

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	1887192	1887192	1887192	1887192
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.01	38.01	38.01	38.01
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1129
N75	179754	79547	311459	786
NG75	179754	112073	311459	691
L50	2	4	1	437
LG50	2	4	1	501
L75	4	8	2	884
LG75	4	7	2	1036
# misassemblies	55	47	87	11
# misassembled contigs	9	13	8	11
Misassembled contigs length	1782615	1752539	1795764	16971
# local misassemblies	70	61	39	15
# unaligned contigs	2 + 0 part	16 + 4 part	0 + 3 part	311 + 113 part
Unaligned length	8340	87718	1270	395800
Genome fraction (%)	84.229	88.849	54.696	65.589
Duplication ratio	1.143	1.118	1.752	1.085
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2520.83	2427.37	3681.10	2074.26
# indels per 100 kbp	89.14	92.44	114.99	66.57
Largest alignment	178056	138984	66377	4706
NA50	39265	55692	7674	907
NGA50	37962	55692	6591	815
NA75	16038	17417	-	507
NGA75	14040	25880	-	-
LA50	13	12	45	552
LGA50	14	12	51	638
LA75	30	28	-	1206
LGA75	33	26	-	-

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

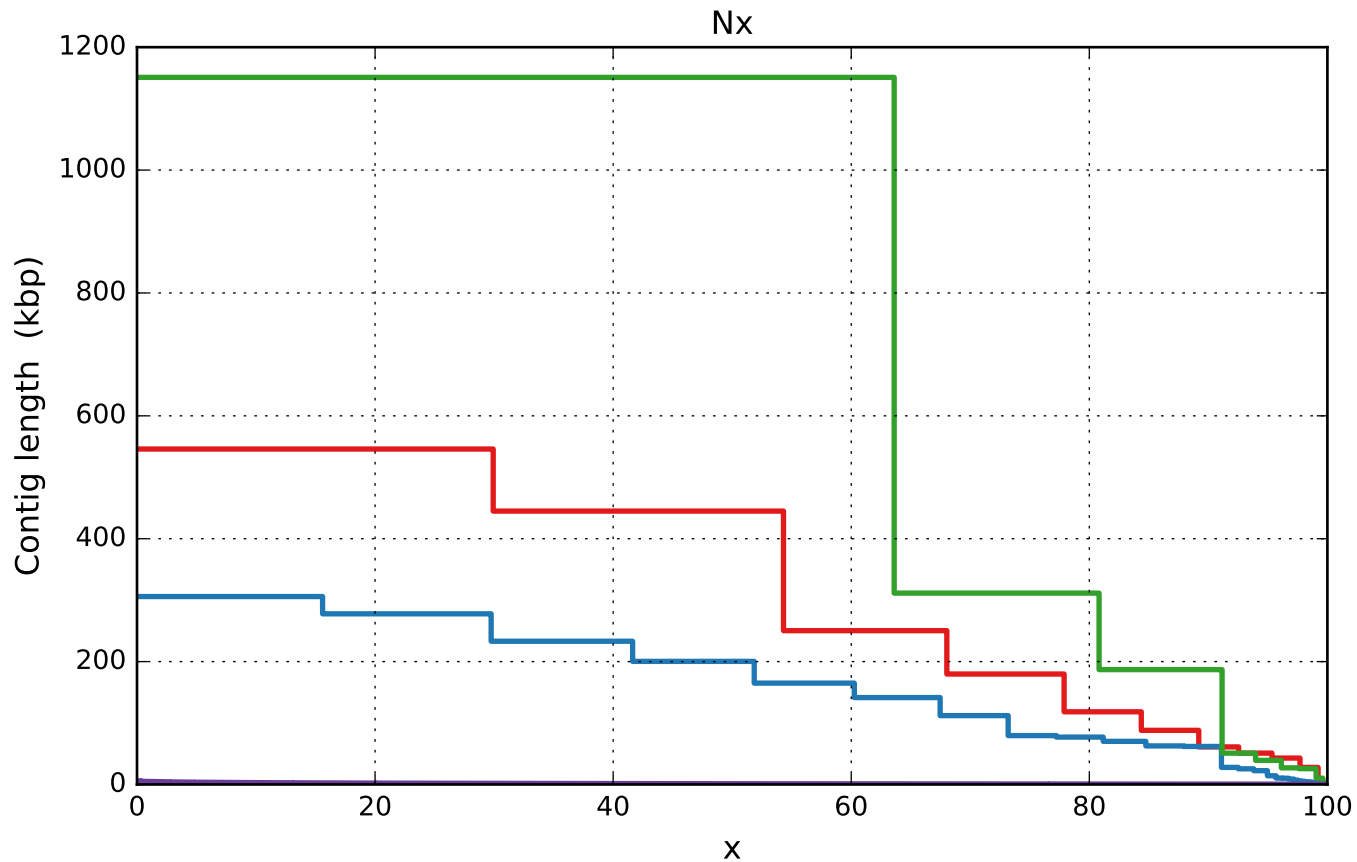
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	55	47	87	11
# relocations	55	47	85	11
# translocations	0	0	0	0
# inversions	0	0	2	0
# misassembled contigs	9	13	8	11
Misassembled contigs length	1782615	1752539	1795764	16971
# local misassemblies	70	61	39	15
# mismatches	40070	40701	37997	25675
# indels	1417	1550	1187	824
# short indels	1303	1416	1100	773
# long indels	114	134	87	51
Indels length	3579	4387	2611	1711

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).

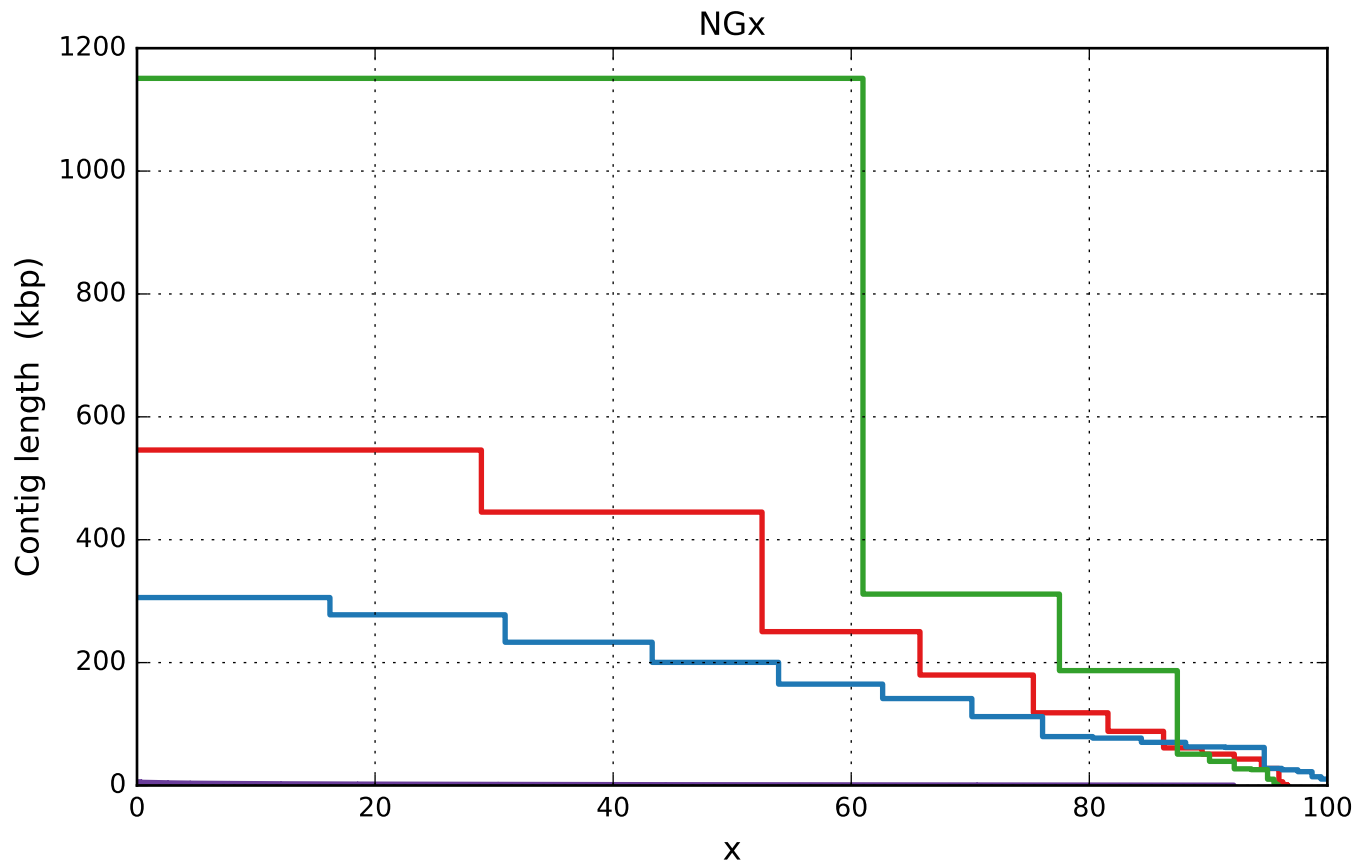
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	2	16	0	311
Fully unaligned length	8340	58065	0	332695
# partially unaligned contigs	0	4	3	113
# with misassembly	0	0	1	2
# both parts are significant	0	2	1	19
Partially unaligned length	0	29653	1270	63105
# N's	1086	1127	693	1471

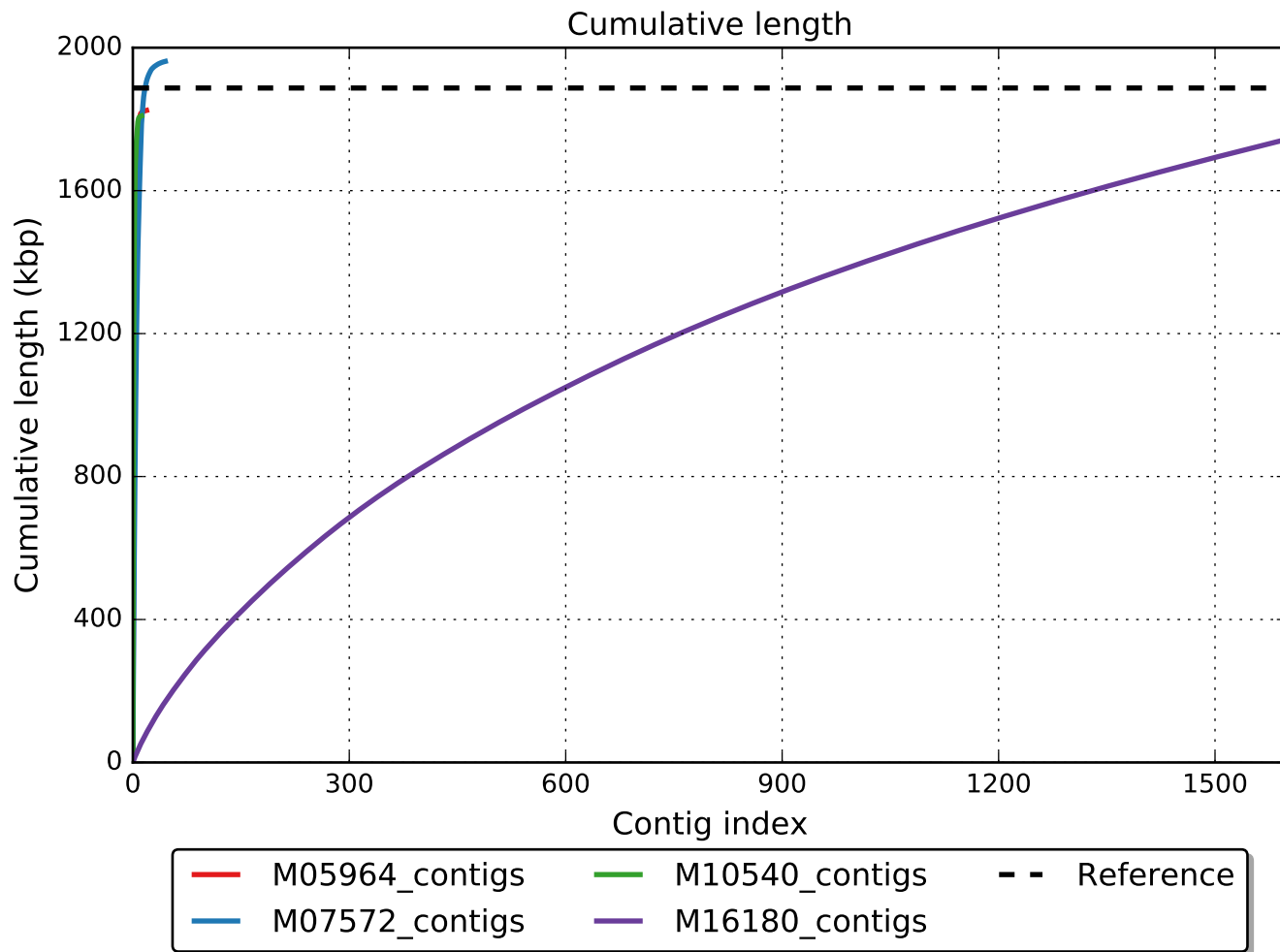
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

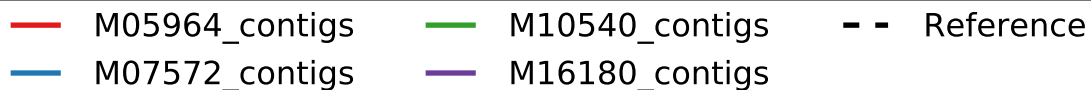
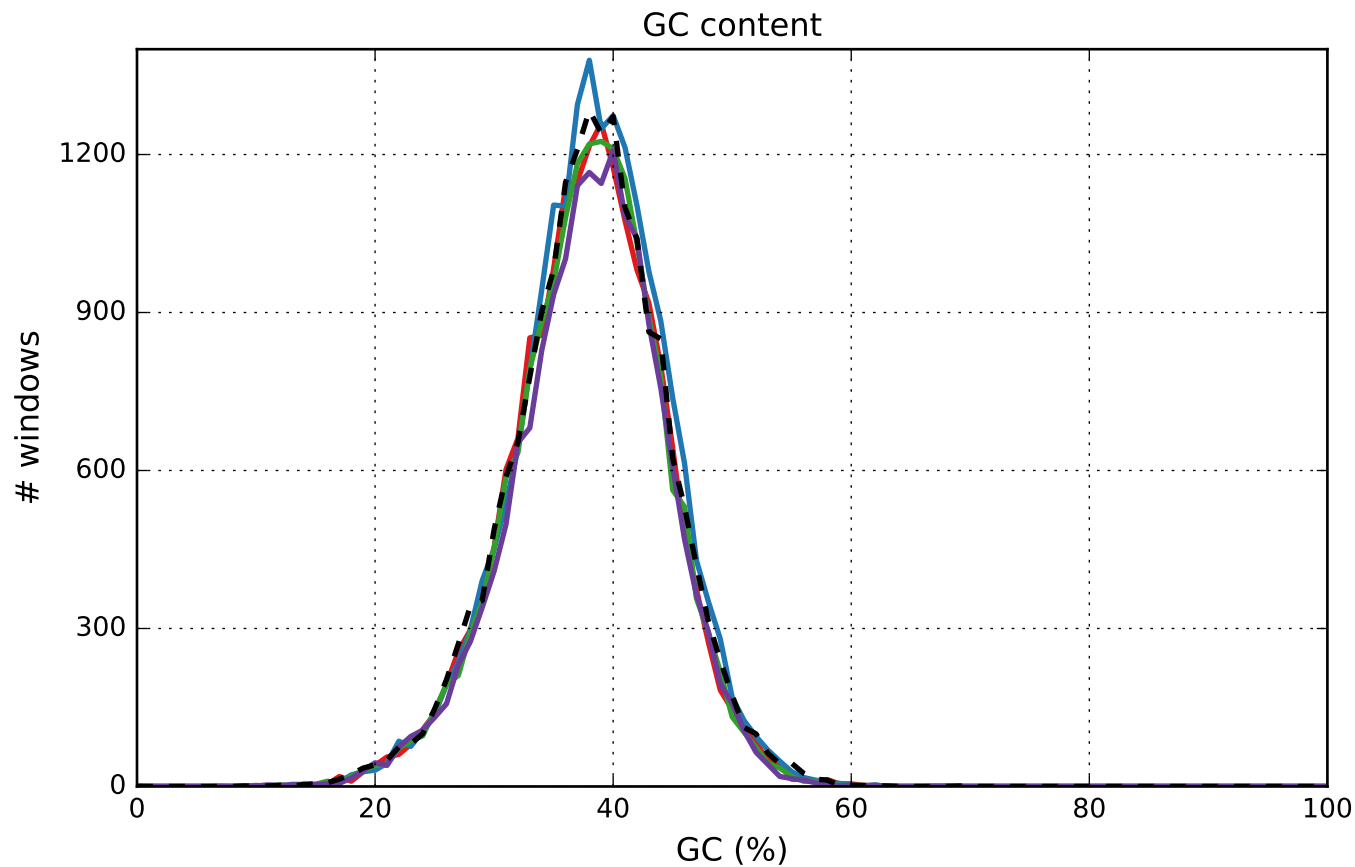


— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

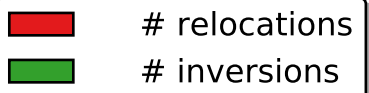
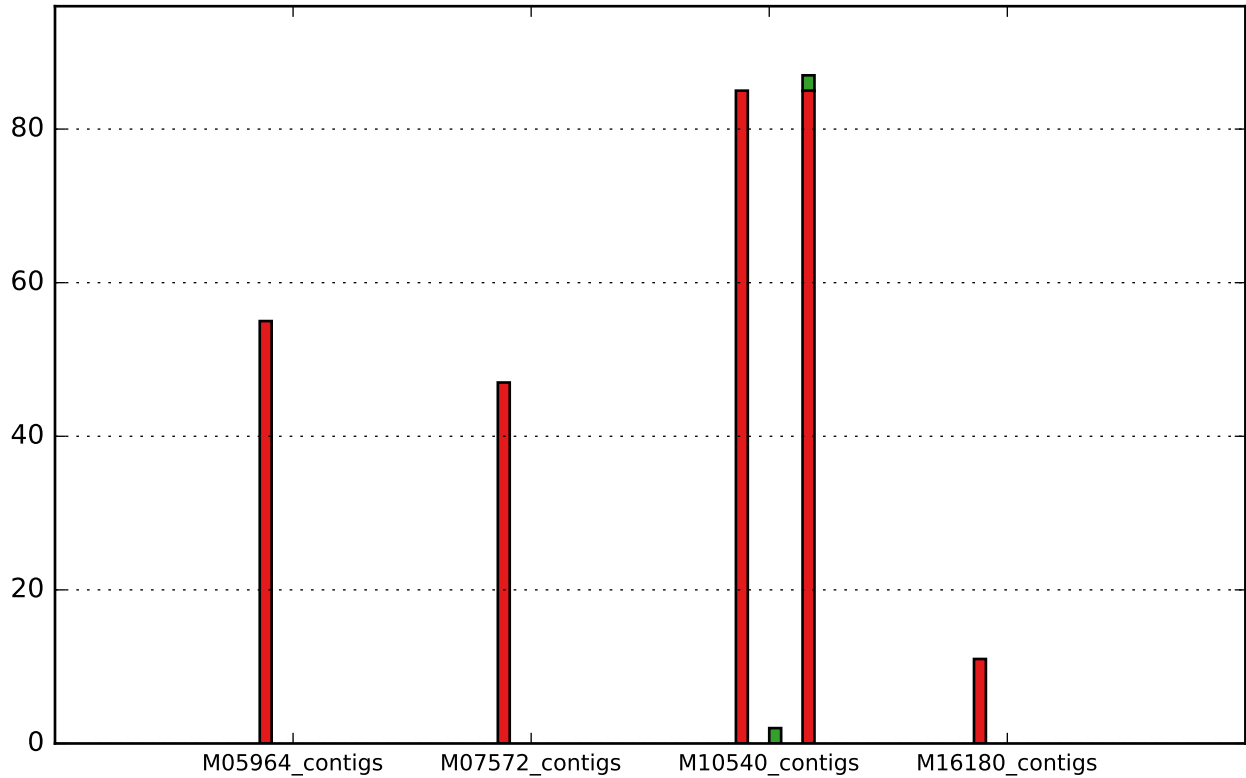


M05964_contigs M10540_contigs M16180_contigs
M07572_contigs

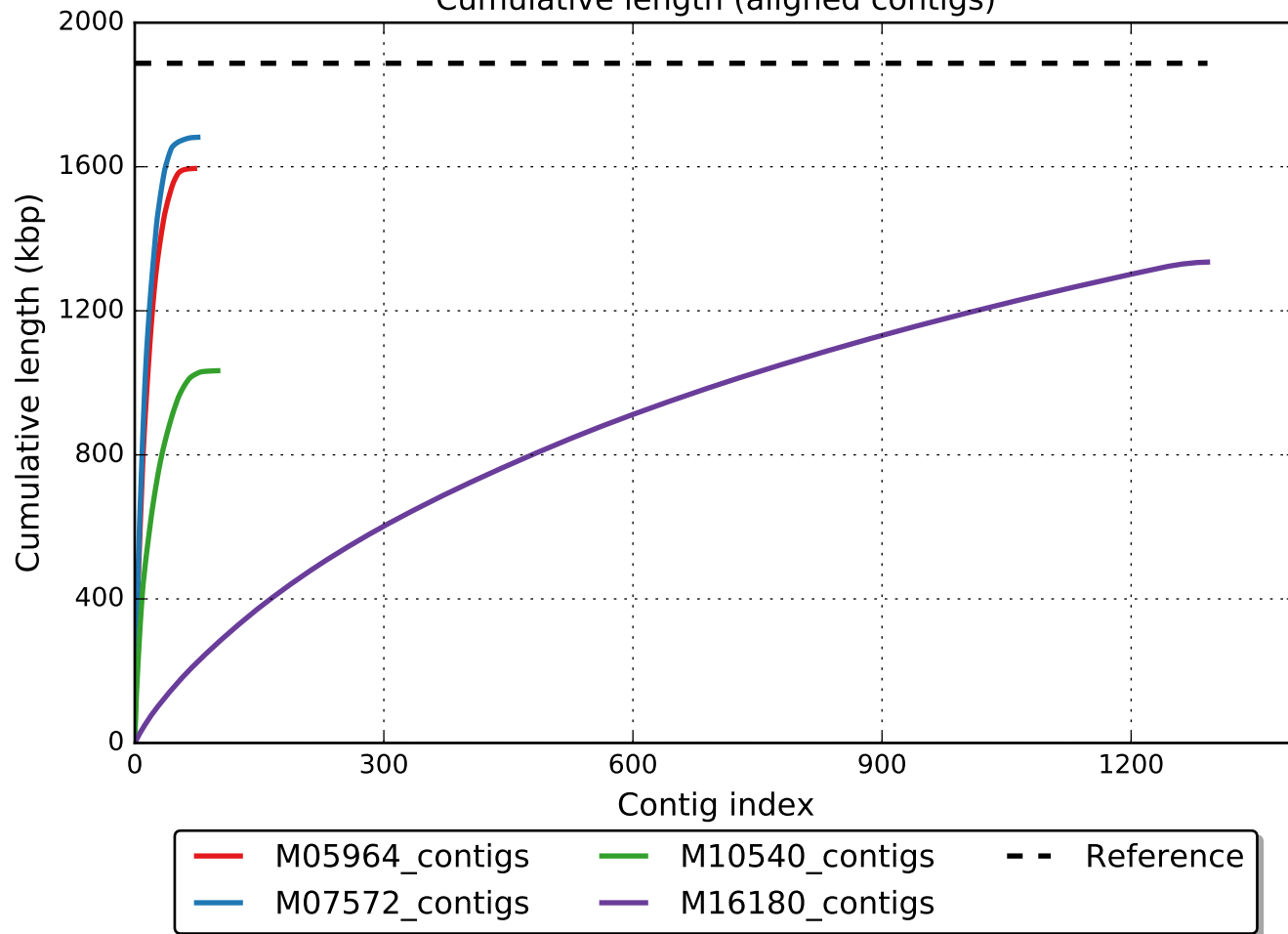




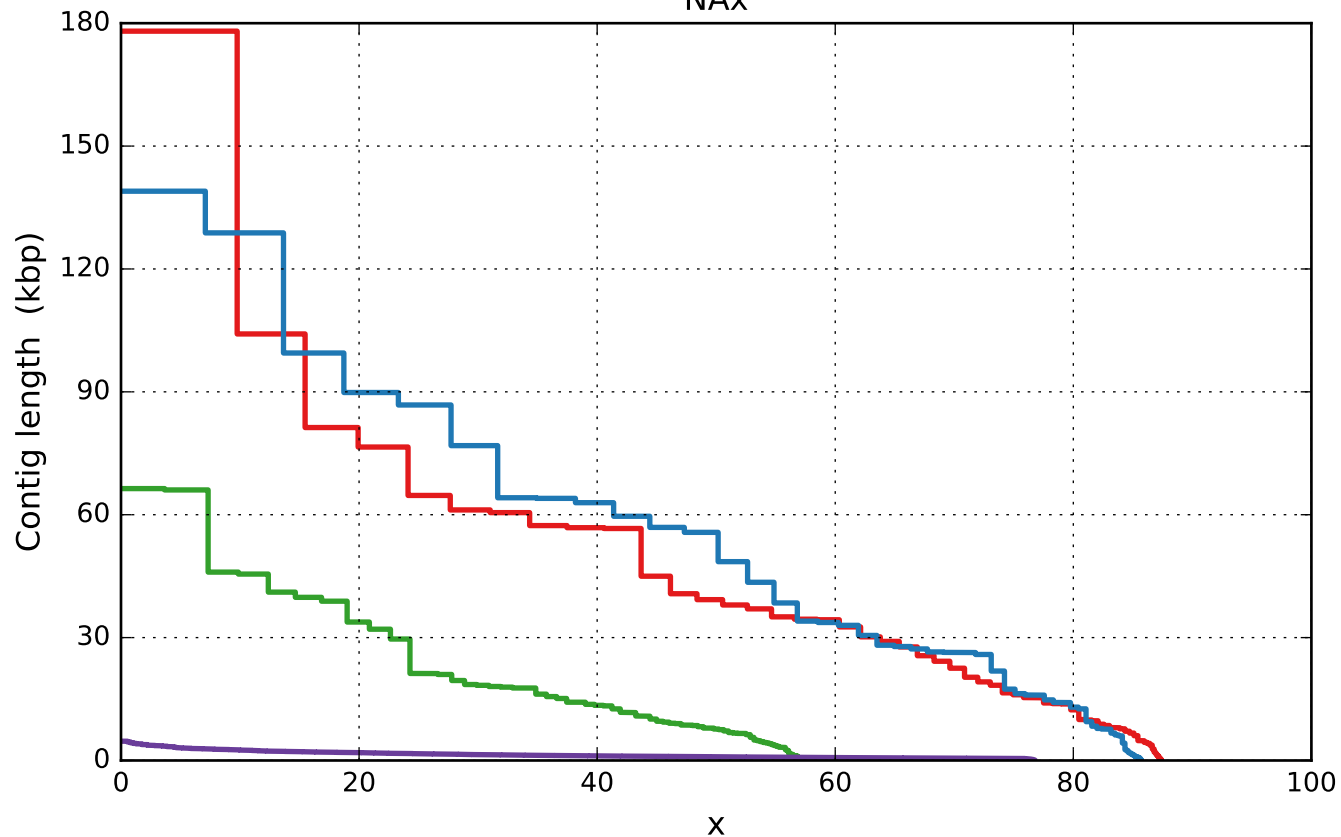
Misassemblies



Cumulative length (aligned contigs)

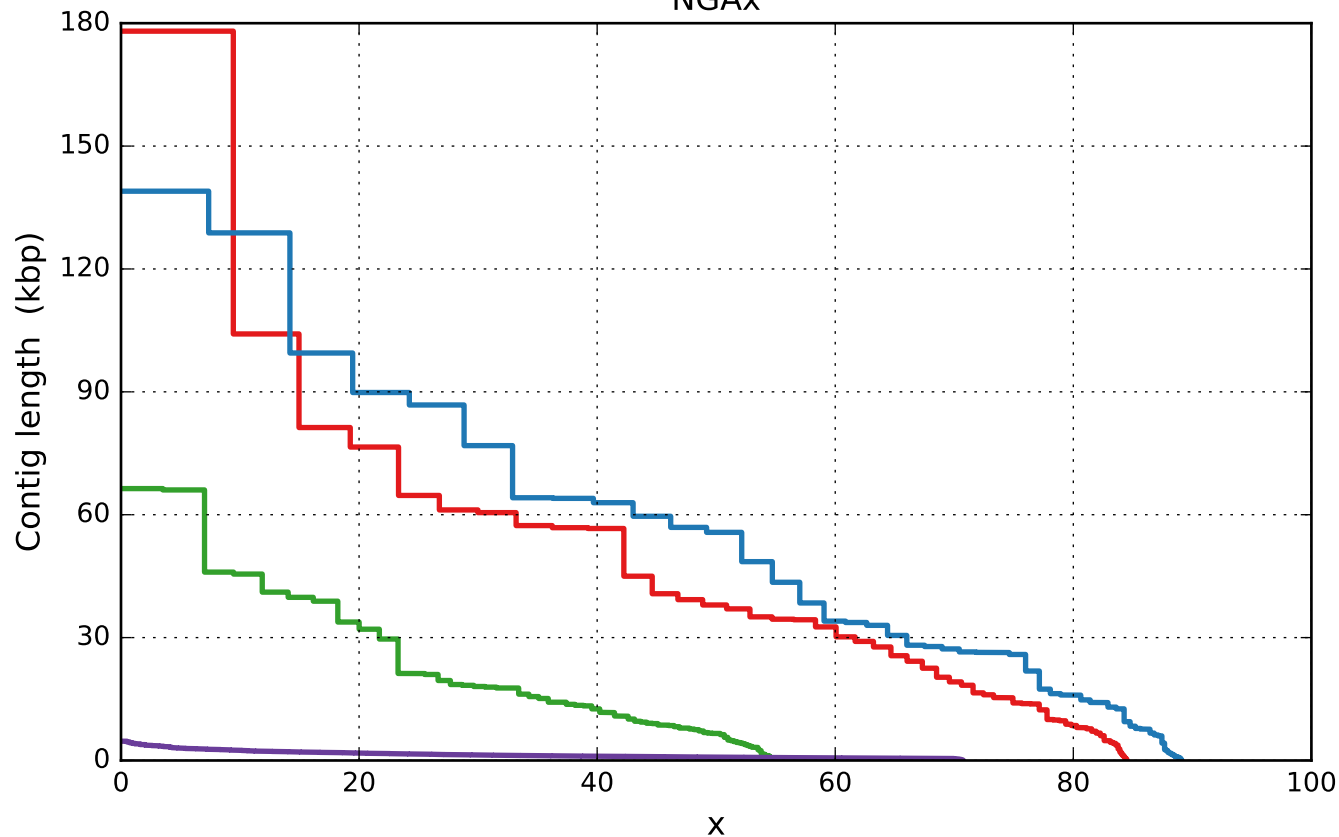


NAx

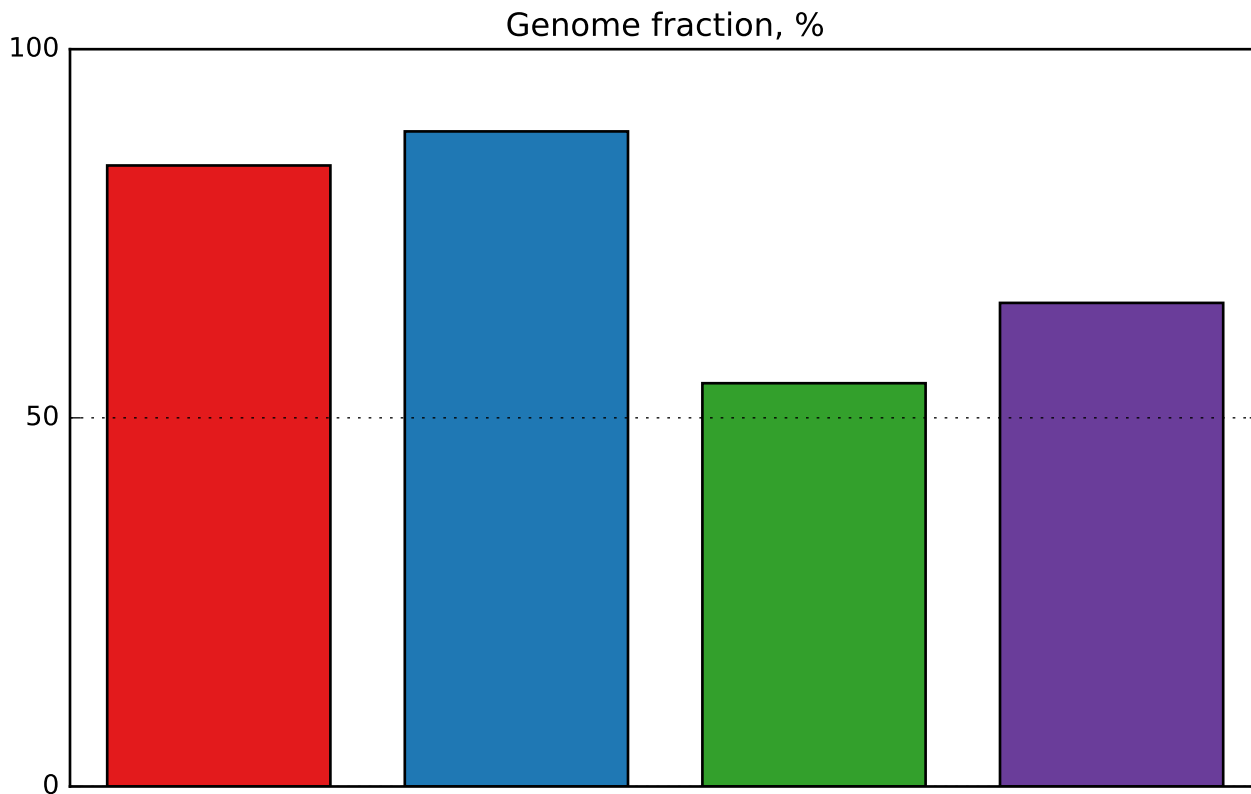


M05964_contigs M10540_contigs M16180_contigs
M07572_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs



■ M05964_contigs ■ M10540_contigs ■ M16180_contigs
■ M07572_contigs