

# 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	1985832	1985832	1985832	1985832
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.22	38.22	38.22	38.22
N50	444952	200368	1150911	1206
NG50	250374	200368	1150911	1068
N75	179754	79547	311459	786
NG75	118299	79547	186938	641
L50	2	4	1	437
LG50	3	4	1	546
L75	4	8	2	884
LG75	5	8	3	1147
# misassemblies	67	73	2	16
# misassembled contigs	9	13	1	15
Misassembled contigs length	1782615	1751746	27072	25297
# local misassemblies	56	73	1	23
# unaligned contigs	2 + 0 part	10 + 10 part	0 + 9 part	376 + 137 part
Unaligned length	8340	119555	965780	507132
Genome fraction (%)	74.665	79.225	41.983	57.236
Duplication ratio	1.225	1.171	1.012	1.084
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2669.41	2605.85	3816.07	2047.14
# indels per 100 kbp	73.45	71.38	90.56	45.31
Largest alignment	110459	121149	38880	5015
NA50	29650	28286	-	791
NGA50	26878	28286	-	669
NA75	9963	6151	-	-
NGA75	-	5572	-	-
LA50	18	20	-	621
LGA50	21	20	-	791
LA75	42	51	-	-
LGA75	-	54	-	-

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

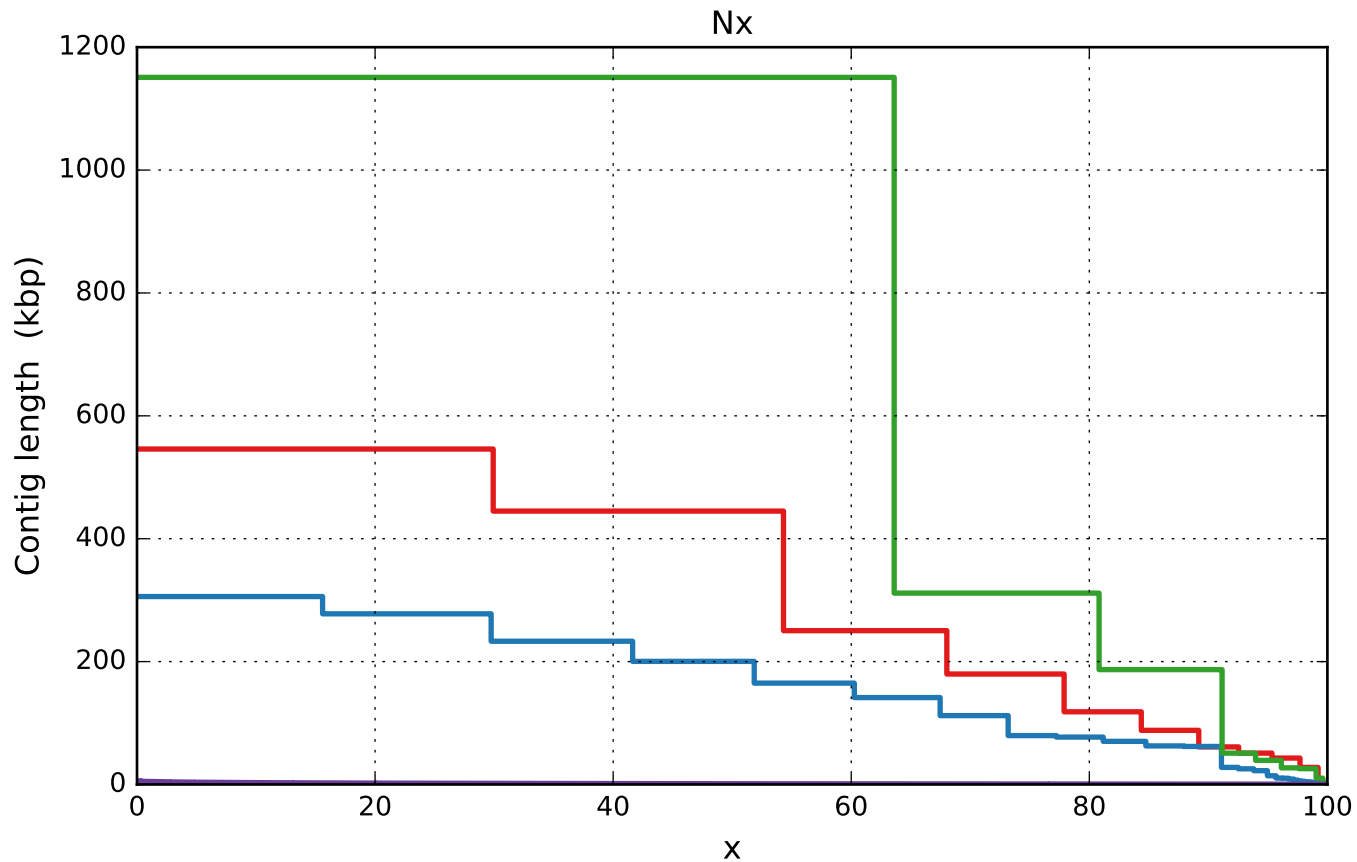
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	67	73	2	16
# relocations	67	73	2	16
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	9	13	1	15
Misassembled contigs length	1782615	1751746	27072	25297
# local misassemblies	56	73	1	23
# mismatches	39580	40997	31815	23268
# indels	1089	1123	755	515
# short indels	960	1002	684	461
# long indels	129	121	71	54
Indels length	3487	3507	1841	1406

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).

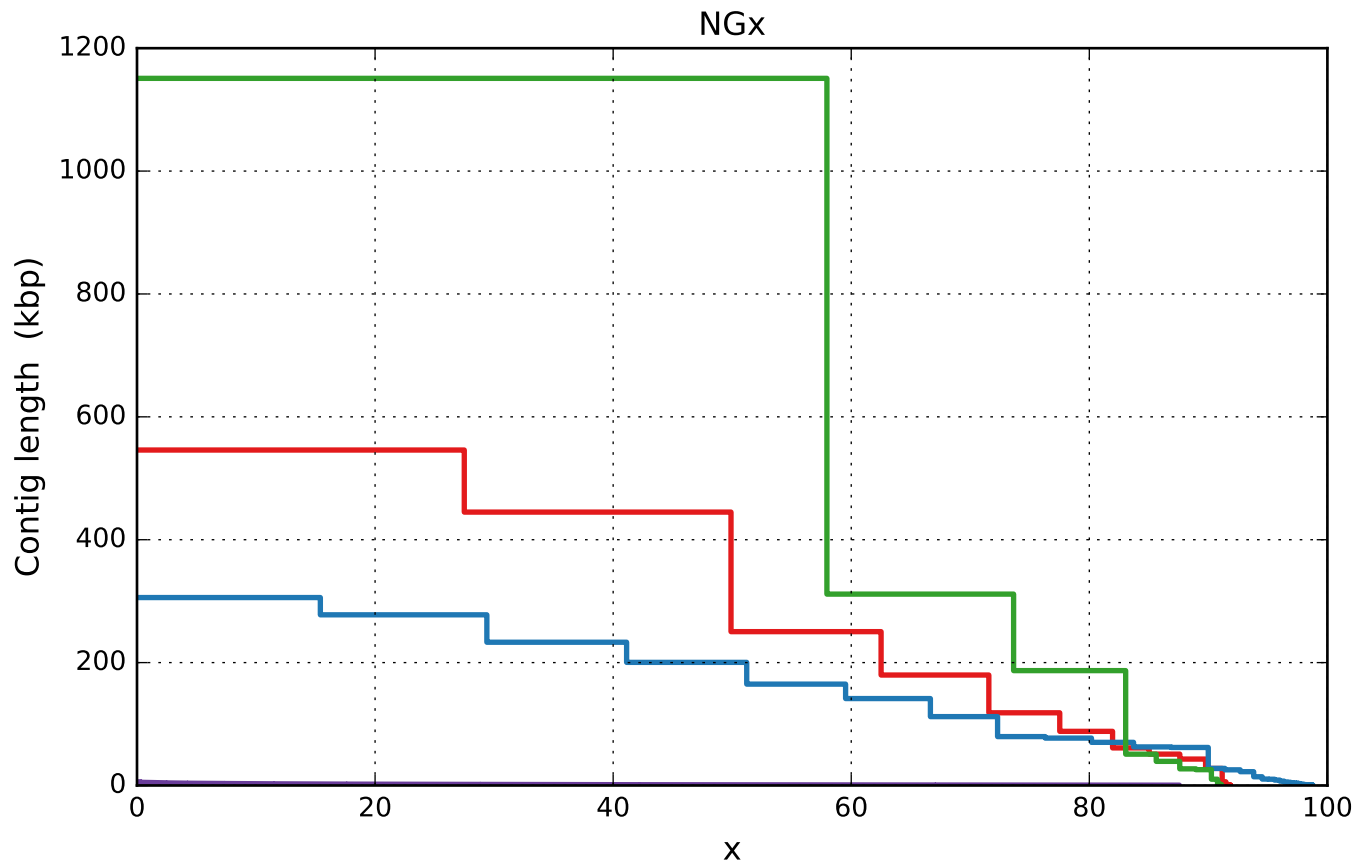
## Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	2	10	0	376
Fully unaligned length	8340	34855	0	424101
# partially unaligned contigs	0	10	9	137
# with misassembly	0	3	7	6
# both parts are significant	0	5	6	24
Partially unaligned length	0	84700	965780	83031
# 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

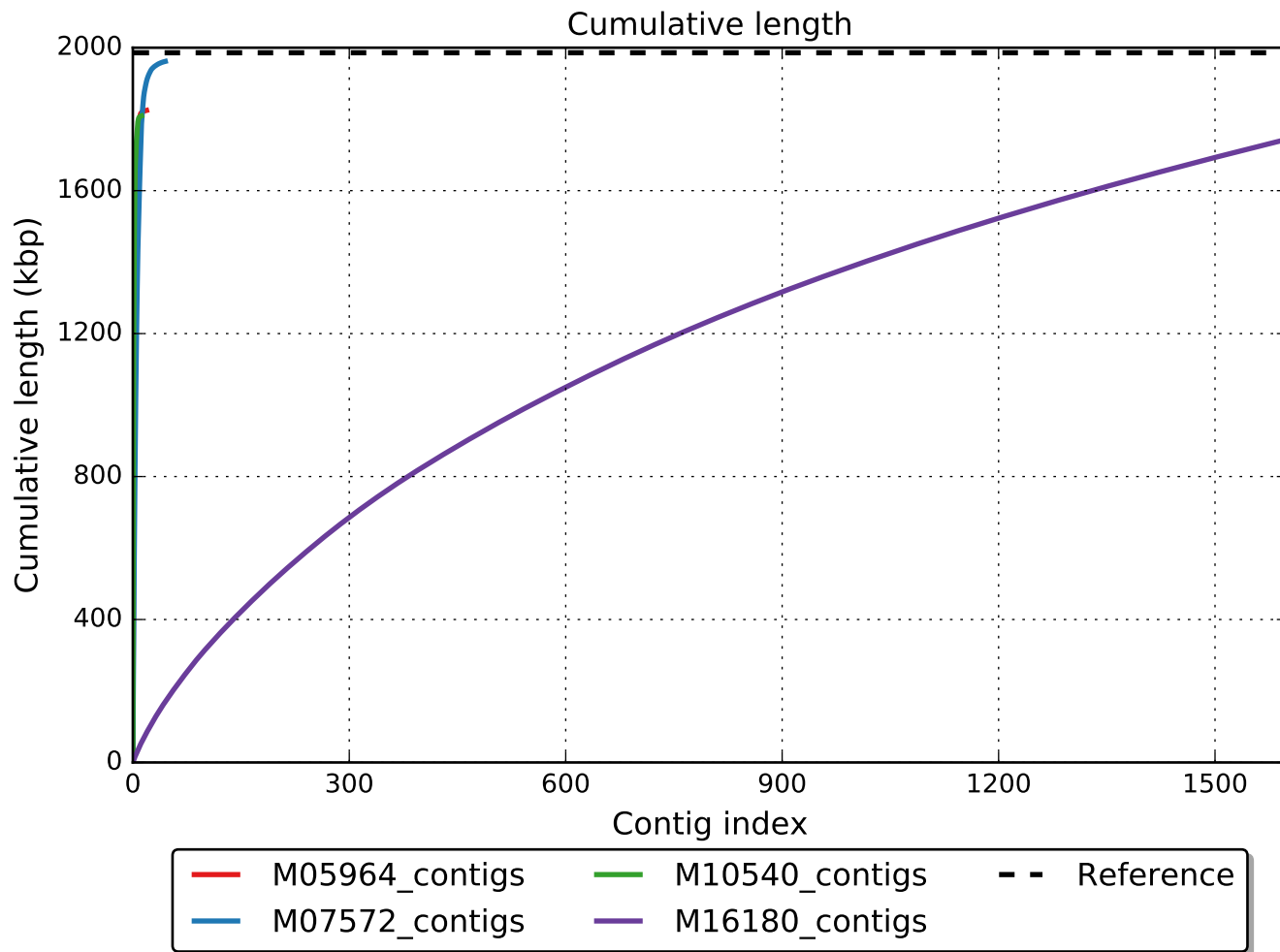


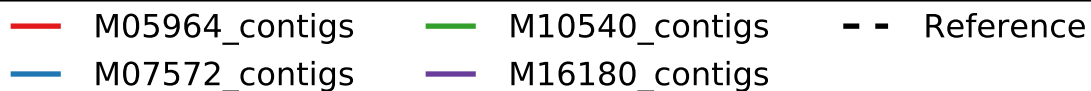
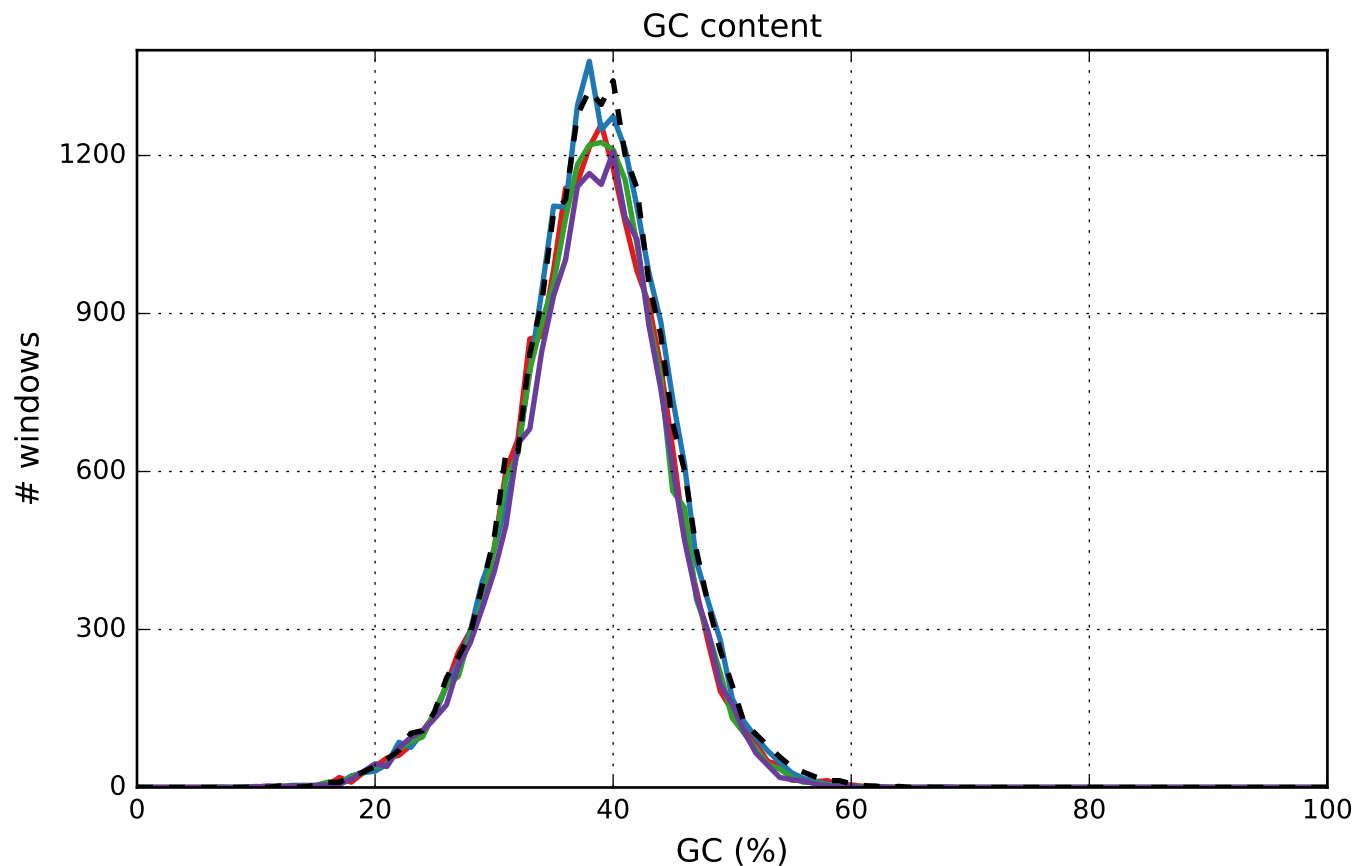
M05964\_contigs

M10540\_contigs

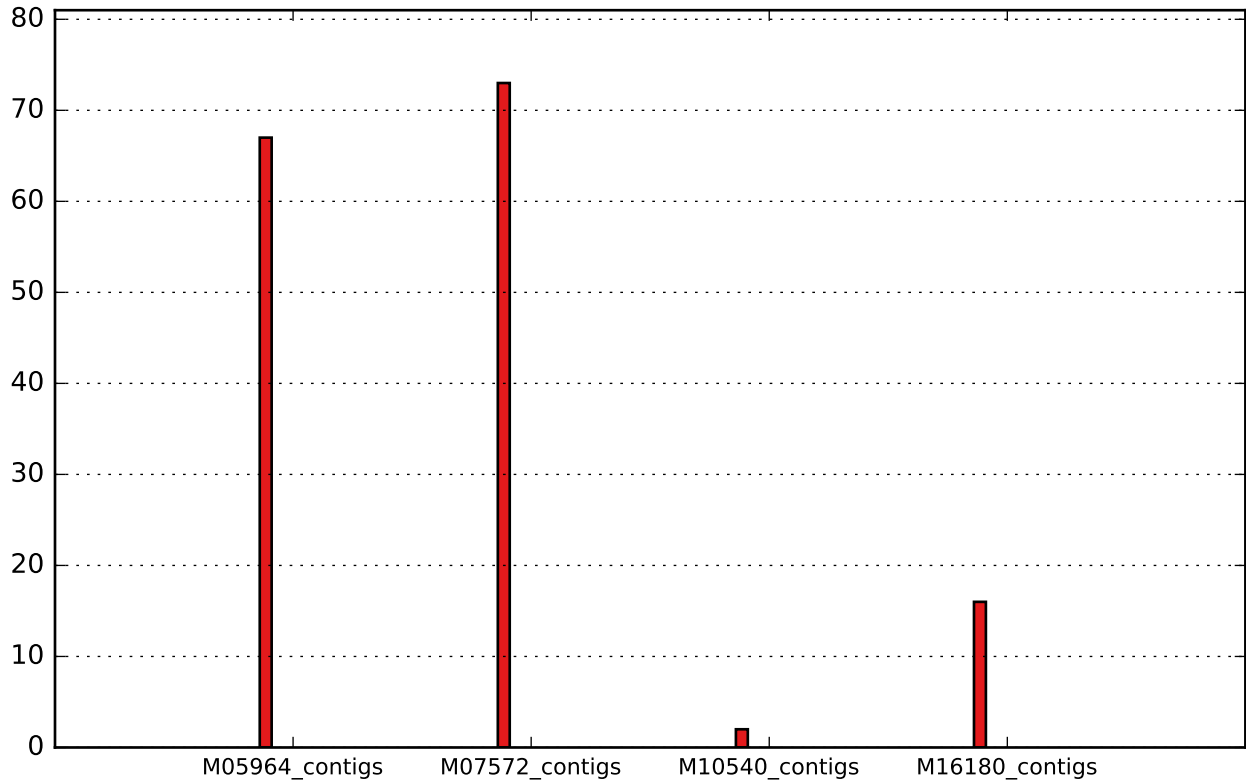
M16180\_contigs

M07572\_contigs





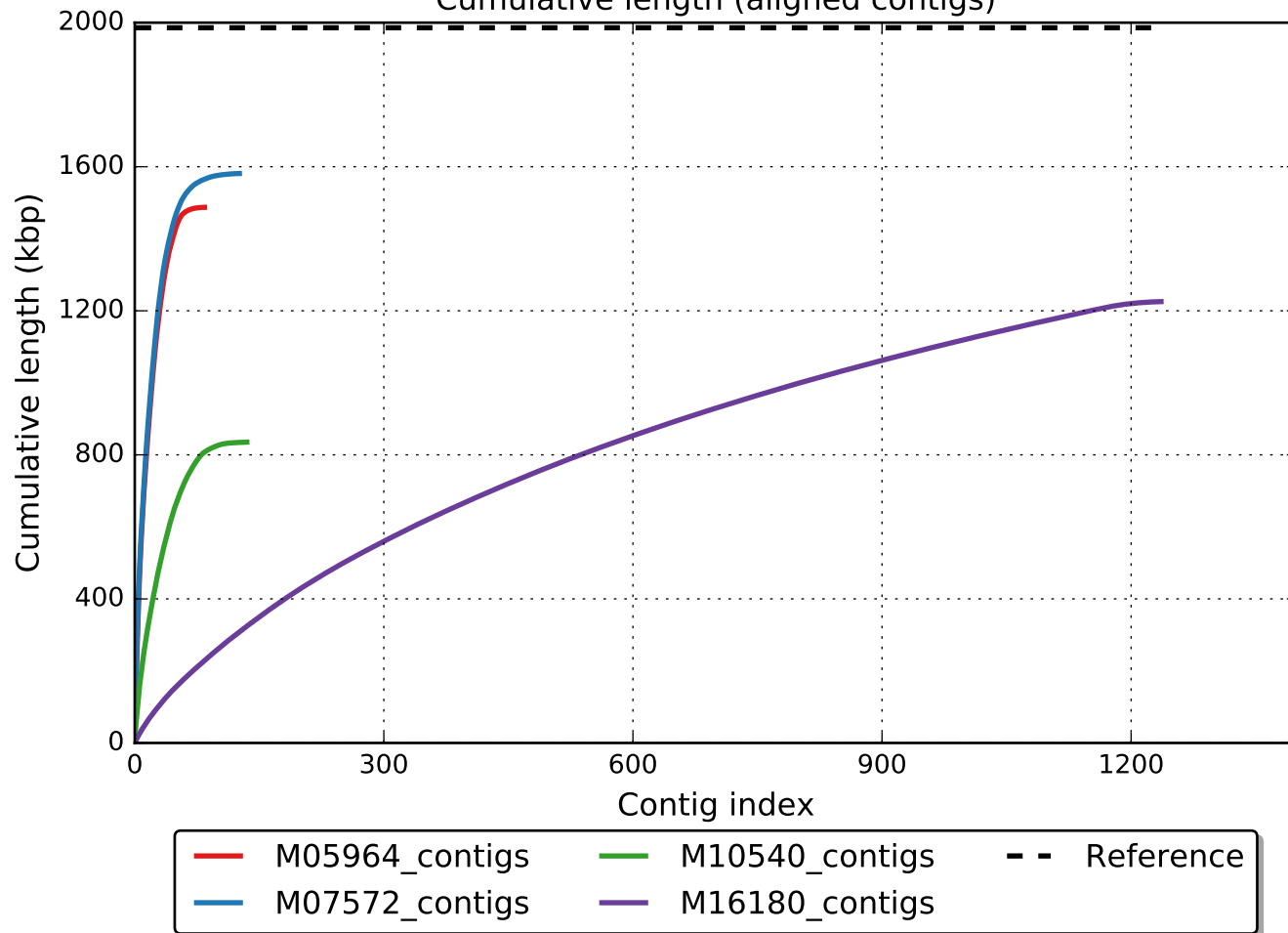
# Misassemblies



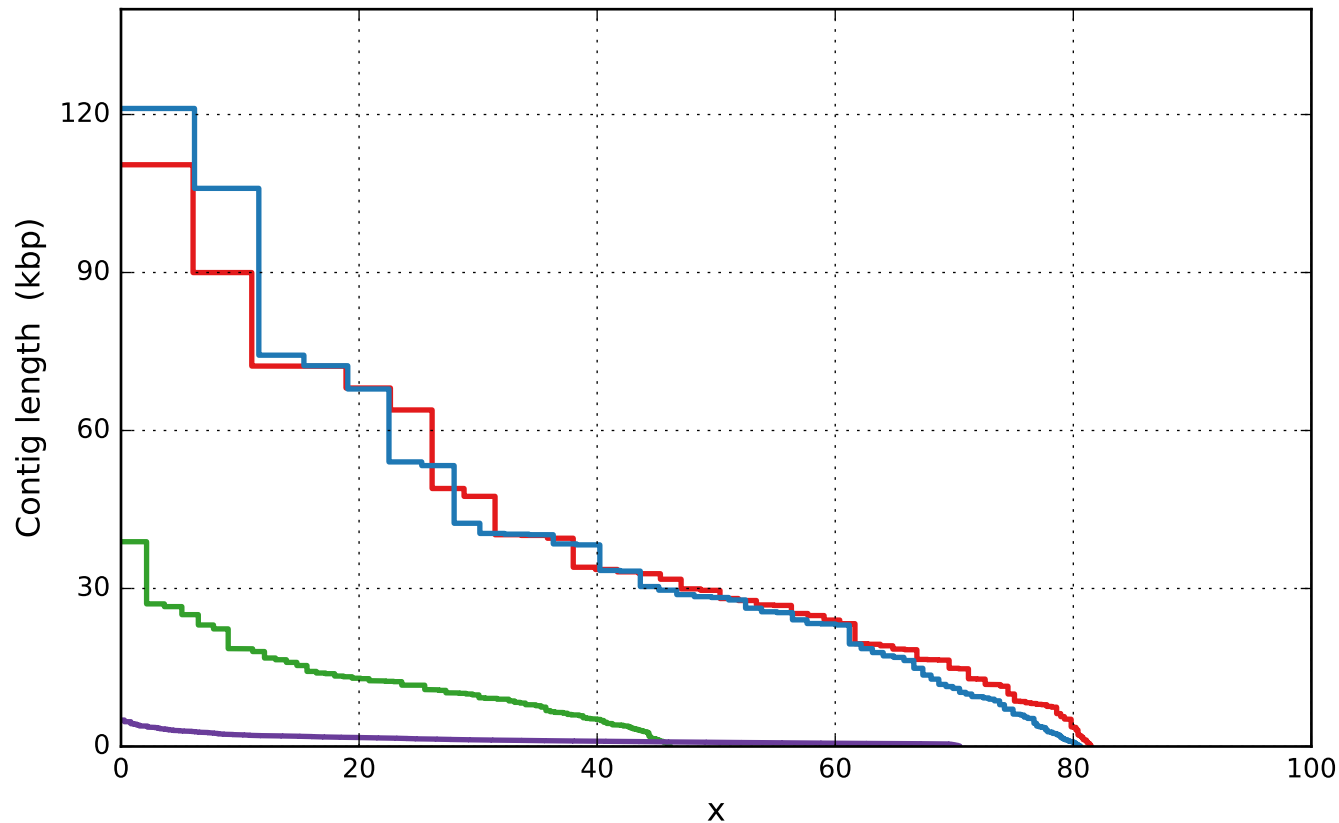
# relocations



Cumulative length (aligned contigs)

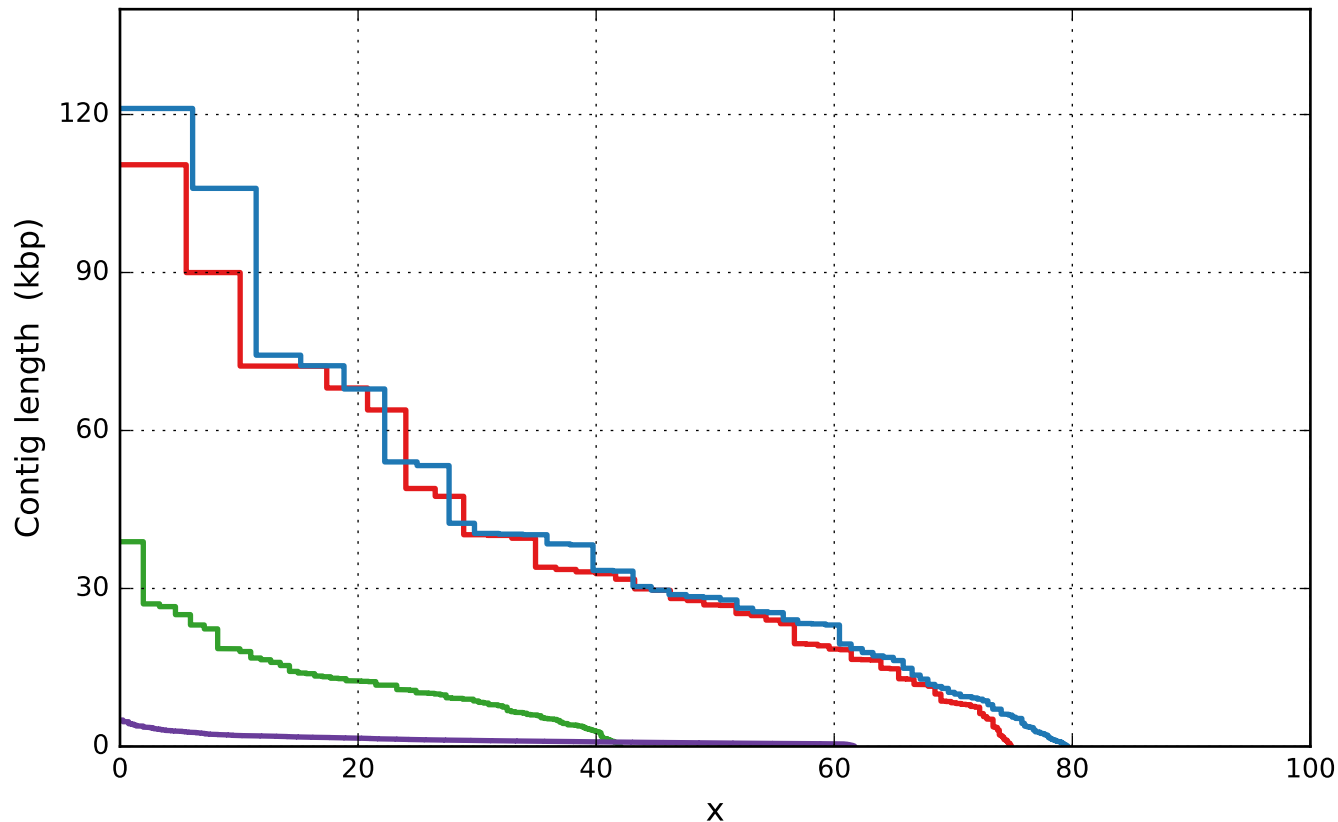


NAx



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

# NGAx



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

