

## 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	1830138	1830138	1830138	1830138
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.15	38.15	38.15	38.15
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1161
N75	179754	79547	311459	786
NG75	179754	112073	311459	723
L50	2	4	1	437
LG50	2	4	1	476
L75	4	8	2	884
LG75	4	7	2	975
# misassemblies	45	43	71	13
# misassembled contigs	9	12	5	13
Misassembled contigs length	1782615	1749842	1715625	25195
# local misassemblies	66	61	36	21
# unaligned contigs	2 + 0 part	23 + 2 part	0 + 4 part	303 + 98 part
Unaligned length	8340	135624	60156	396461
Genome fraction (%)	86.012	88.078	54.174	67.222
Duplication ratio	1.154	1.133	1.764	1.091
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2443.17	2306.14	3739.71	1959.02
# indels per 100 kbp	73.75	74.57	97.33	53.08
Largest alignment	146760	112787	74272	4706
NA50	40061	38818	6605	889
NGA50	40061	40982	6271	836
NA75	14912	12623	-	510
NGA75	14138	18801	-	-
LA50	13	15	42	561
LGA50	13	13	44	614
LA75	28	34	-	1219
LGA75	29	28	-	-

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

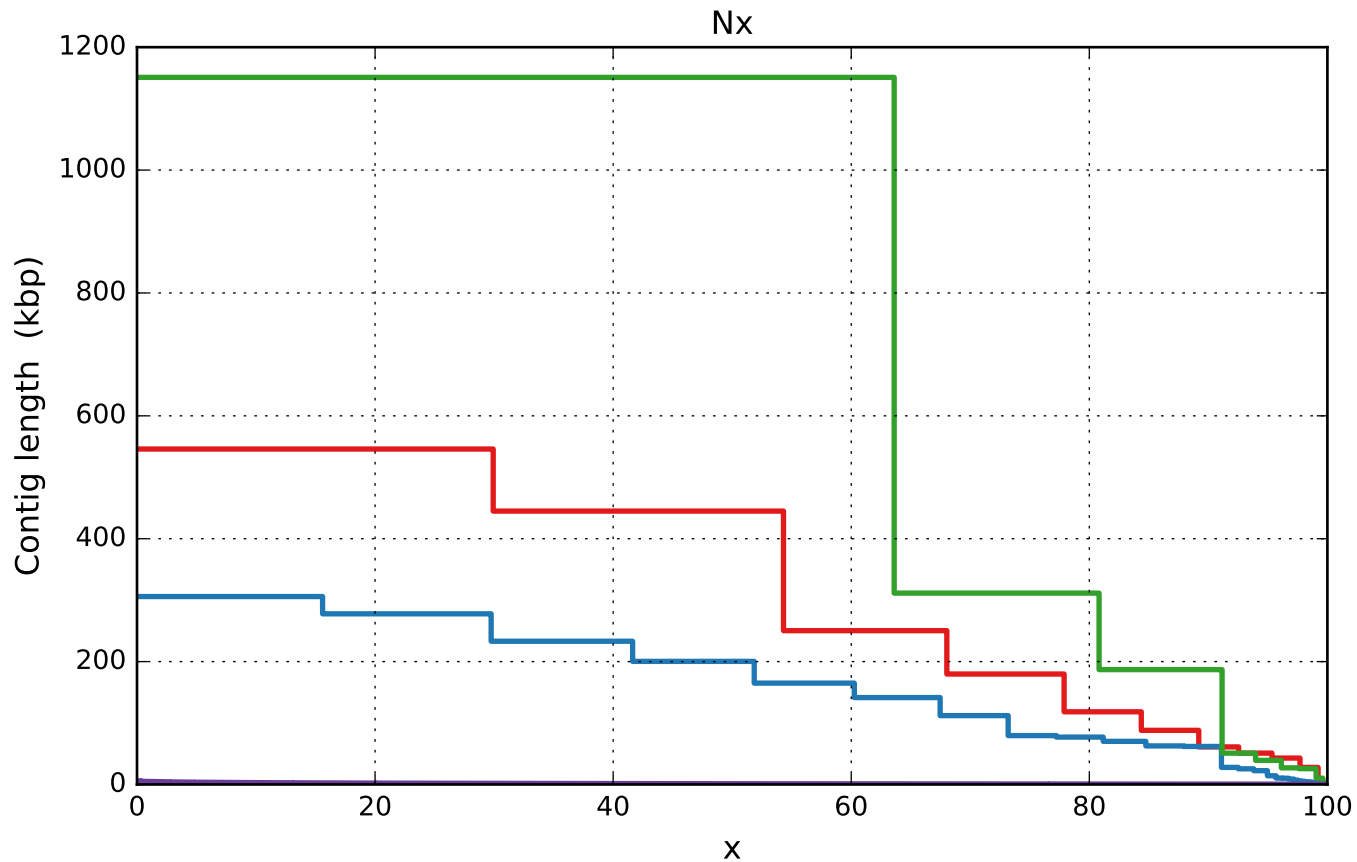
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	45	43	71	13
# relocations	45	43	71	13
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	9	12	5	13
Misassembled contigs length	1782615	1749842	1715625	25195
# local misassemblies	66	61	36	21
# mismatches	38459	37174	37078	24101
# indels	1161	1202	965	653
# short indels	1044	1086	891	599
# long indels	117	116	74	54
Indels length	3222	3374	2052	1620

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

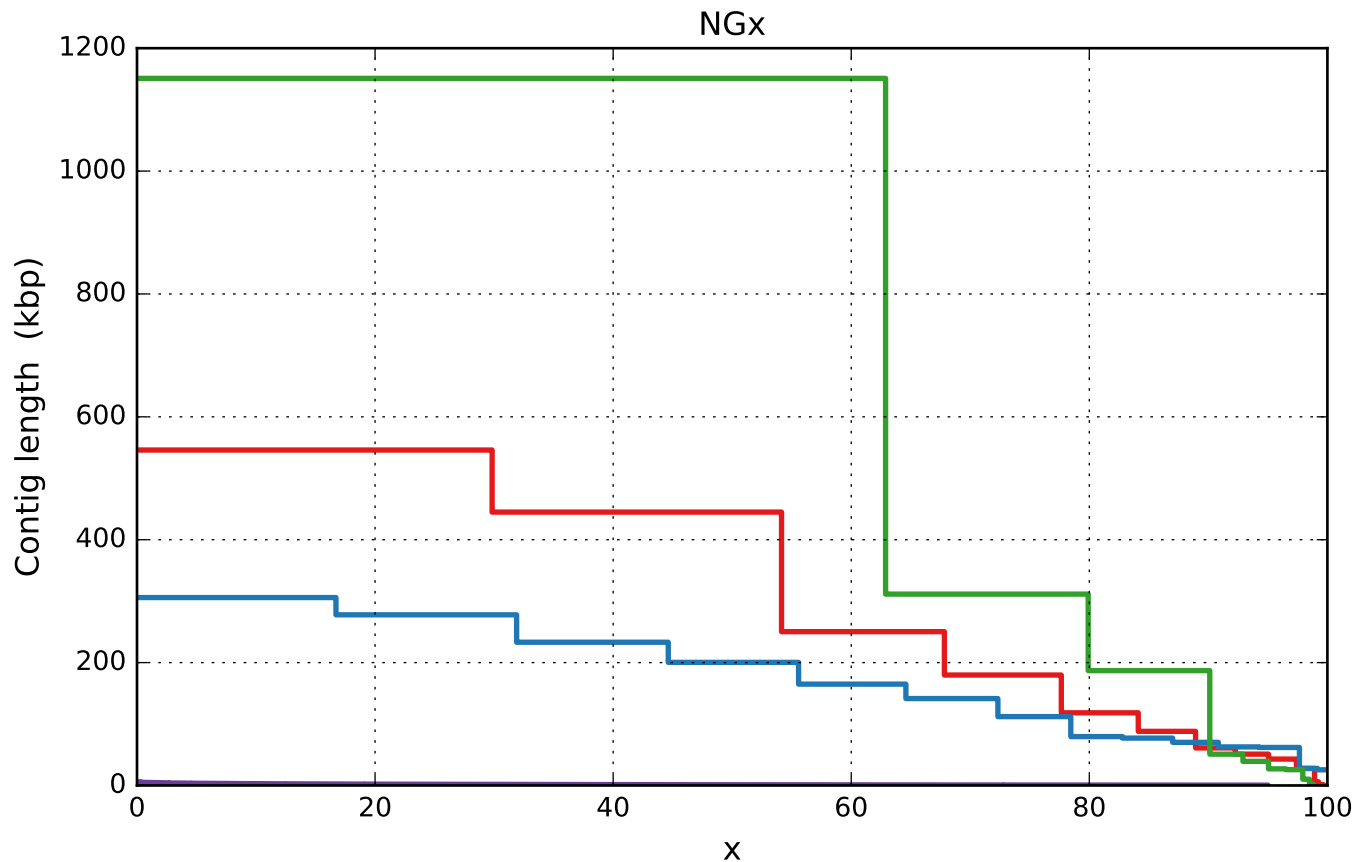
## Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	2	23	0	303
Fully unaligned length	8340	100393	0	347396
# partially unaligned contigs	0	2	4	98
# with misassembly	0	1	3	1
# both parts are significant	0	1	3	14
Partially unaligned length	0	35231	60156	49065
# N's	1086	1127	693	1471

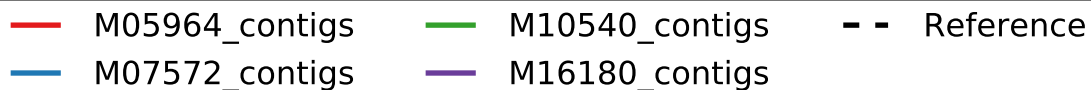
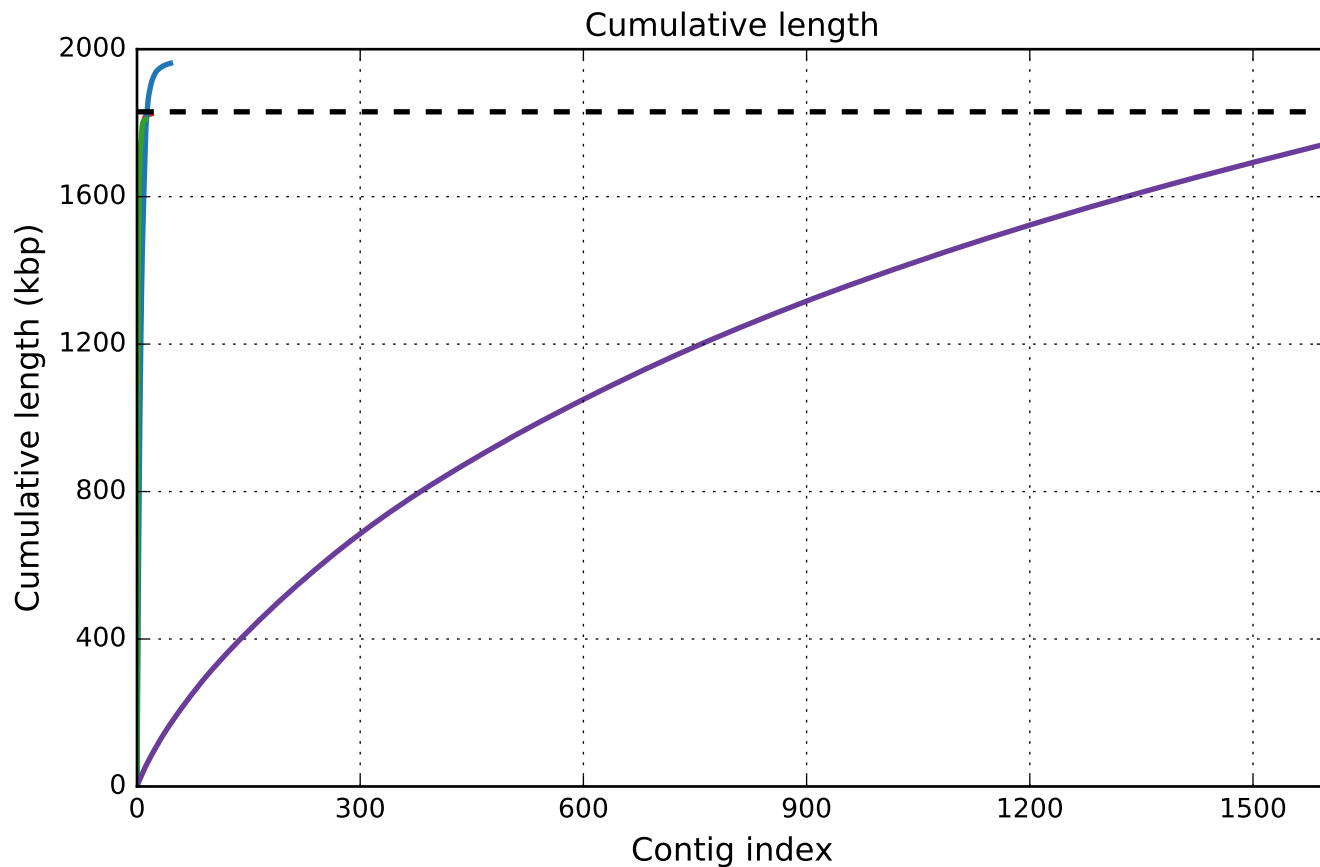
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

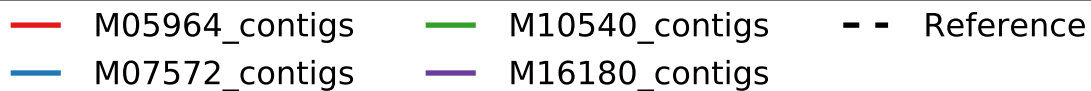
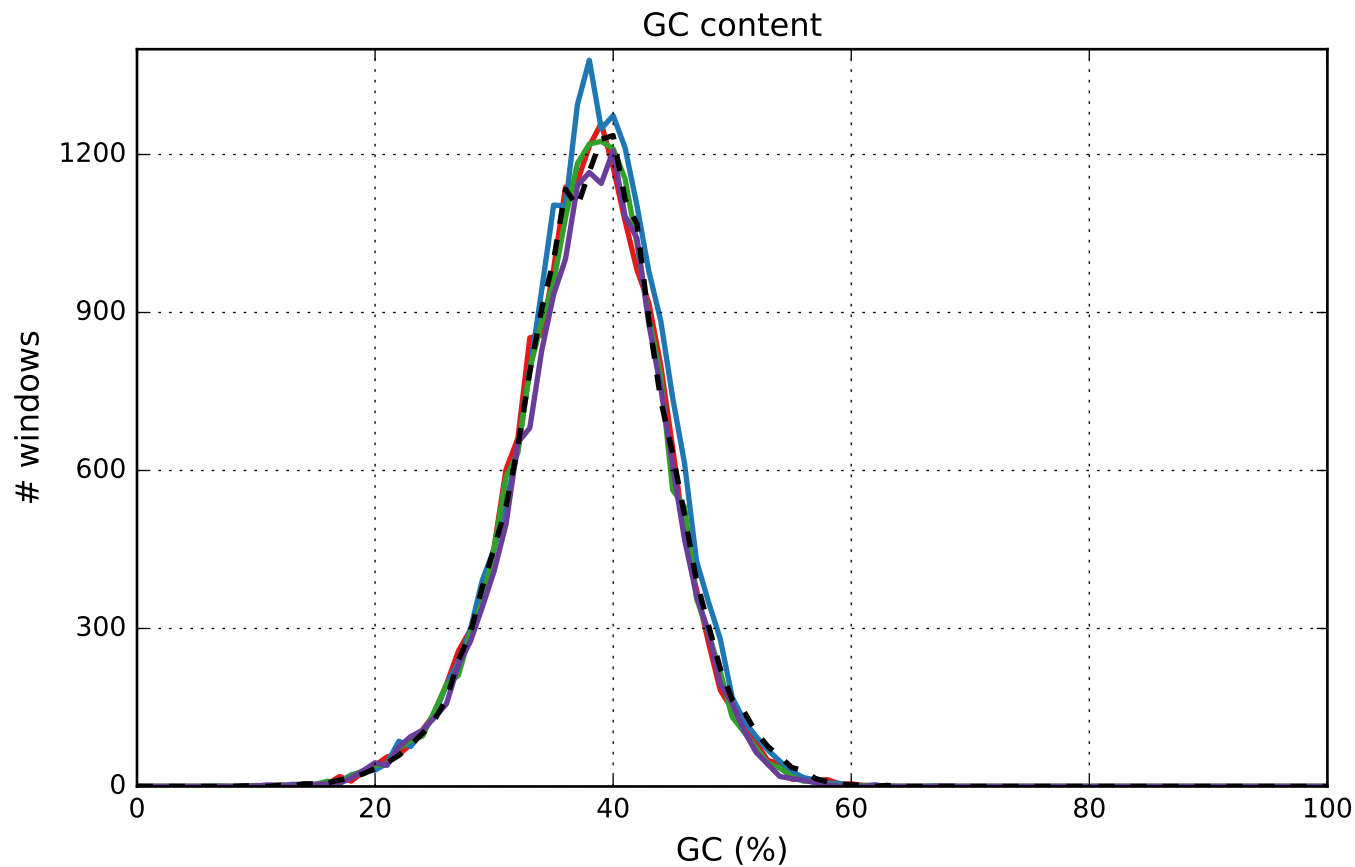


— M05964\_contigs    — M10540\_contigs    — M16180\_contigs  
— M07572\_contigs

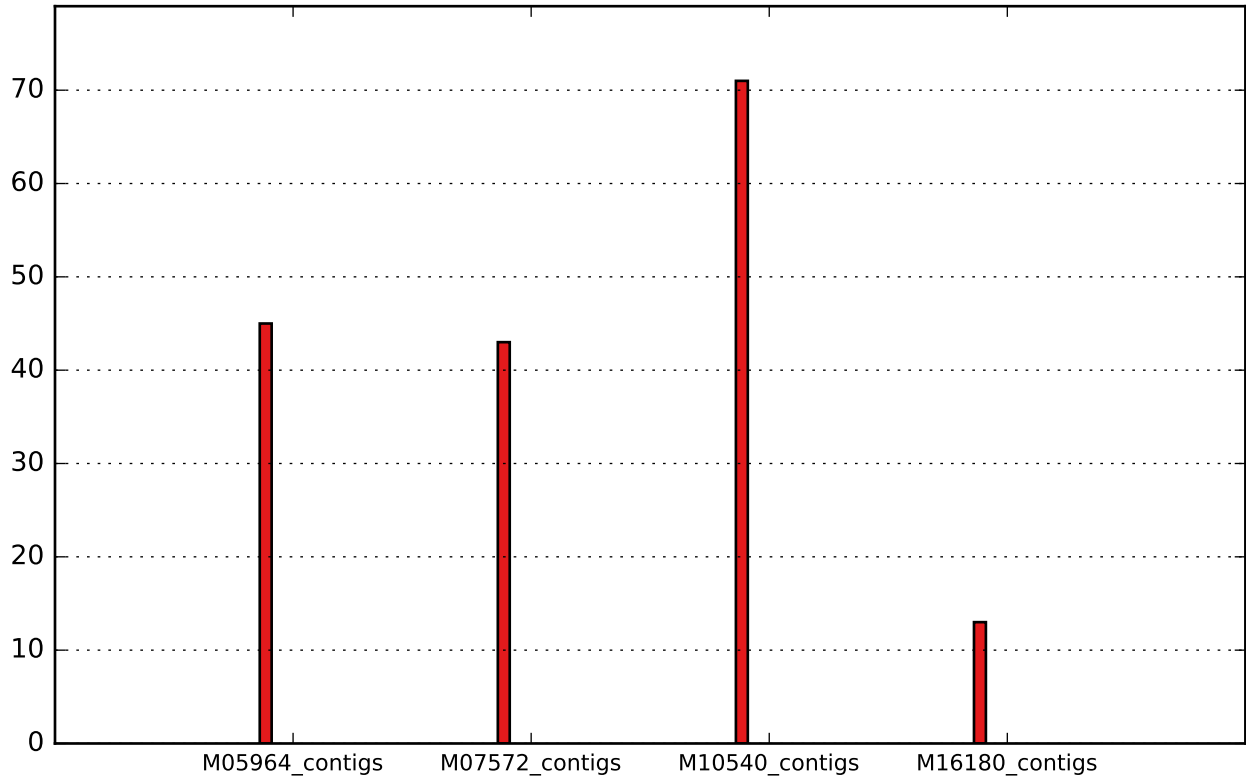


M05964\_contigs    M10540\_contigs    M16180\_contigs  
M07572\_contigs





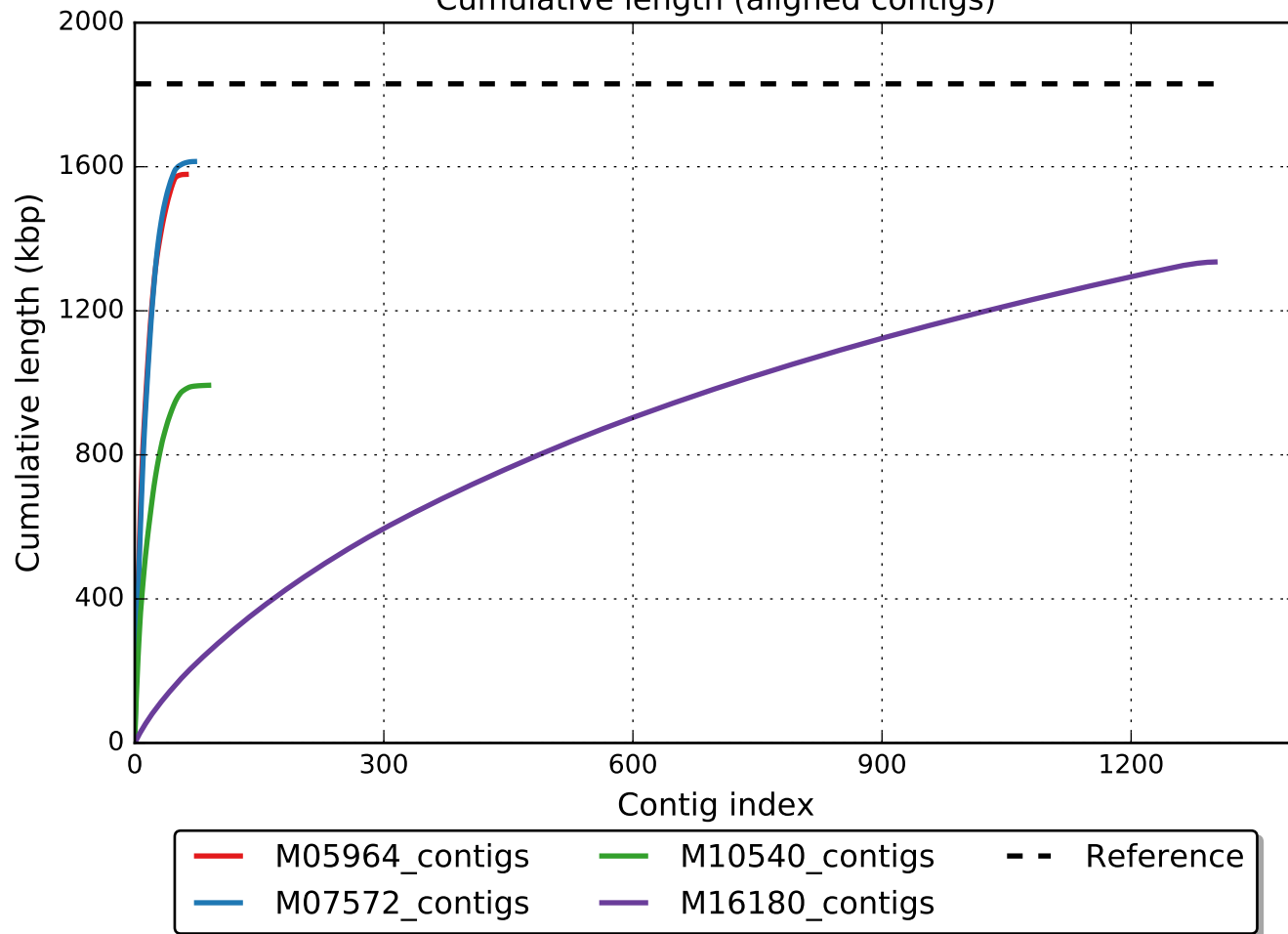
# Misassemblies



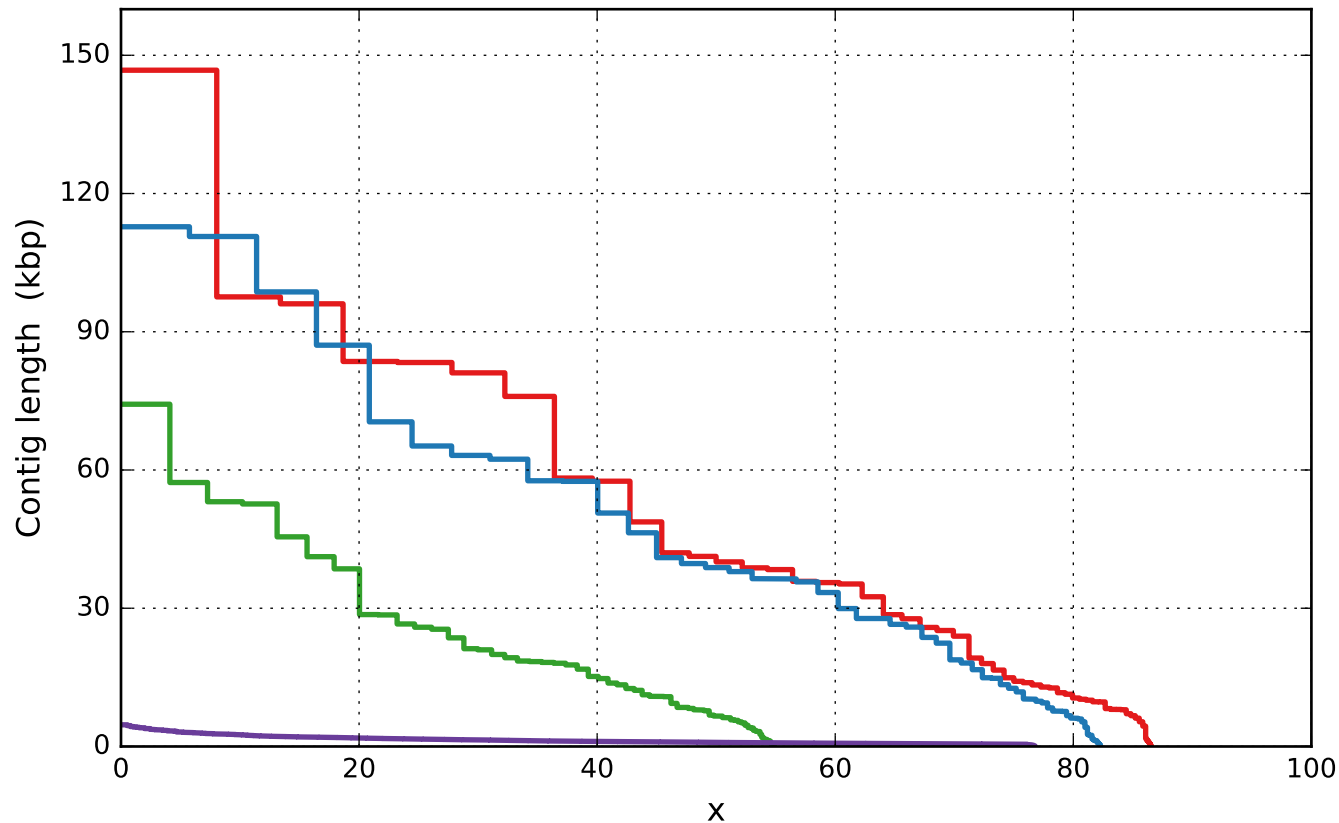
 # relocations



Cumulative length (aligned contigs)

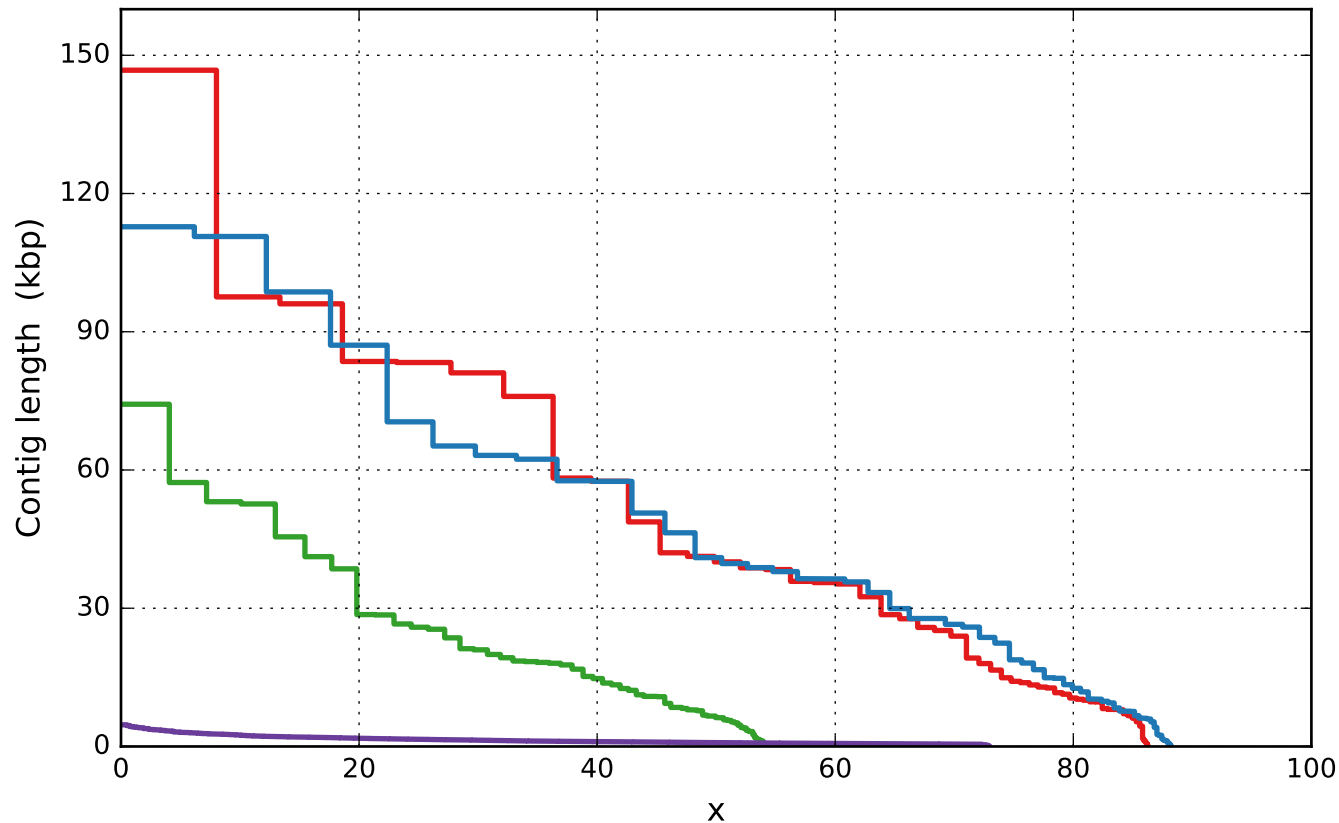


NAx

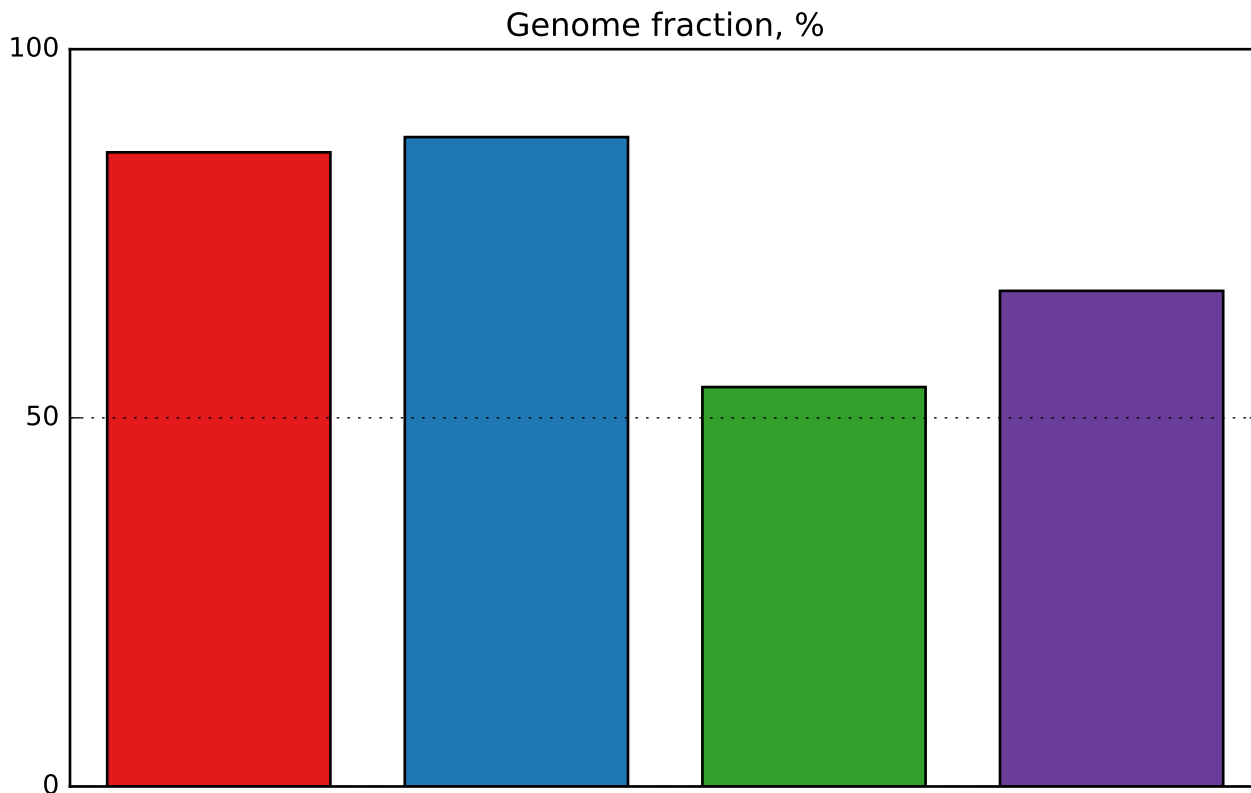


— M05964\_contigs    — M10540\_contigs    — M16180\_contigs  
— M07572\_contigs

# NGAx



— M05964\_contigs    — M10540\_contigs    — M16180\_contigs  
— M07572\_contigs



■ M05964\_contigs   ■ M10540\_contigs   ■ M16180\_contigs  
■ M07572\_contigs