

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	1969659	1969659	1969659	1969659
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.31	38.31	38.31	38.31
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1076
N75	179754	79547	311459	786
NG75	118299	79547	186938	650
L50	2	4	1	437
LG50	2	4	1	538
L75	4	8	2	884
LG75	5	8	3	1128
# misassemblies	51	41	80	19
# misassembled contigs	9	11	5	18
Misassembled contigs length	1782615	1724360	1714276	25175
# local misassemblies	58	63	40	13
# unaligned contigs	1 + 1 part	12 + 9 part	0 + 3 part	348 + 122 part
Unaligned length	6205	141309	35701	437687
Genome fraction (%)	81.628	80.704	51.663	61.139
Duplication ratio	1.131	1.145	1.743	1.080
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2506.23	2314.55	3464.49	2072.78
# indels per 100 kbp	70.22	59.26	77.14	41.69
Largest alignment	178366	153176	51310	5015
NA50	60140	34879	6605	869
NGA50	59822	34879	3284	741
NA75	21200	14240	-	-
NGA75	14907	14240	-	-
LA50	9	14	47	569
LGA50	10	14	62	713
LA75	22	33	-	-
LGA75	28	33	-	-

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

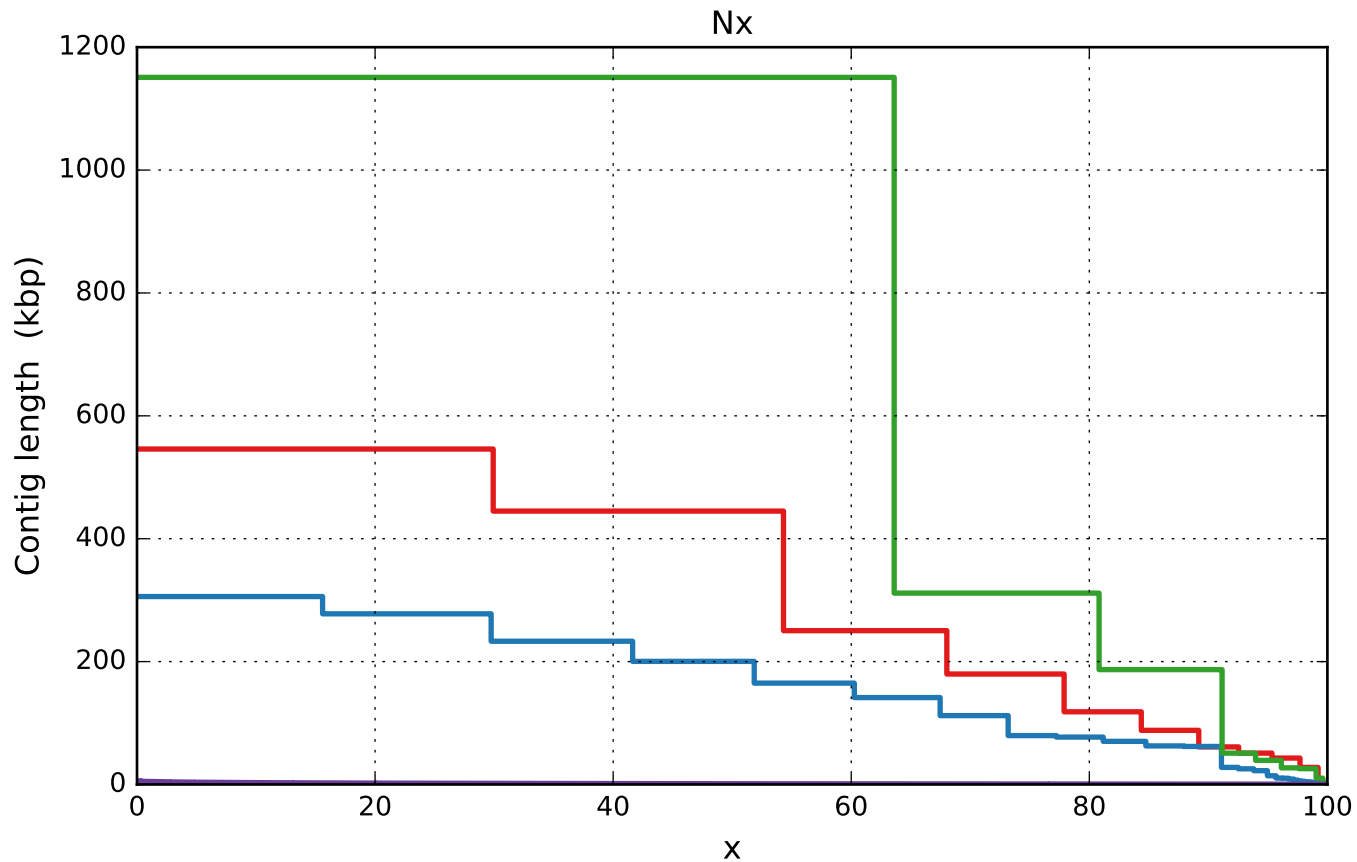
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	51	41	80	19
# relocations	51	41	79	19
# translocations	0	0	0	0
# inversions	0	0	1	0
# misassembled contigs	9	11	5	18
Misassembled contigs length	1782615	1724360	1714276	25175
# local misassemblies	58	63	40	13
# mismatches	40295	36792	35254	24961
# indels	1129	942	785	502
# short indels	990	843	726	464
# long indels	139	99	59	38
Indels length	3495	2821	1813	1157

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).

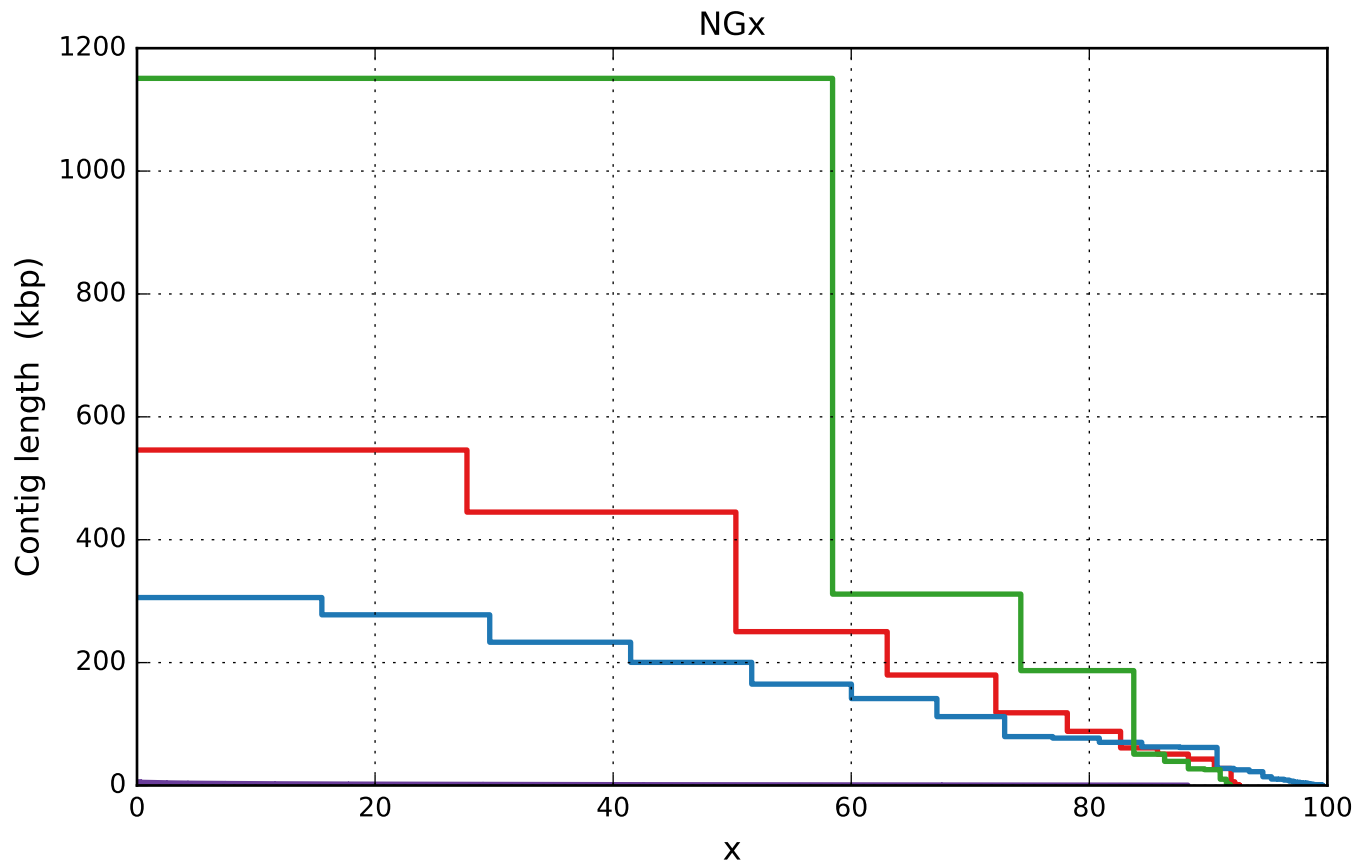
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	1	12	0	348
Fully unaligned length	2293	47640	0	356237
# partially unaligned contigs	1	9	3	122
# with misassembly	0	3	1	7
# both parts are significant	1	5	2	30
Partially unaligned length	3912	93669	35701	81450
# 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

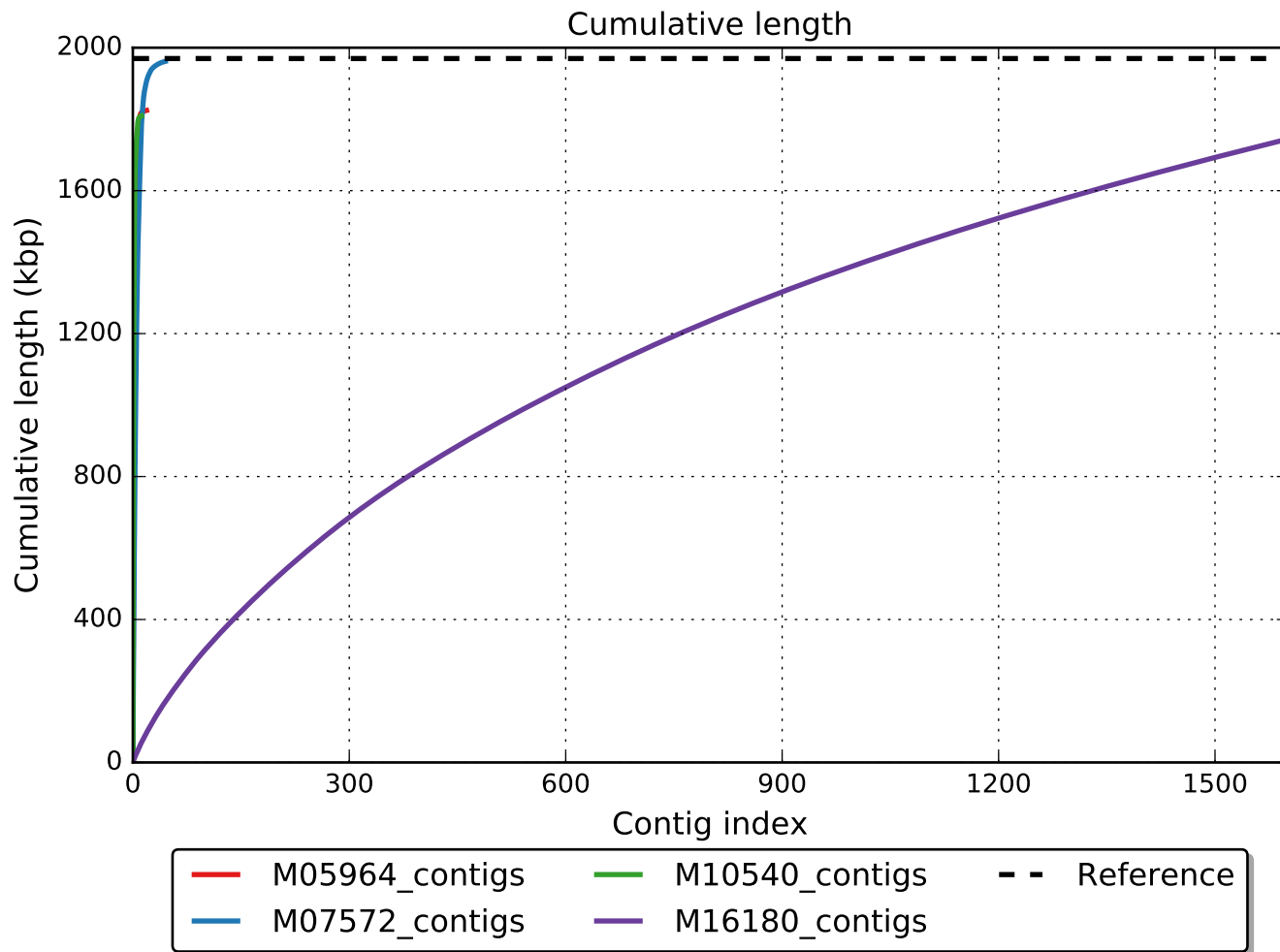


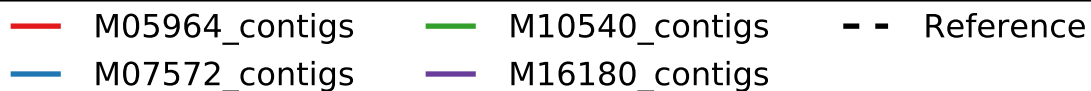
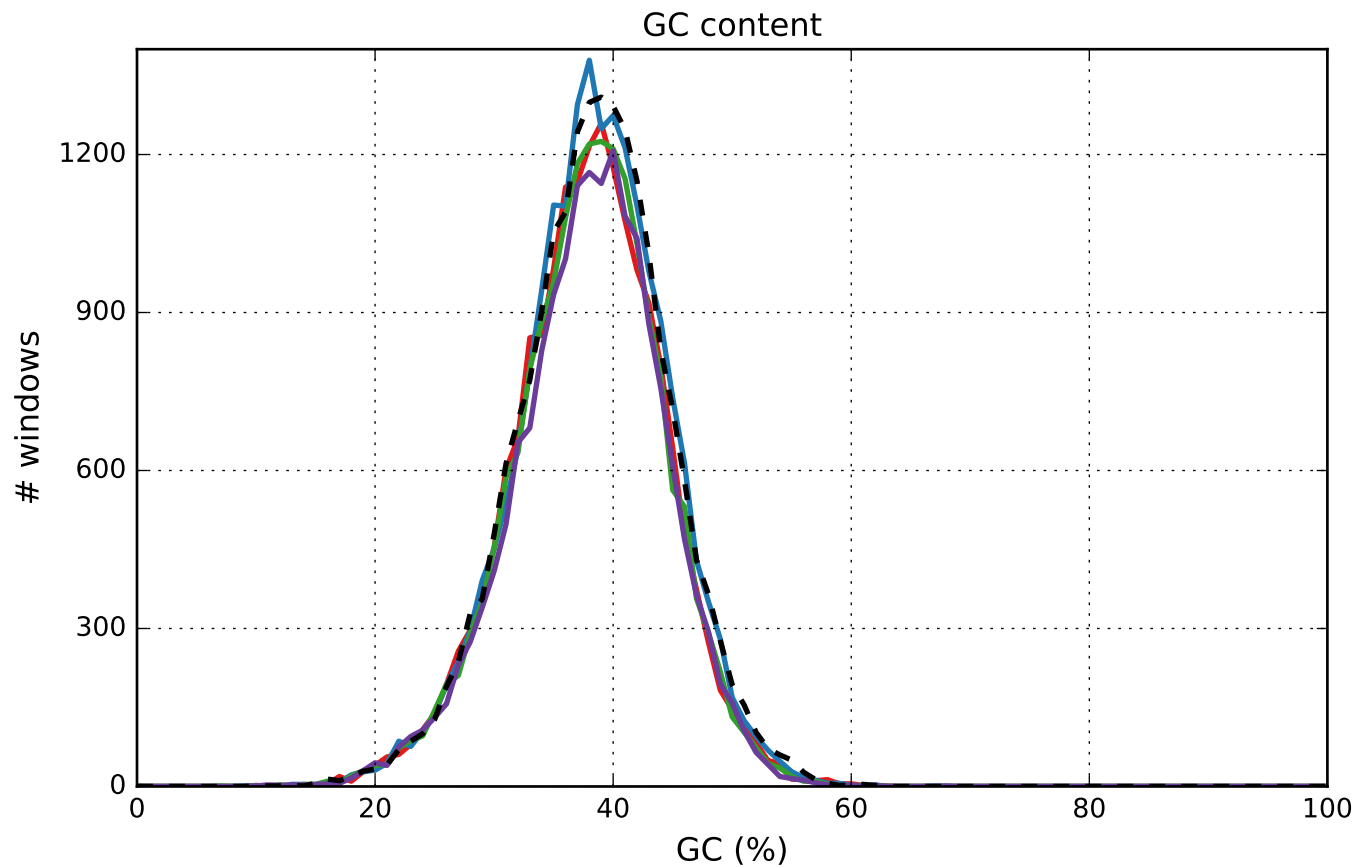
M05964_contigs

M10540_contigs

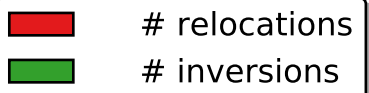
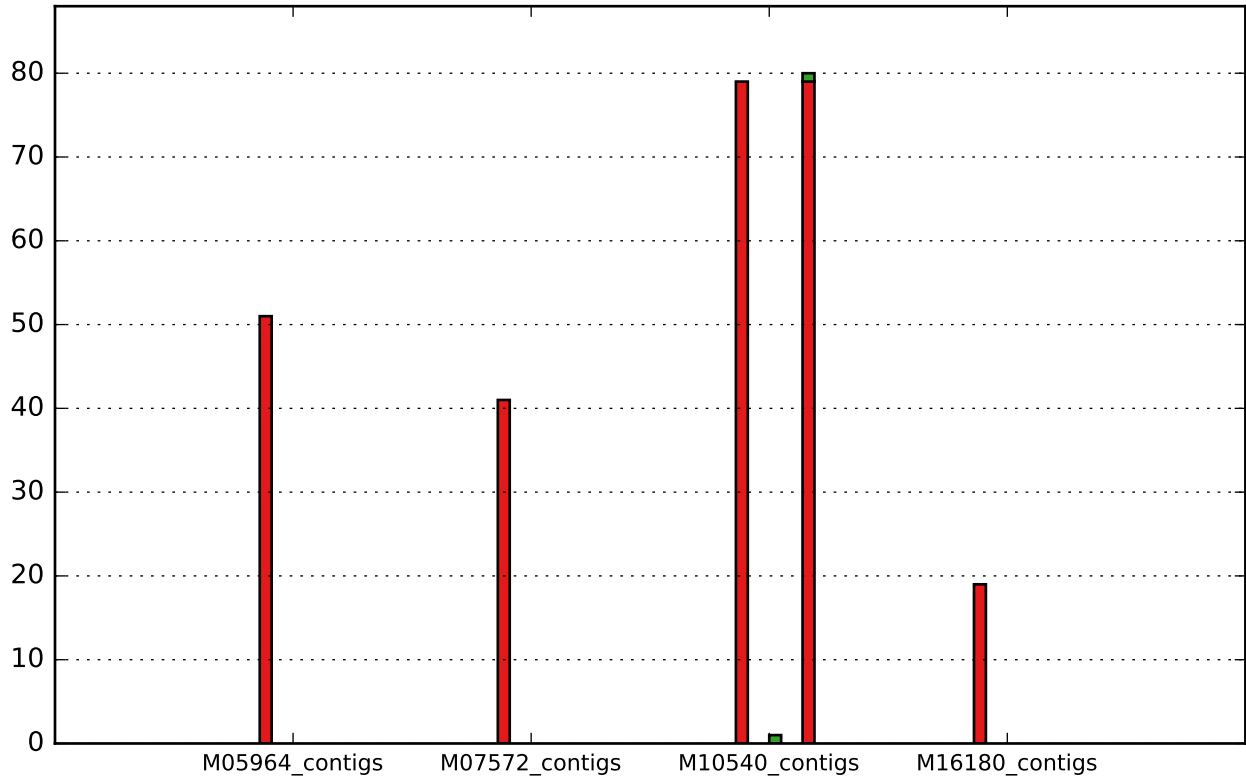
M16180_contigs

M07572_contigs

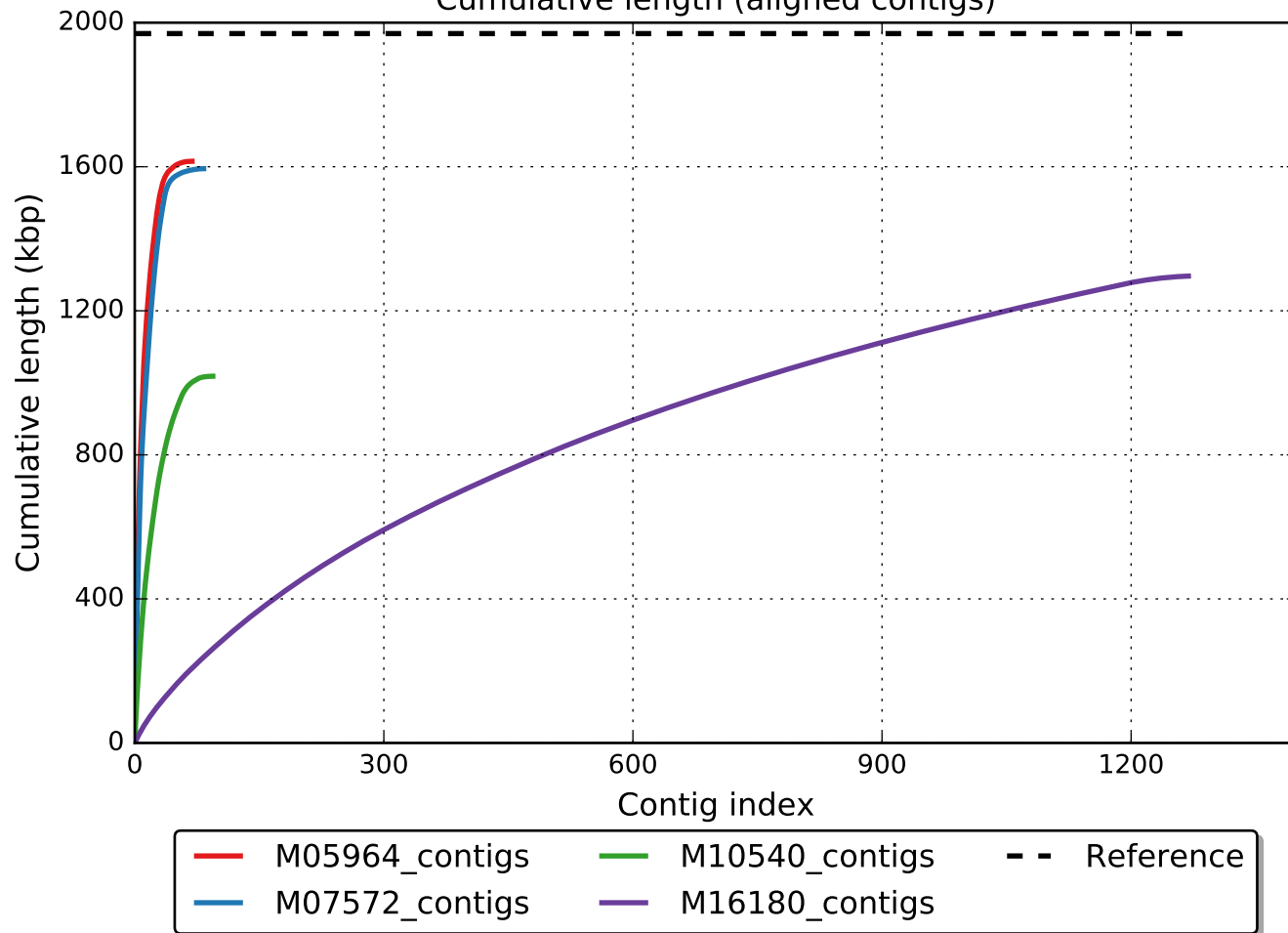




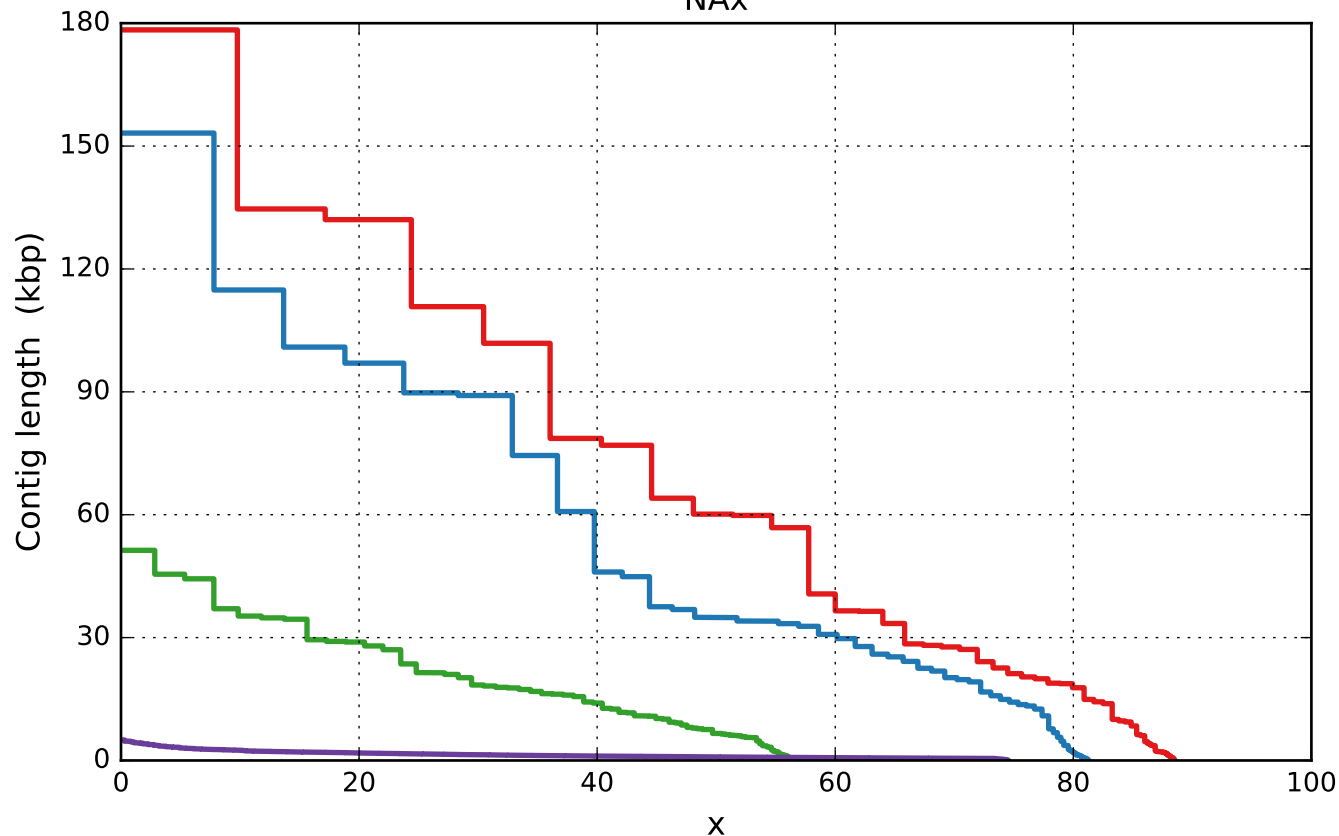
Misassemblies



Cumulative length (aligned contigs)

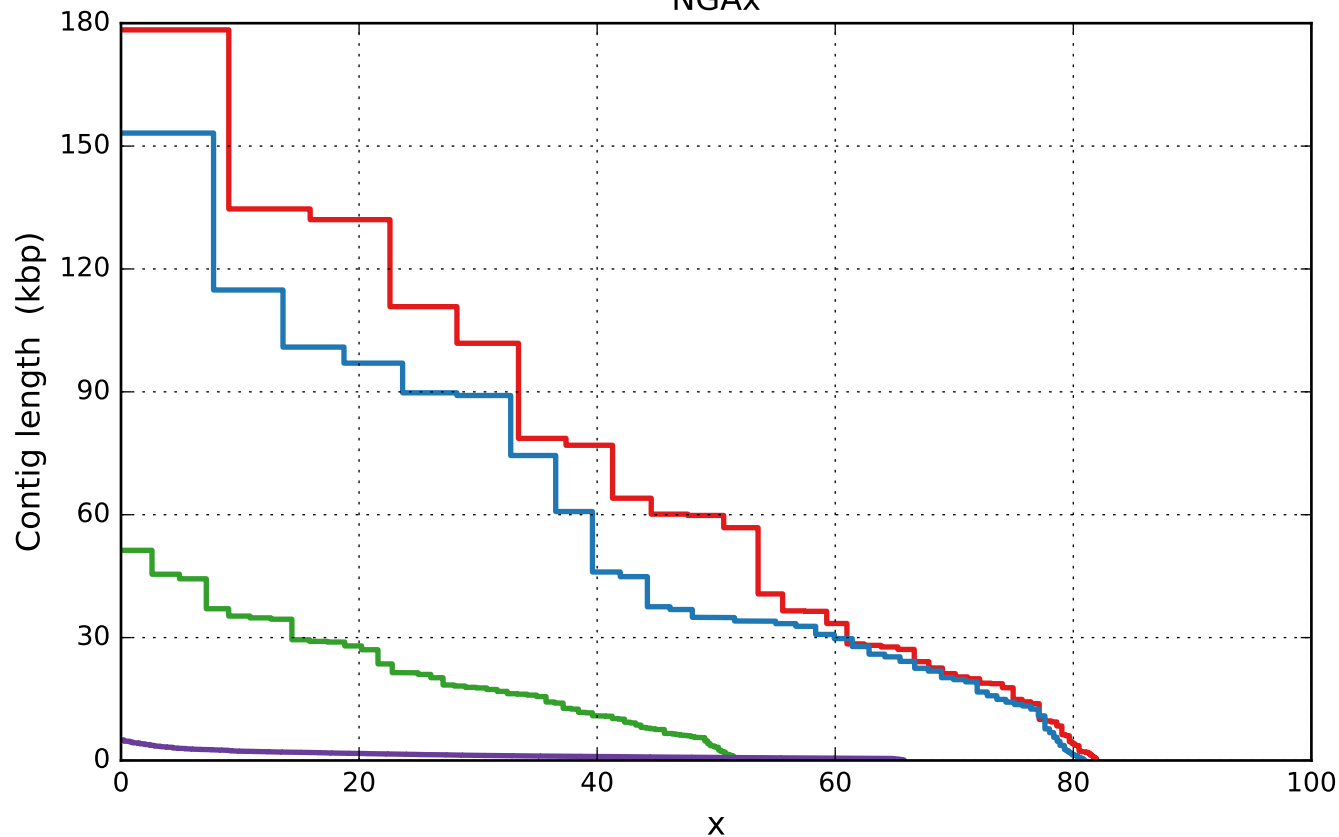


NAx



M05964_contigs M07572_contigs M10540_contigs M16180_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

