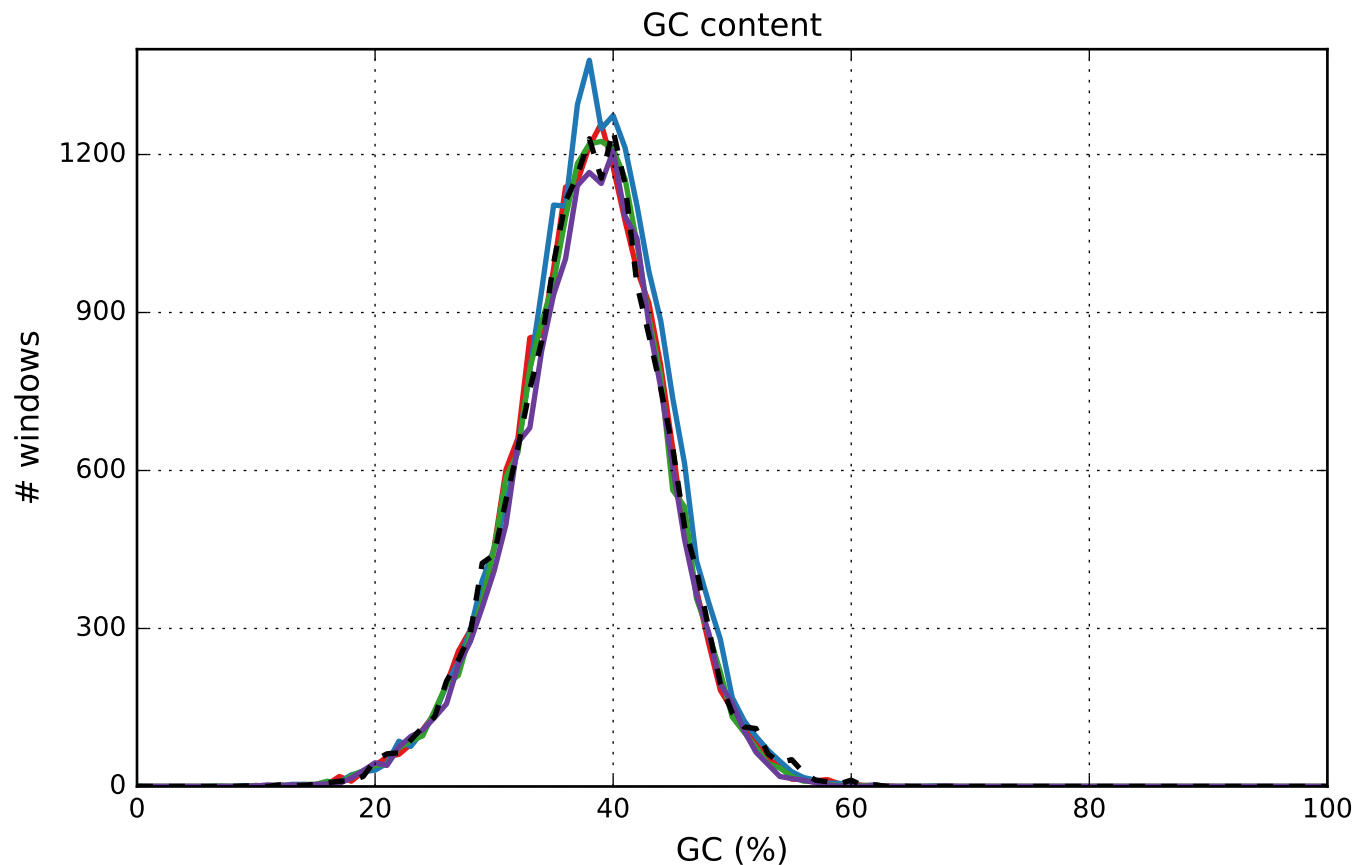
— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs



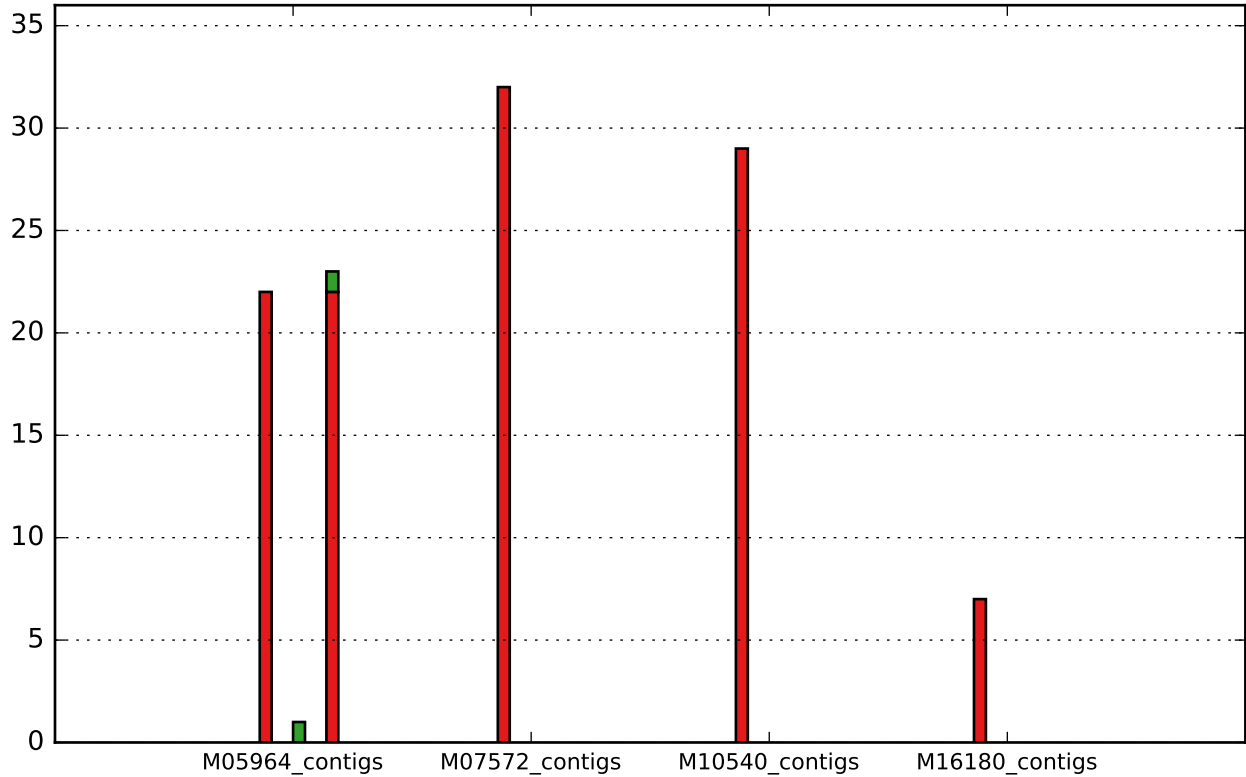
— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs



M05964_contigs	M10540_contigs	- - Reference
M07572_contigs	M16180_contigs	



Misassemblies

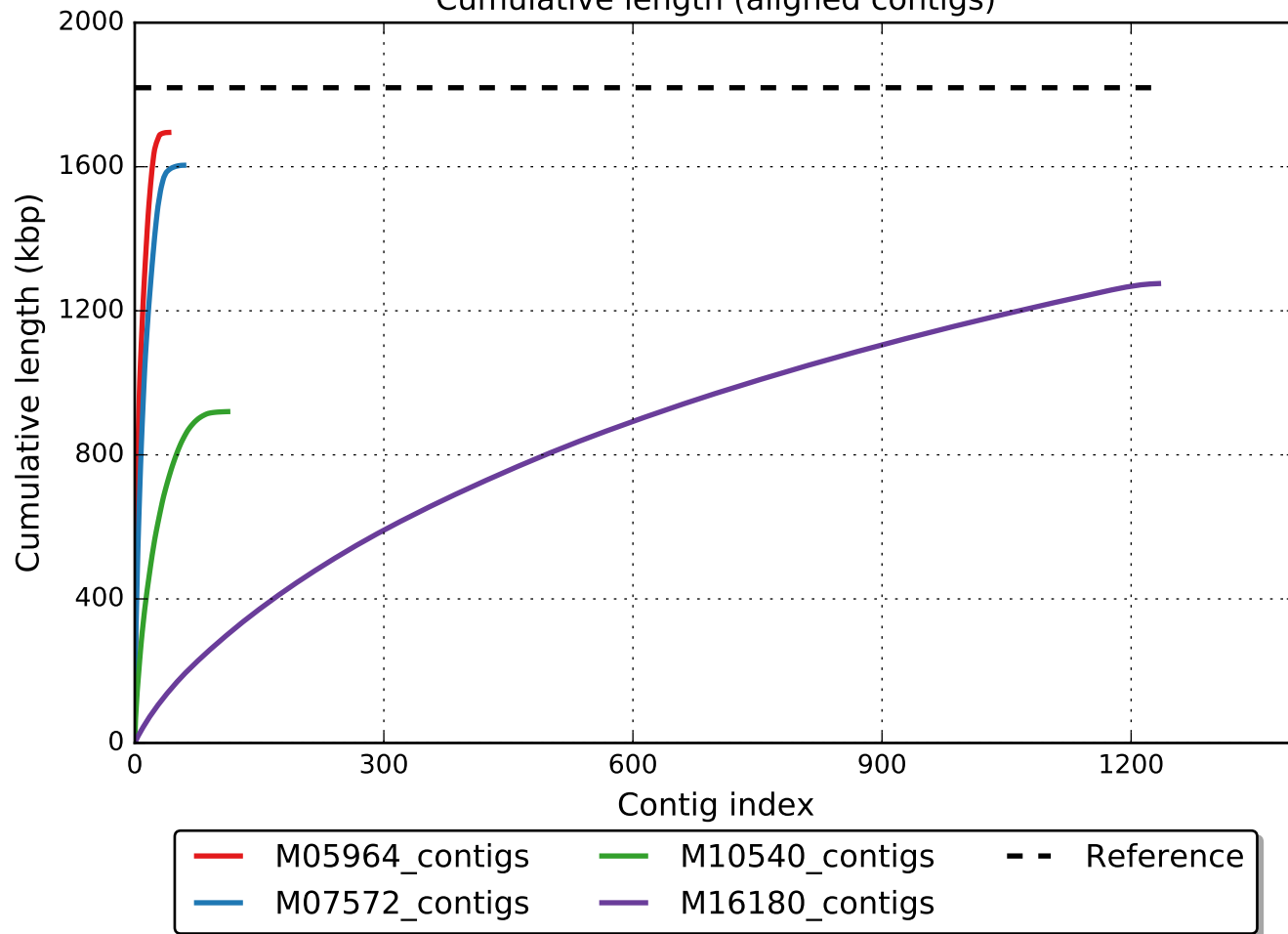


relocations

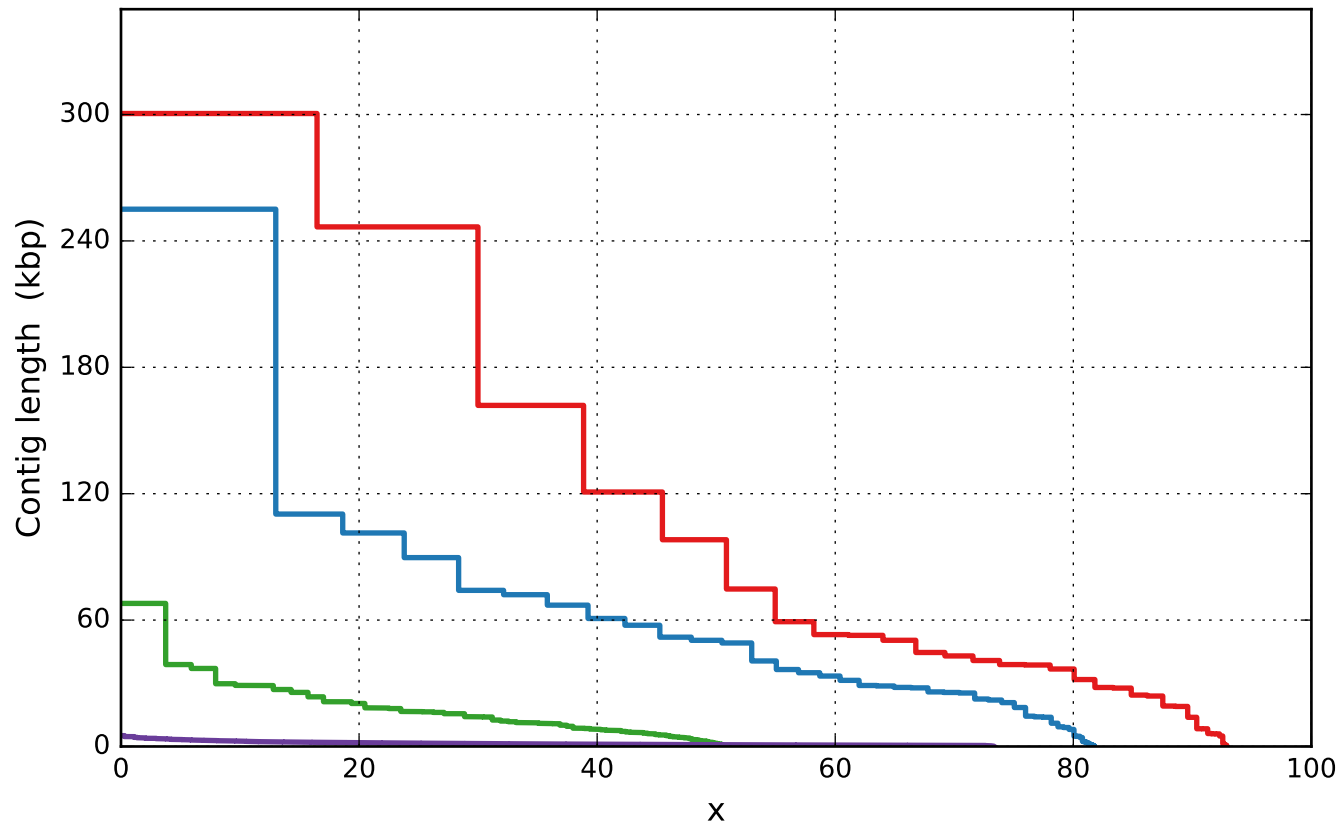


inversions

Cumulative length (aligned contigs)

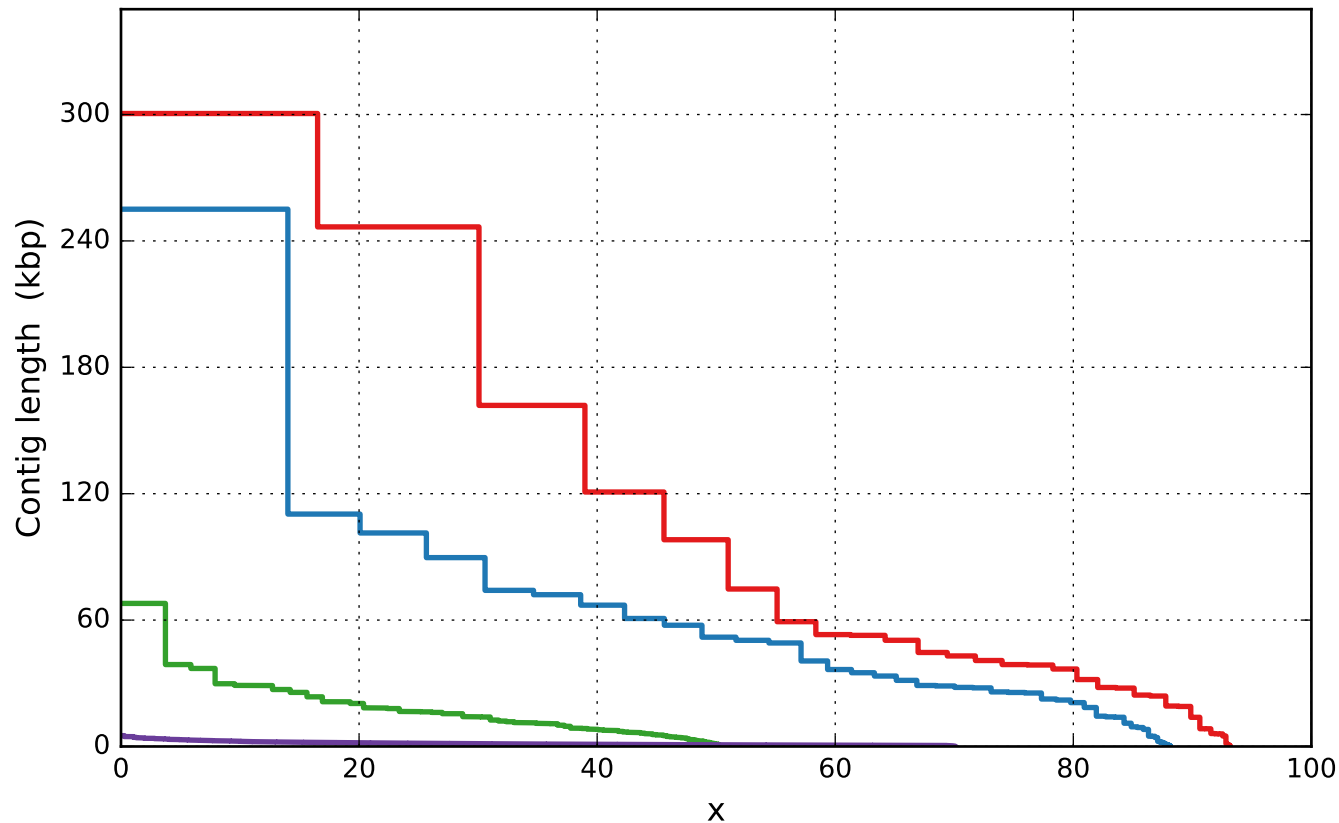


NAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

