

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	1914490	1914490	1914490	1914490
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.16	38.16	38.16	38.16
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1113
N75	179754	79547	311459	786
NG75	118299	79547	311459	682
L50	2	4	1	437
LG50	2	4	1	513
L75	4	8	2	884
LG75	5	8	2	1066
# misassemblies	40	15	80	10
# misassembled contigs	9	9	6	10
Misassembled contigs length	1782615	1259117	1741348	13212
# local misassemblies	68	32	43	10
# unaligned contigs	1 + 1 part	13 + 3 part	0 + 3 part	287 + 92 part
Unaligned length	3693	112545	34749	343445
Genome fraction (%)	84.455	89.903	55.037	67.508
Duplication ratio	1.126	1.074	1.684	1.080
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2135.04	1109.24	3530.65	1482.46
# indels per 100 kbp	57.77	36.31	84.94	29.25
Largest alignment	157989	241111	64661	5486
NA50	56831	100516	8353	982
NGA50	51861	112073	6983	870
NA75	24899	39767	-	549
NGA75	20262	44262	-	-
LA50	10	6	42	517
LGA50	11	5	49	612
LA75	23	14	-	1117
LGA75	26	13	-	-

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

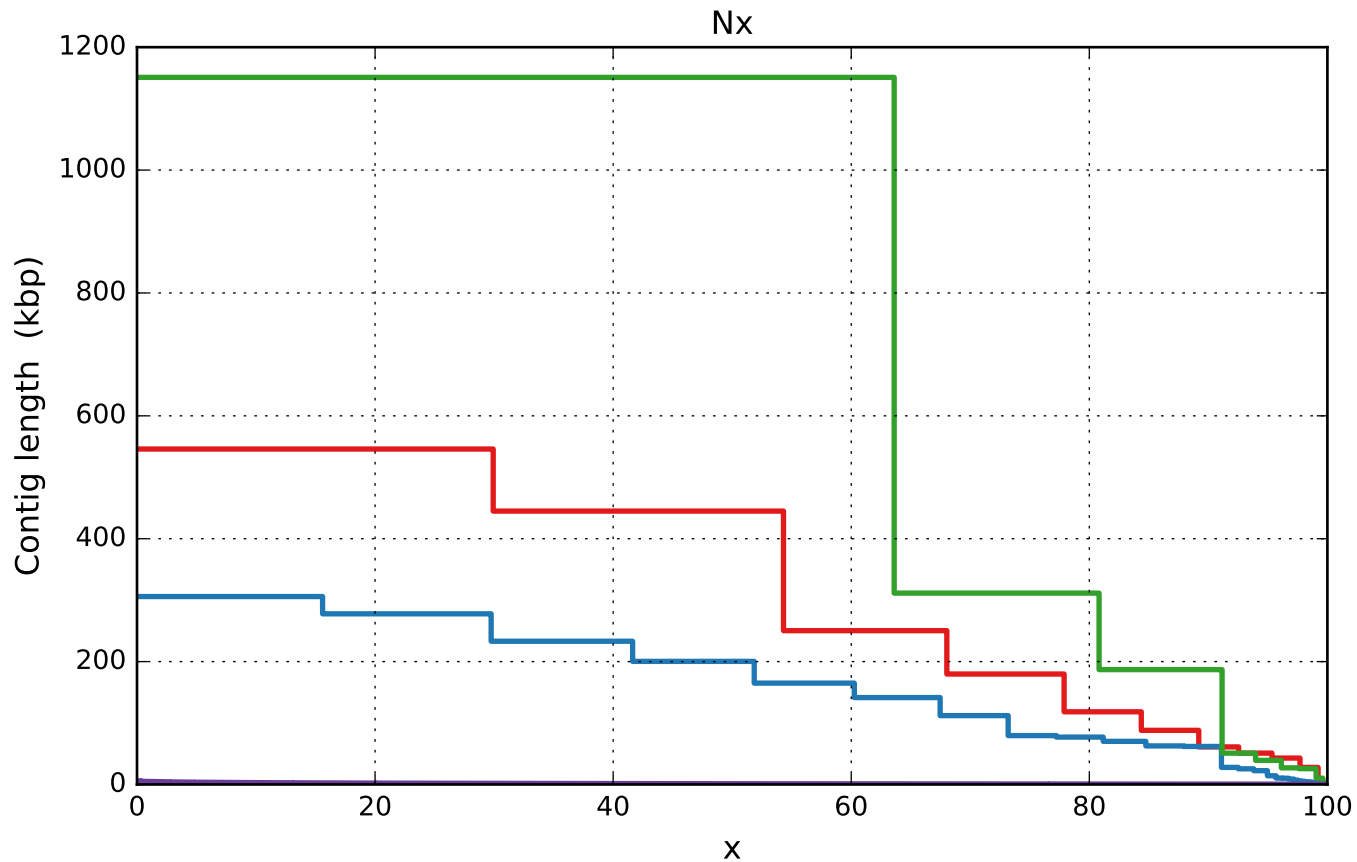
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	40	15	80	10
# relocations	40	15	78	10
# translocations	0	0	0	0
# inversions	0	0	2	0
# misassembled contigs	9	9	6	10
Misassembled contigs length	1782615	1259117	1741348	13212
# local misassemblies	68	32	43	10
# mismatches	34521	19092	37202	19160
# indels	934	625	895	378
# short indels	816	549	809	342
# long indels	118	76	86	36
Indels length	3288	2260	2313	1033

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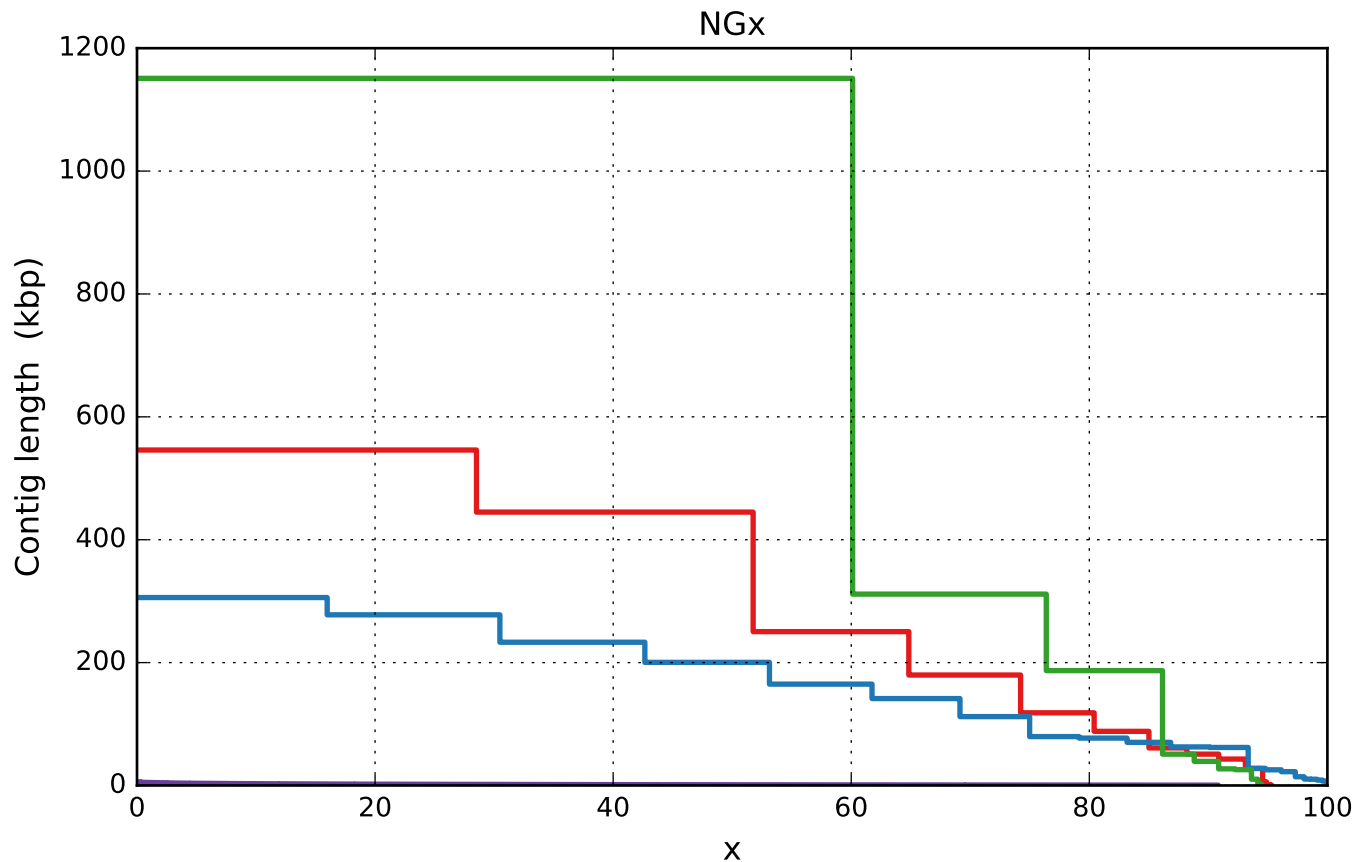
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	1	13	0	287
Fully unaligned length	2293	70733	0	288749
# partially unaligned contigs	1	3	3	92
# with misassembly	0	1	2	1
# both parts are significant	1	2	1	11
Partially unaligned length	1400	41812	34749	54696
# 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

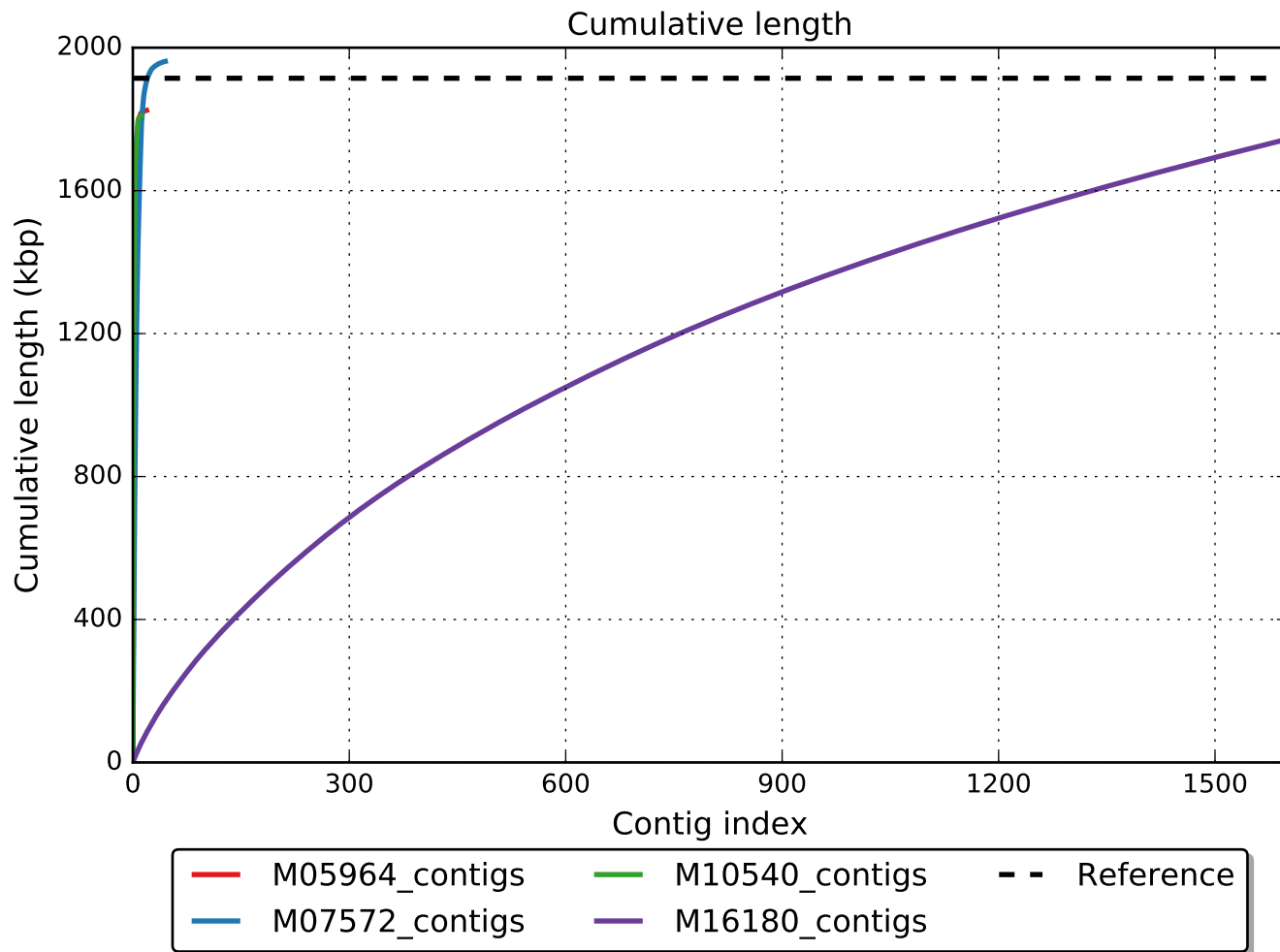


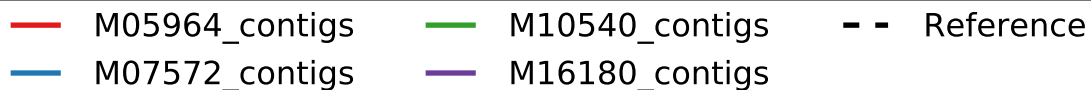
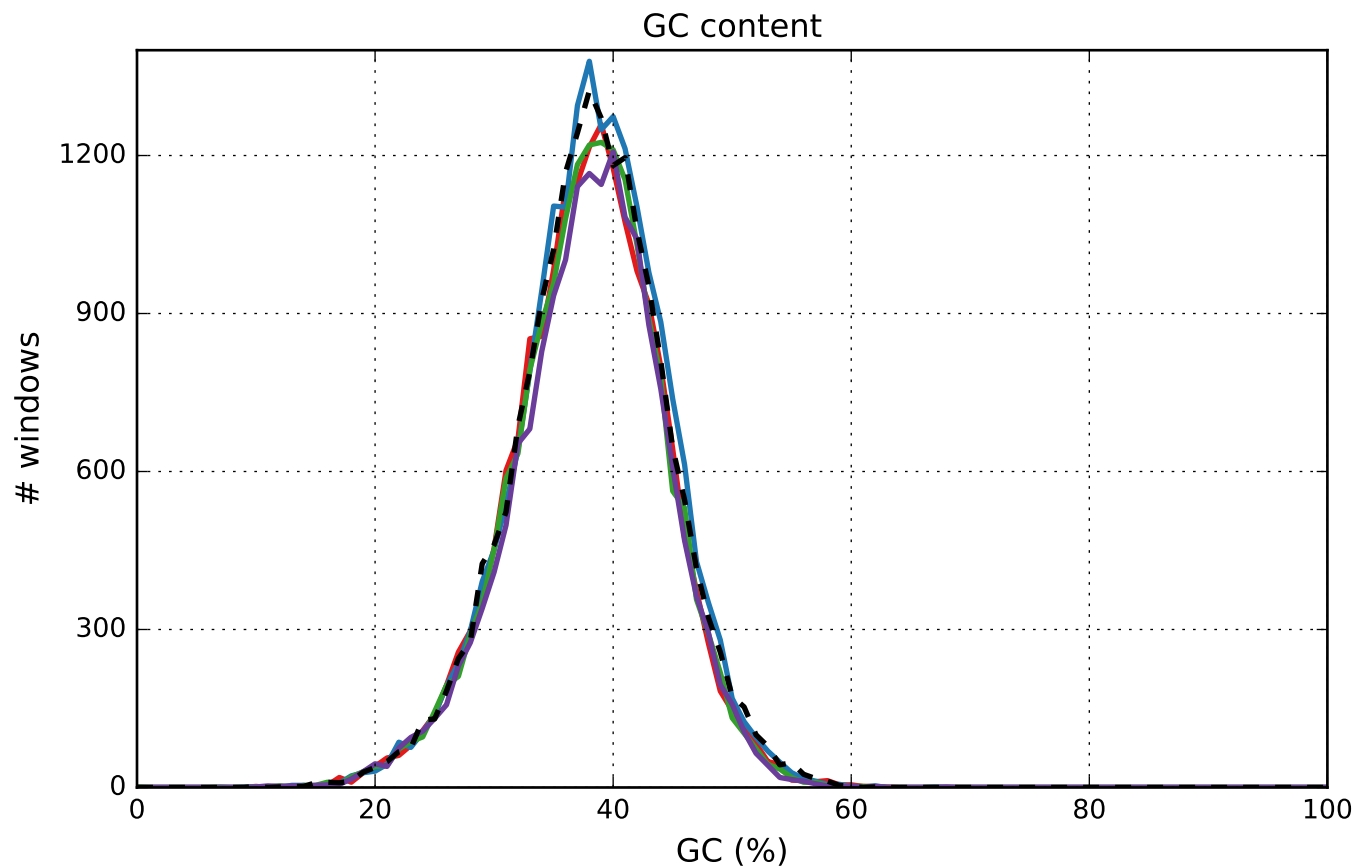
M05964_contigs

M10540_contigs

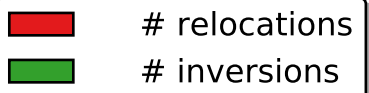
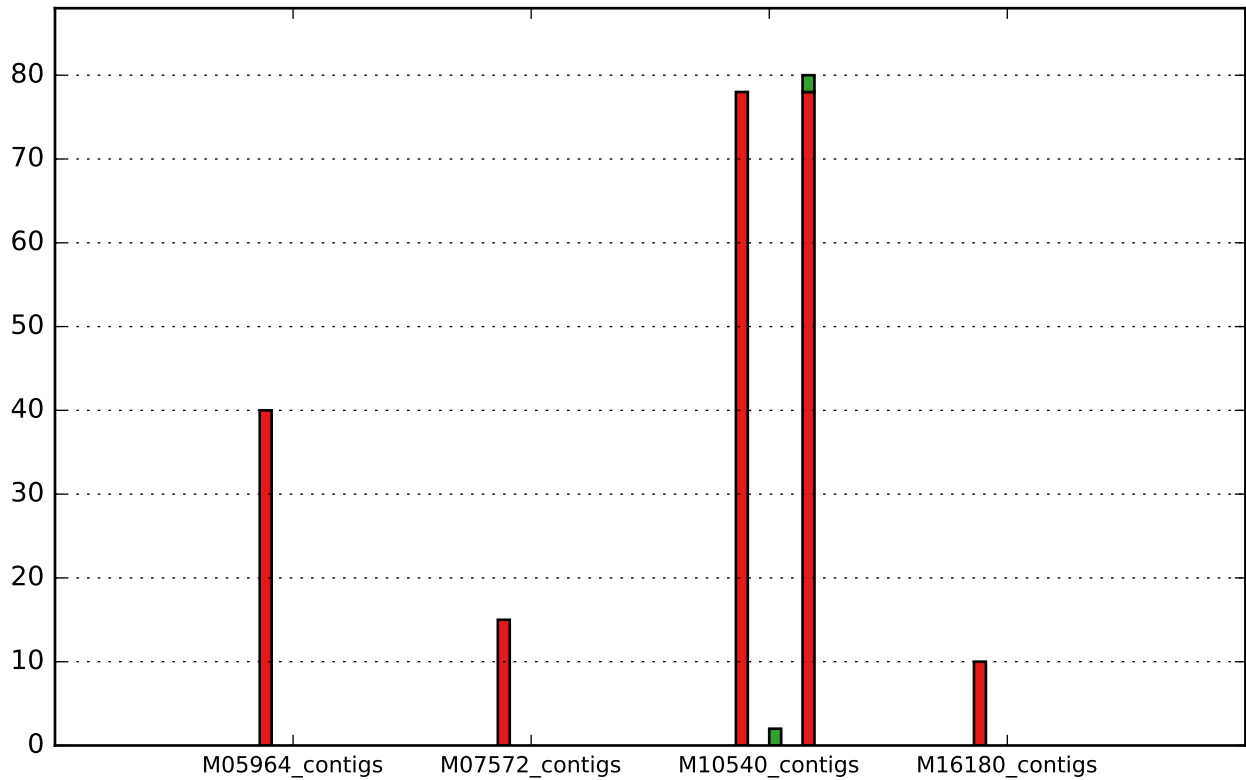
M16180_contigs

M07572_contigs

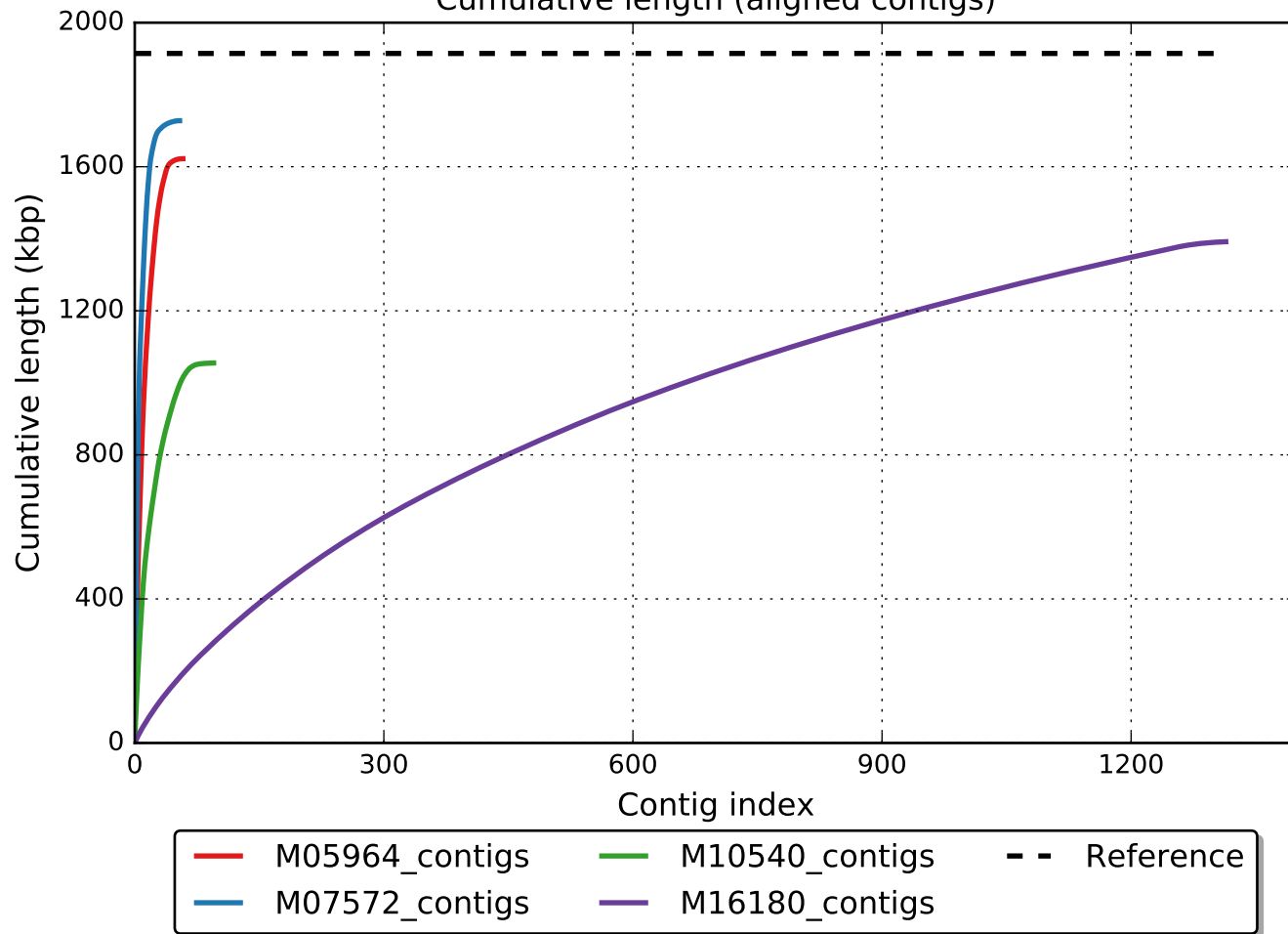




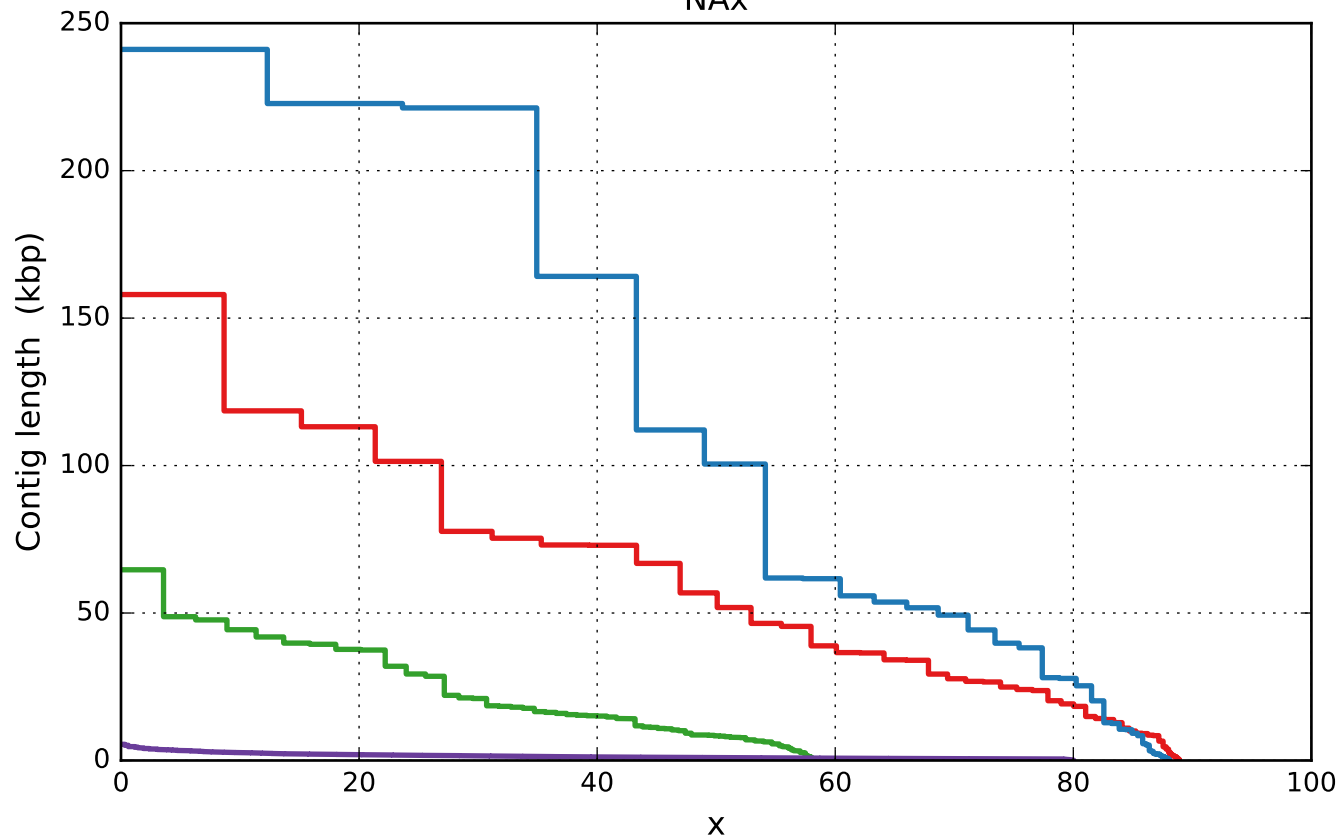
Misassemblies



Cumulative length (aligned contigs)



NAx



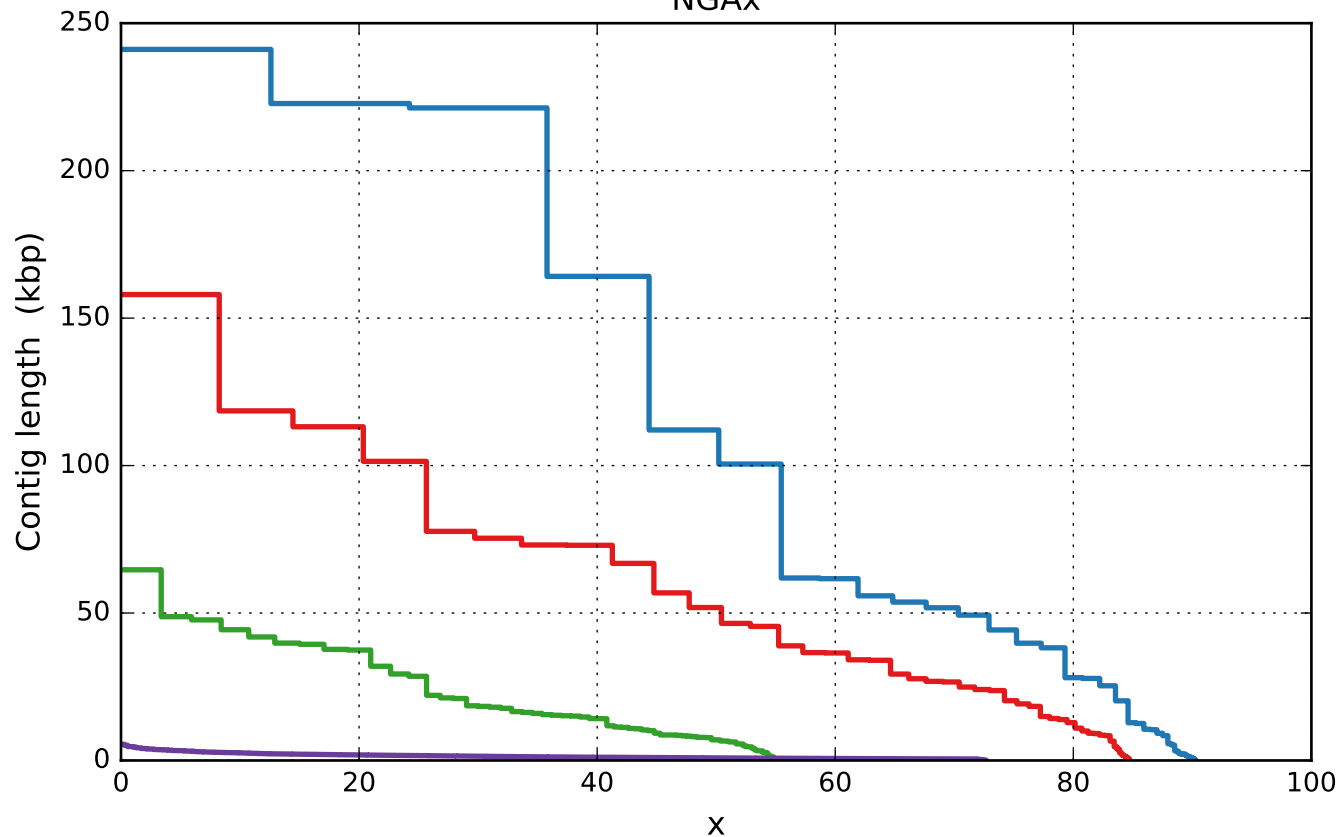
M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

