

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	1811802	1811802	1811802	1811802
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.07	38.07	38.07	38.07
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1166
N75	179754	79547	311459	786
NG75	179754	112073	311459	729
L50	2	4	1	437
LG50	2	4	1	468
L75	4	8	2	884
LG75	4	7	2	957
# misassemblies	46	41	81	12
# misassembled contigs	9	12	6	12
Misassembled contigs length	1782615	1749842	1717730	19886
# local misassemblies	67	67	40	23
# unaligned contigs	2 + 0 part	20 + 3 part	0 + 2 part	401 + 113 part
Unaligned length	8340	138865	35428	487650
Genome fraction (%)	88.773	86.519	60.357	63.849
Duplication ratio	1.129	1.163	1.622	1.082
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2561.02	2667.60	3656.47	2320.43
# indels per 100 kbp	69.45	63.86	92.91	46.59
Largest alignment	148362	226003	81875	5147
NA50	56818	34304	10744	826
NGA50	59035	38532	10744	791
NA75	18855	9452	-	-
NGA75	18855	15896	-	-
LA50	10	13	38	588
LGA50	9	11	38	633
LA75	25	38	-	-
LGA75	25	29	-	-

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

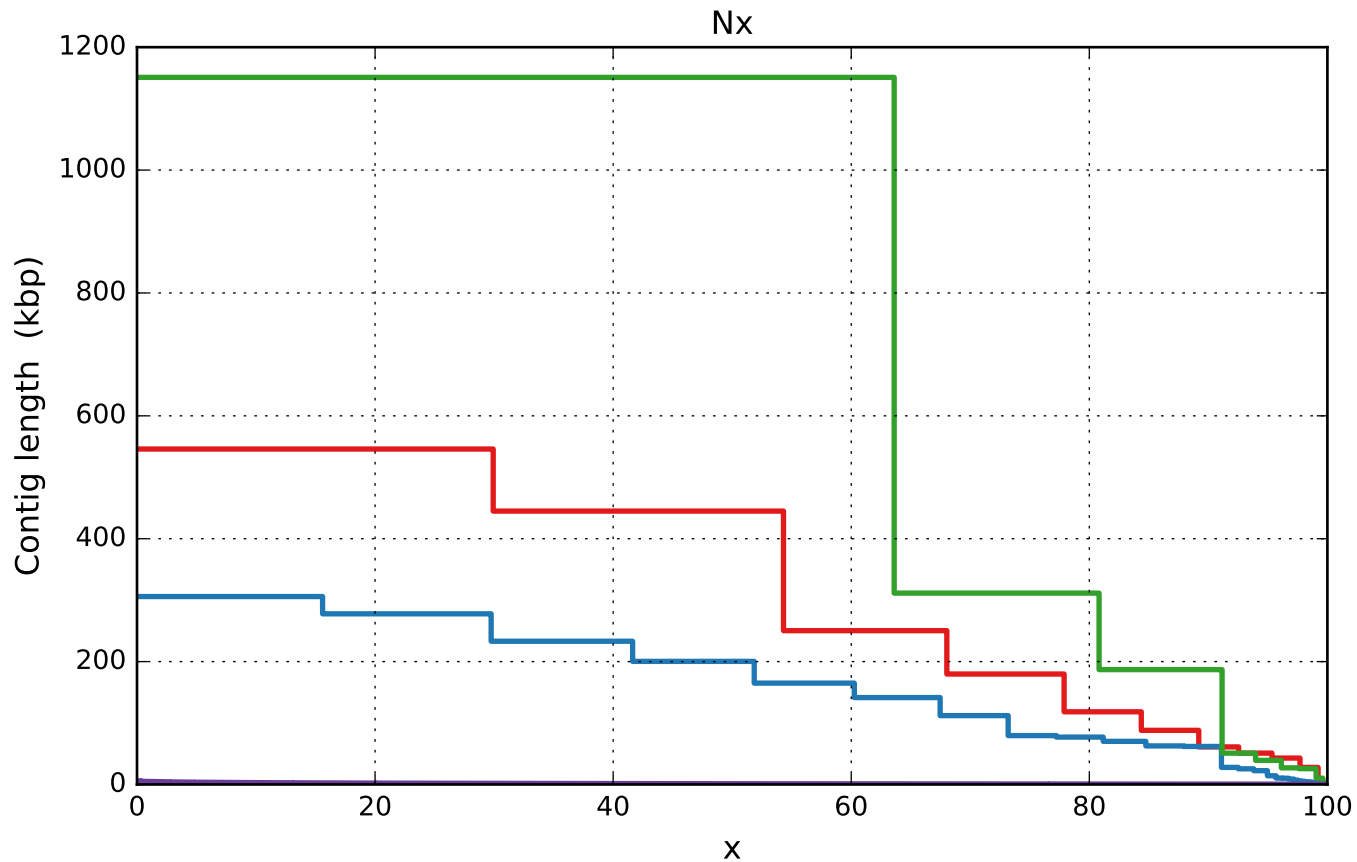
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	46	41	81	12
# relocations	46	41	81	12
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	9	12	6	12
Misassembled contigs length	1782615	1749842	1717730	19886
# local misassemblies	67	67	40	23
# mismatches	41191	41816	39985	26843
# indels	1117	1001	1016	539
# short indels	976	885	920	496
# long indels	141	116	96	43
Indels length	3502	2986	2481	1313

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).

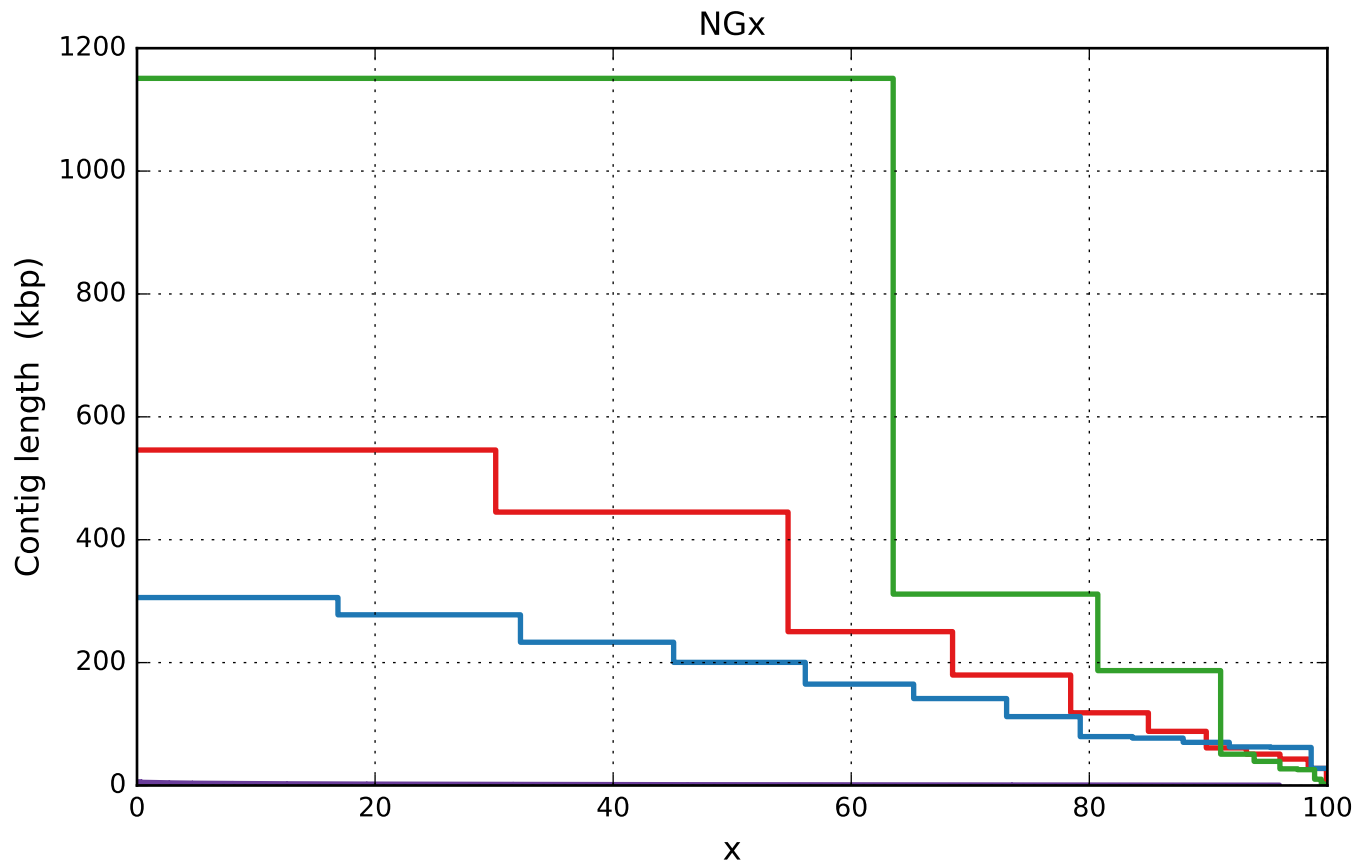
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	2	20	0	401
Fully unaligned length	8340	90575	0	431781
# partially unaligned contigs	0	3	2	113
# with misassembly	0	2	1	2
# both parts are significant	0	2	2	24
Partially unaligned length	0	48290	35428	55869
# N's	1086	1127	693	1471

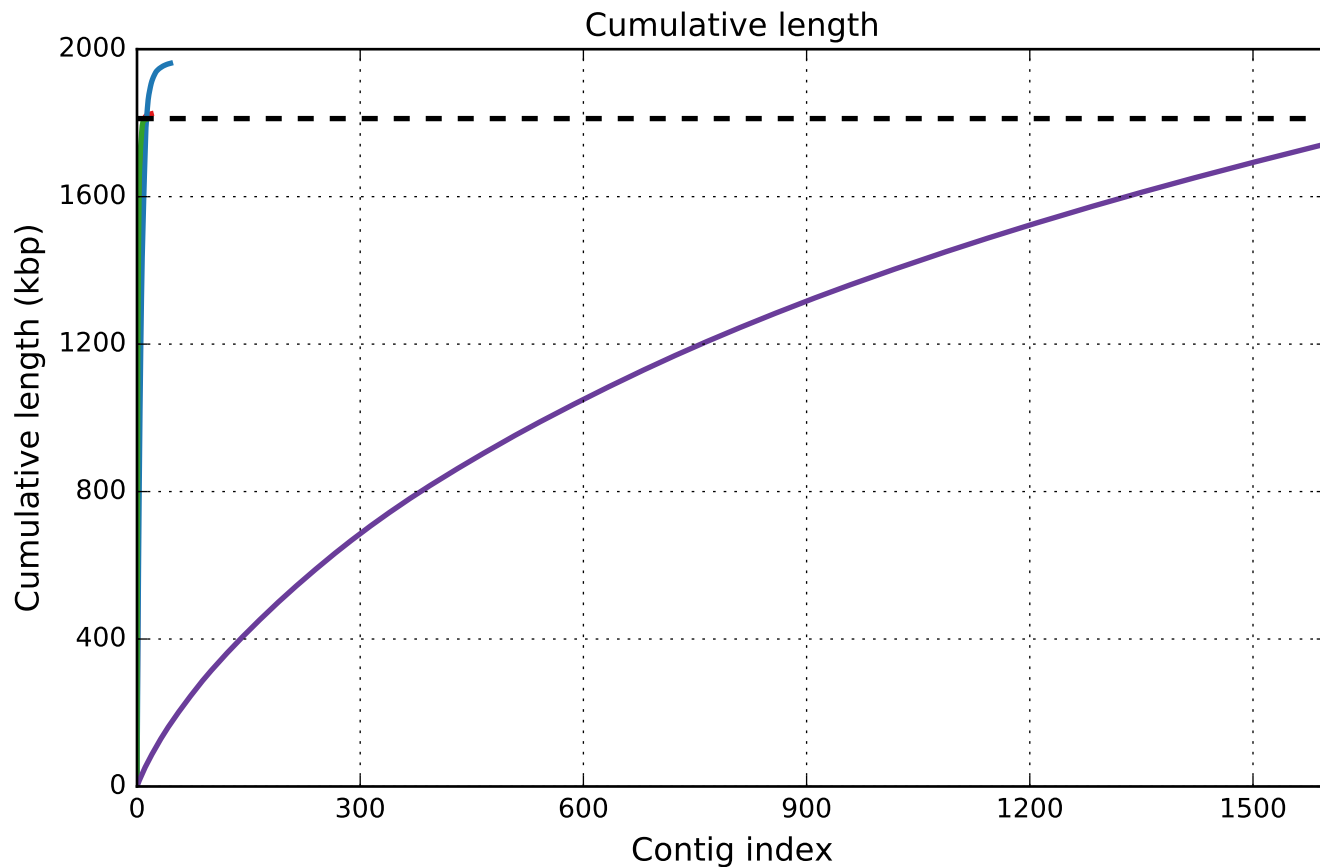
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



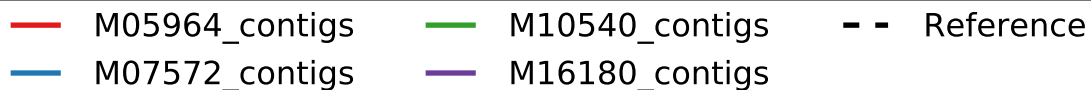
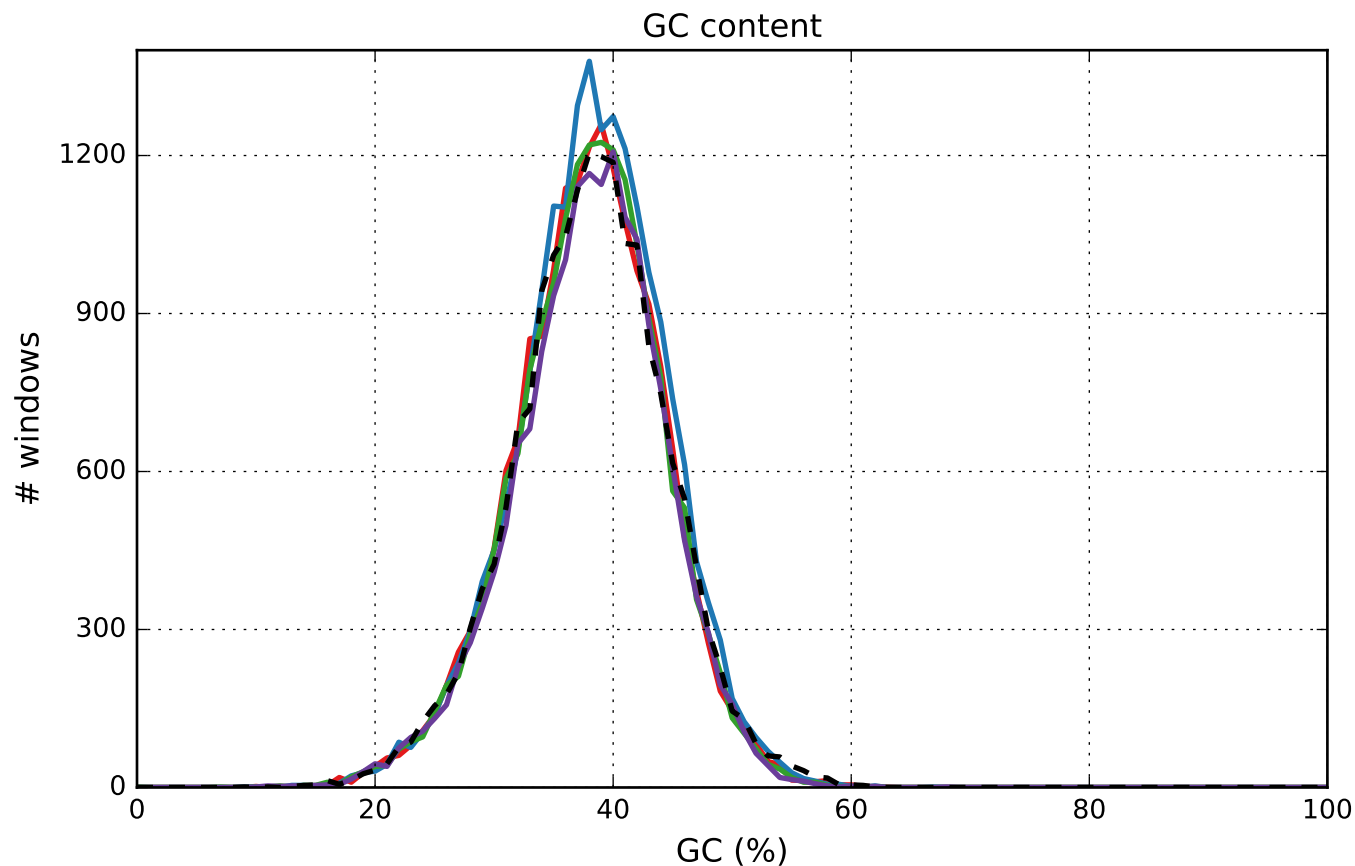
— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

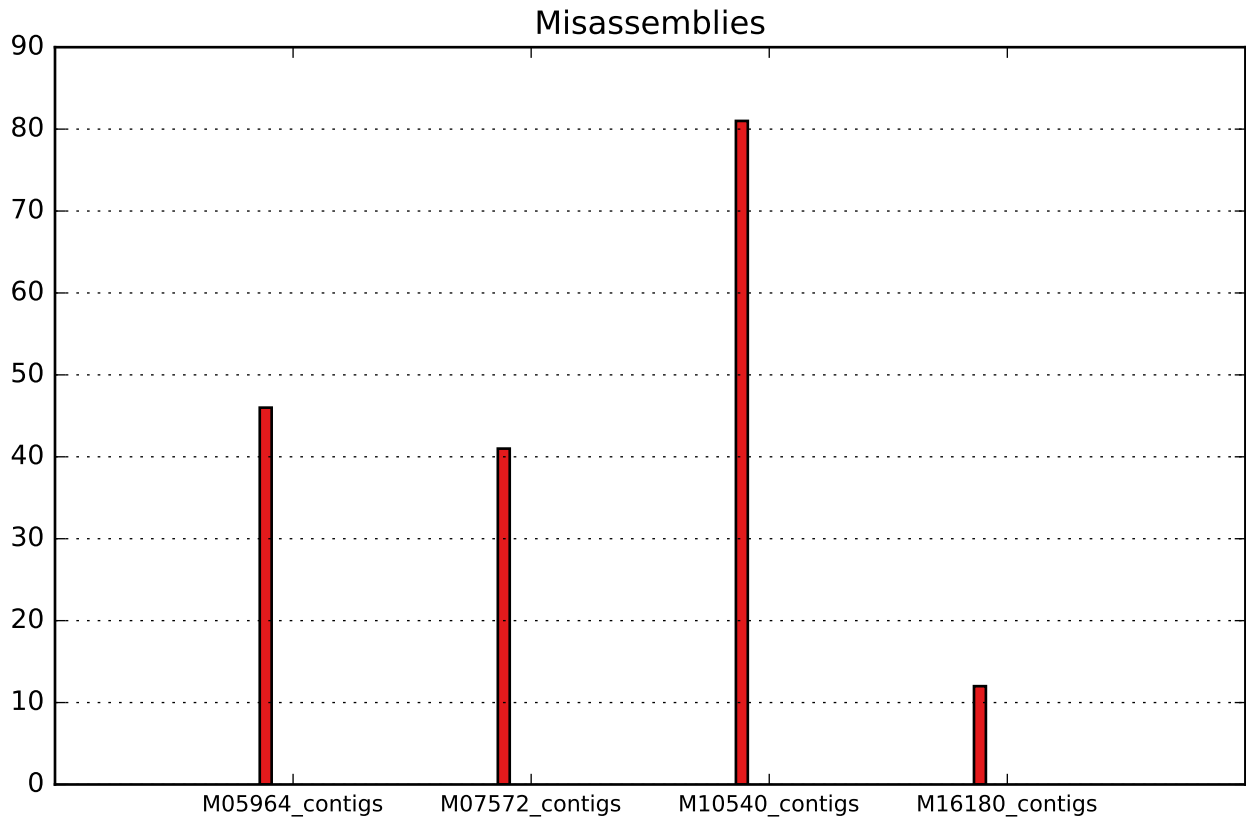


— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs



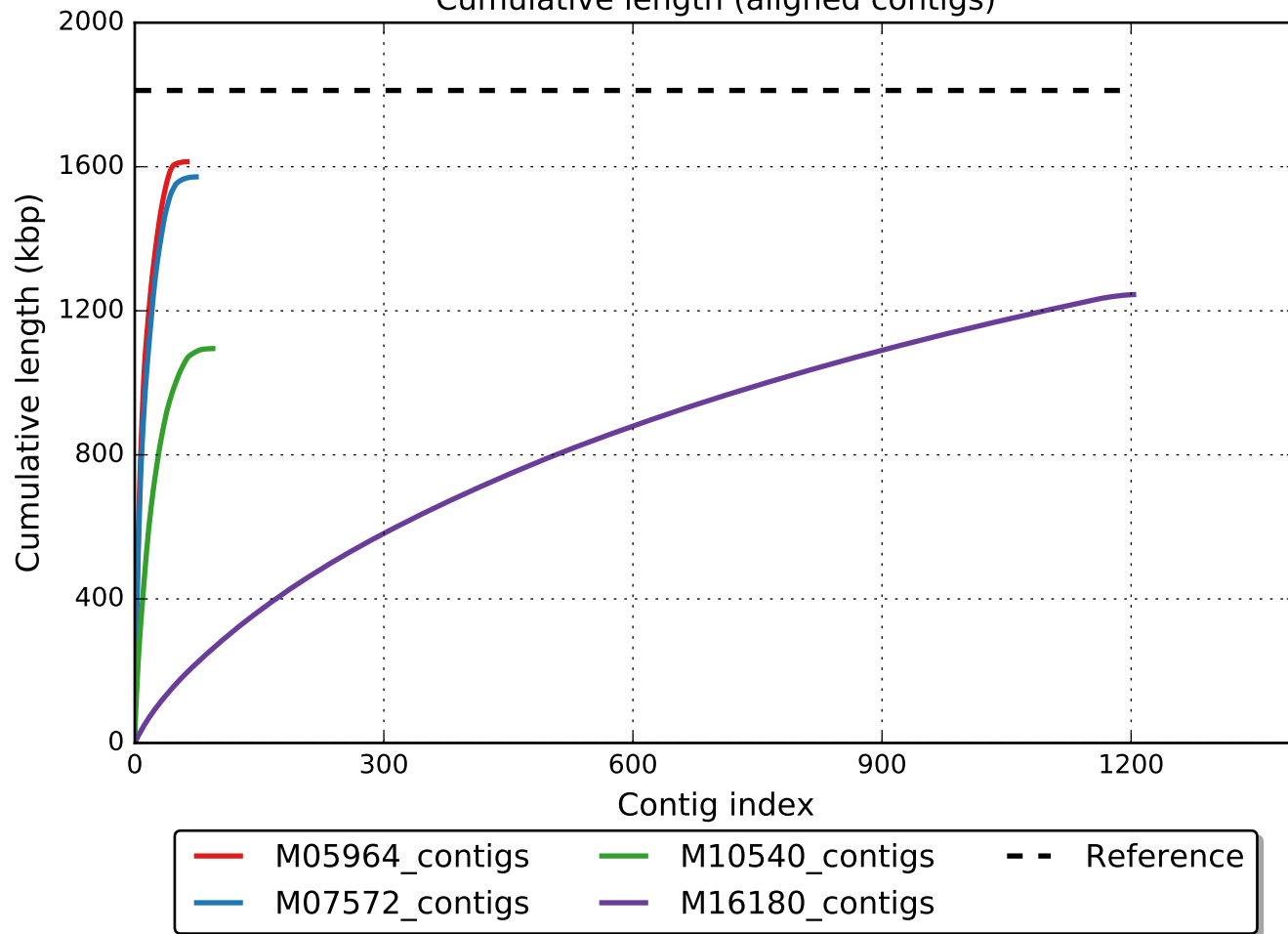
M05964_contigs	M10540_contigs	- - Reference
M07572_contigs	M16180_contigs	



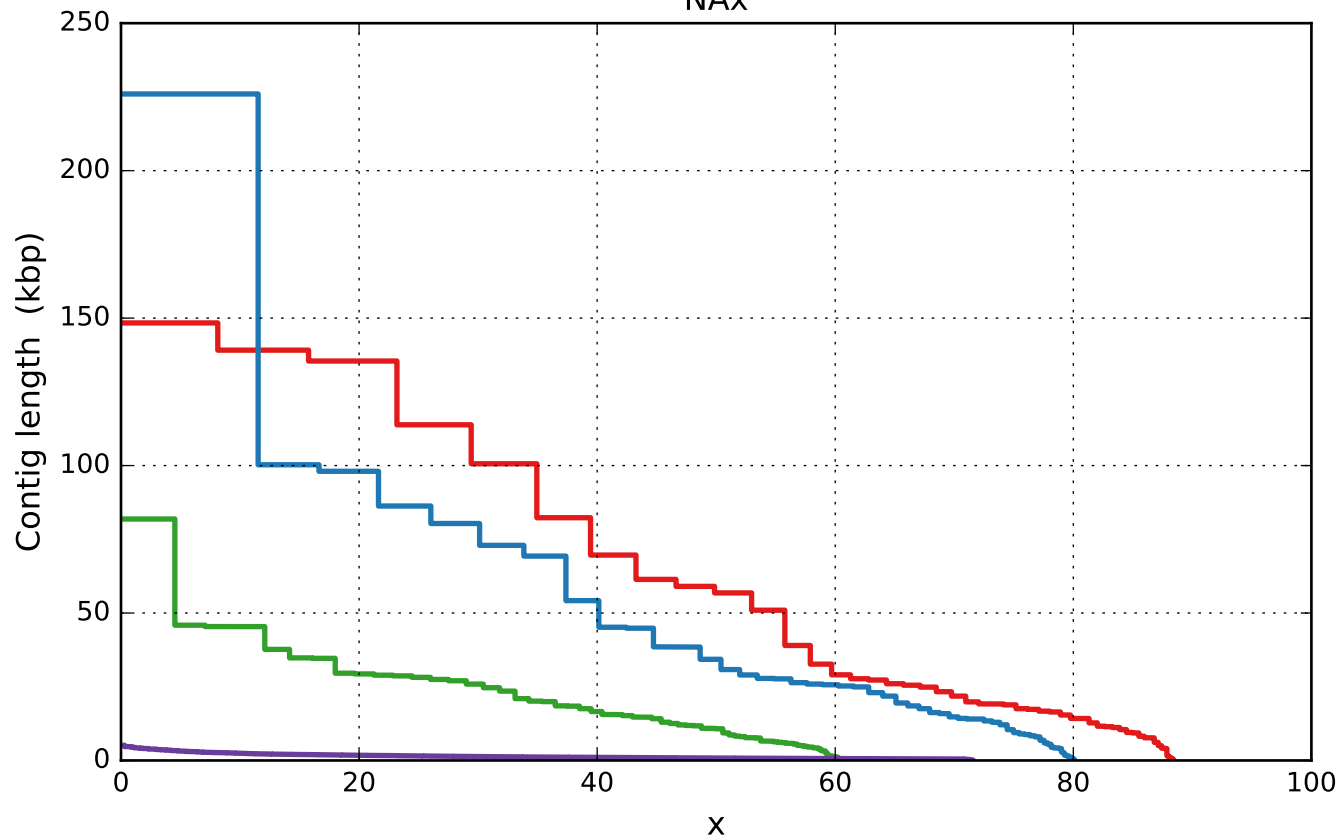


 # relocations

Cumulative length (aligned contigs)



NAx



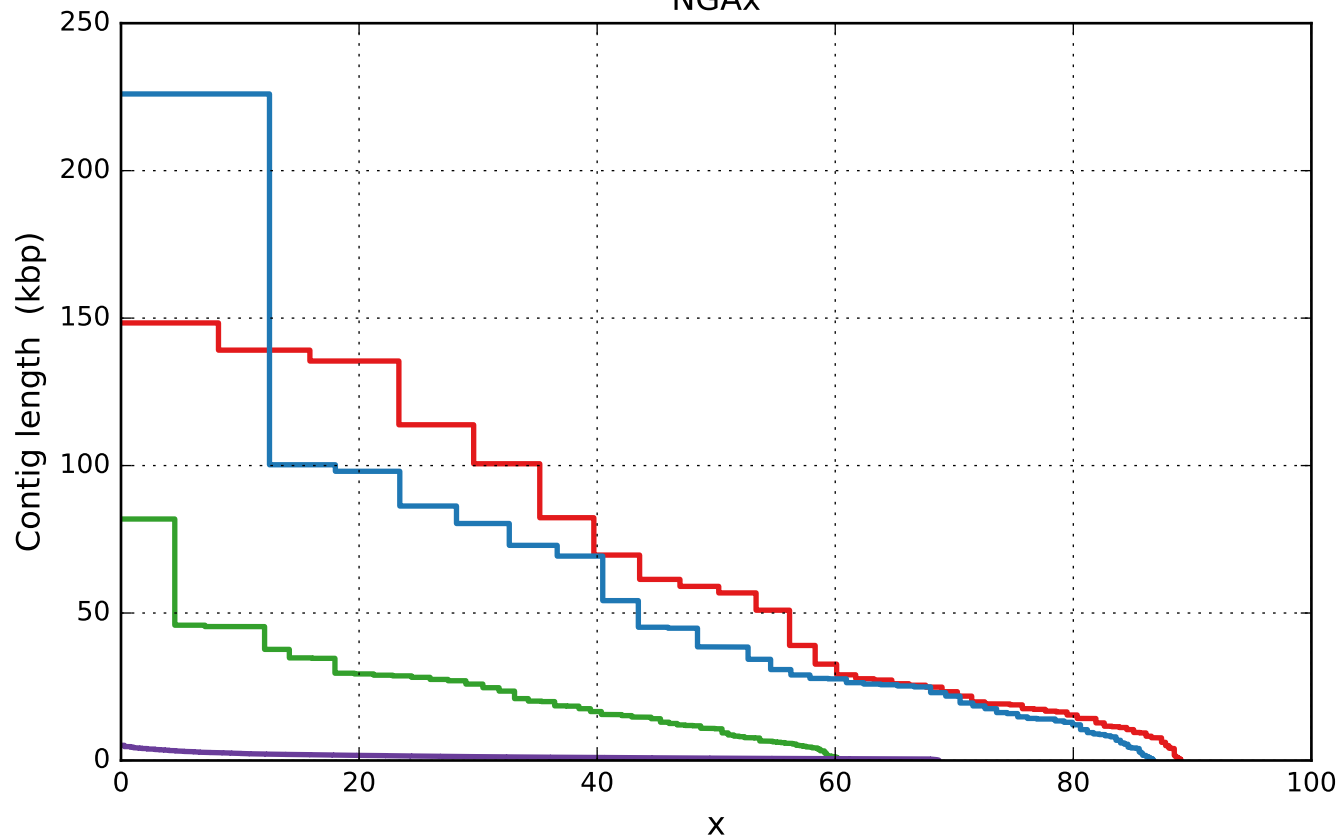
M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

NGAx



M05964_contigs M10540_contigs M16180_contigs
M07572_contigs

