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	1981535	1981535	1981535	1981535
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.14	38.14	38.14	38.14
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1069
N75	179754	79547	311459	786
NG75	118299	79547	186938	642
L50	2	4	1	437
LG50	2	4	1	544
L75	4	8	2	884
LG75	5	8	3	1142
# misassemblies	58	52	54	14
# misassembled contigs	9	12	3	14
Misassembled contigs length	1782615	1749842	1215879	28359
# local misassemblies	61	56	27	17
# unaligned contigs	2 + 0 part	13 + 8 part	0 + 6 part	226 + 106 part
Unaligned length	8340	120269	294954	345446
Genome fraction (%)	81.179	81.429	50.172	64.499
Duplication ratio	1.129	1.141	1.523	1.090
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2424.93	2349.93	3734.24	1862.49
# indels per 100 kbp	65.59	64.89	85.80	36.85
Largest alignment	122175	111107	67998	4699
NA50	44409	35717	6271	907
NGA50	39479	35717	713	786
NA75	19190	9517	-	539
NGA75	9732	9216	-	-
LA50	13	17	51	561
LGA50	15	17	80	706
LA75	28	41	-	1192
LGA75	37	43	-	-

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

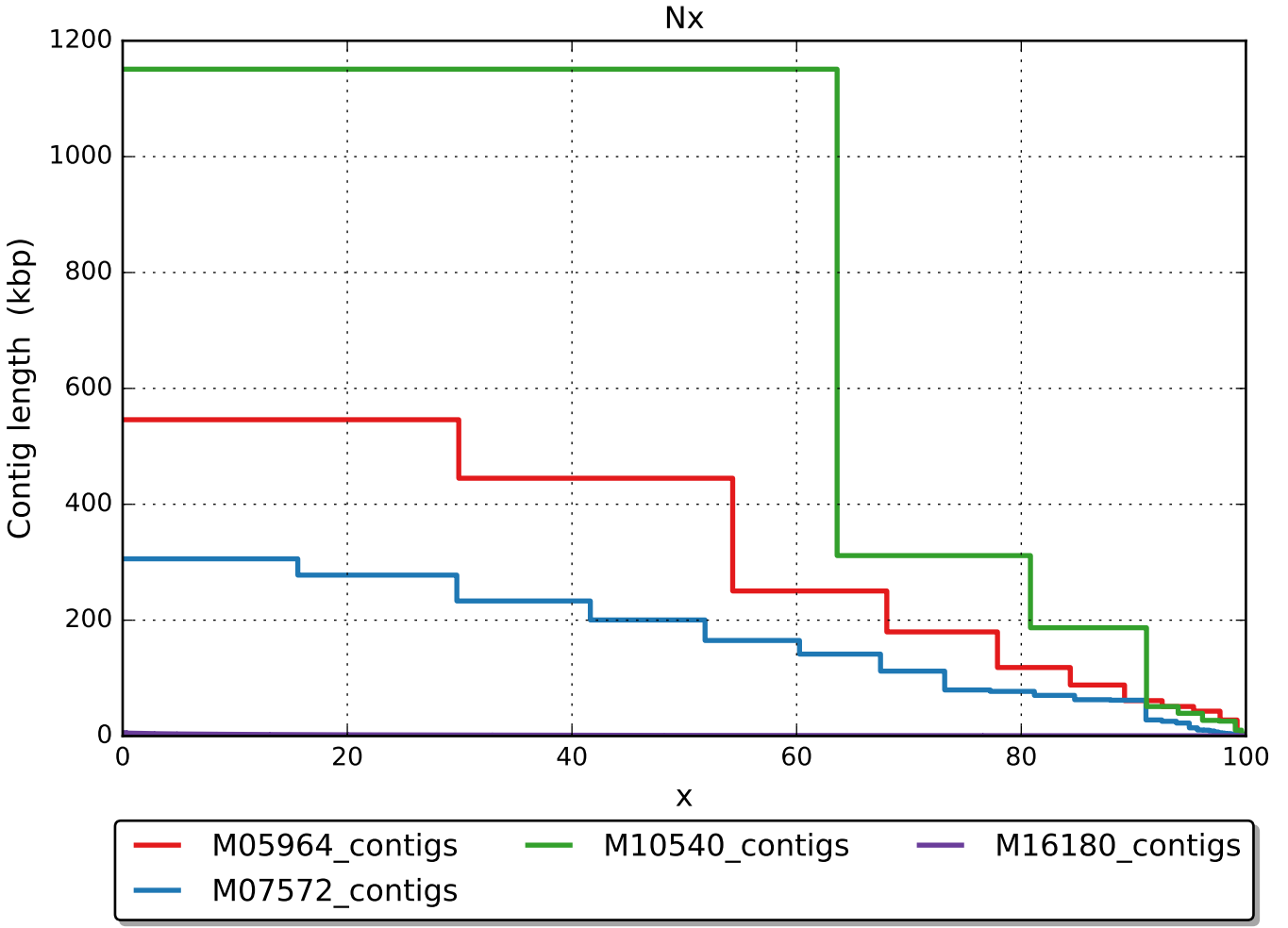
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	58	52	54	14
# relocations	58	52	54	14
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	9	12	3	14
Misassembled contigs length	1782615	1749842	1215879	28359
# local misassemblies	61	56	27	17
# mismatches	39007	37917	37125	23804
# indels	1055	1047	853	471
# short indels	926	921	786	418
# long indels	129	126	67	53
Indels length	3552	3511	1997	1535

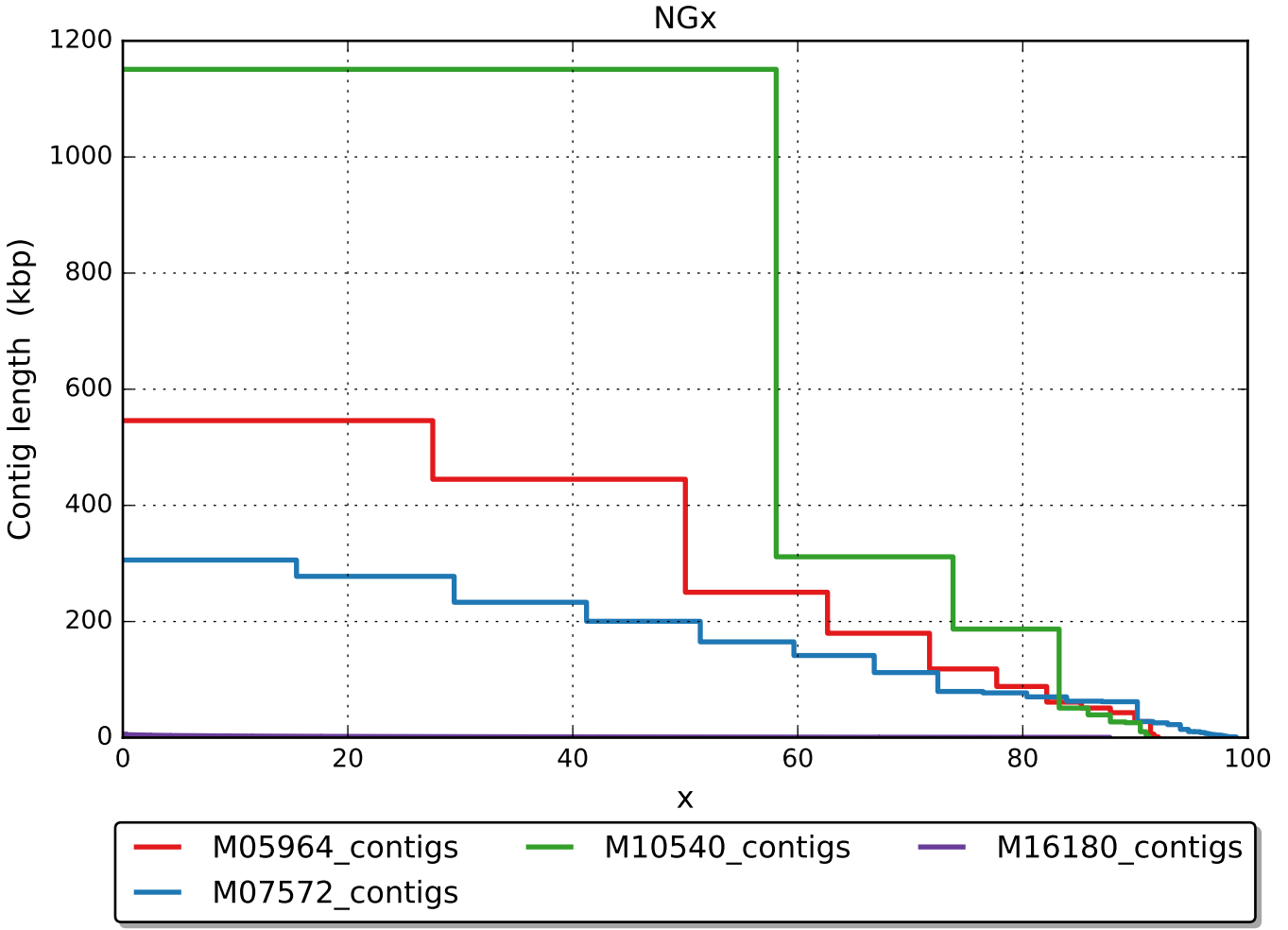
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

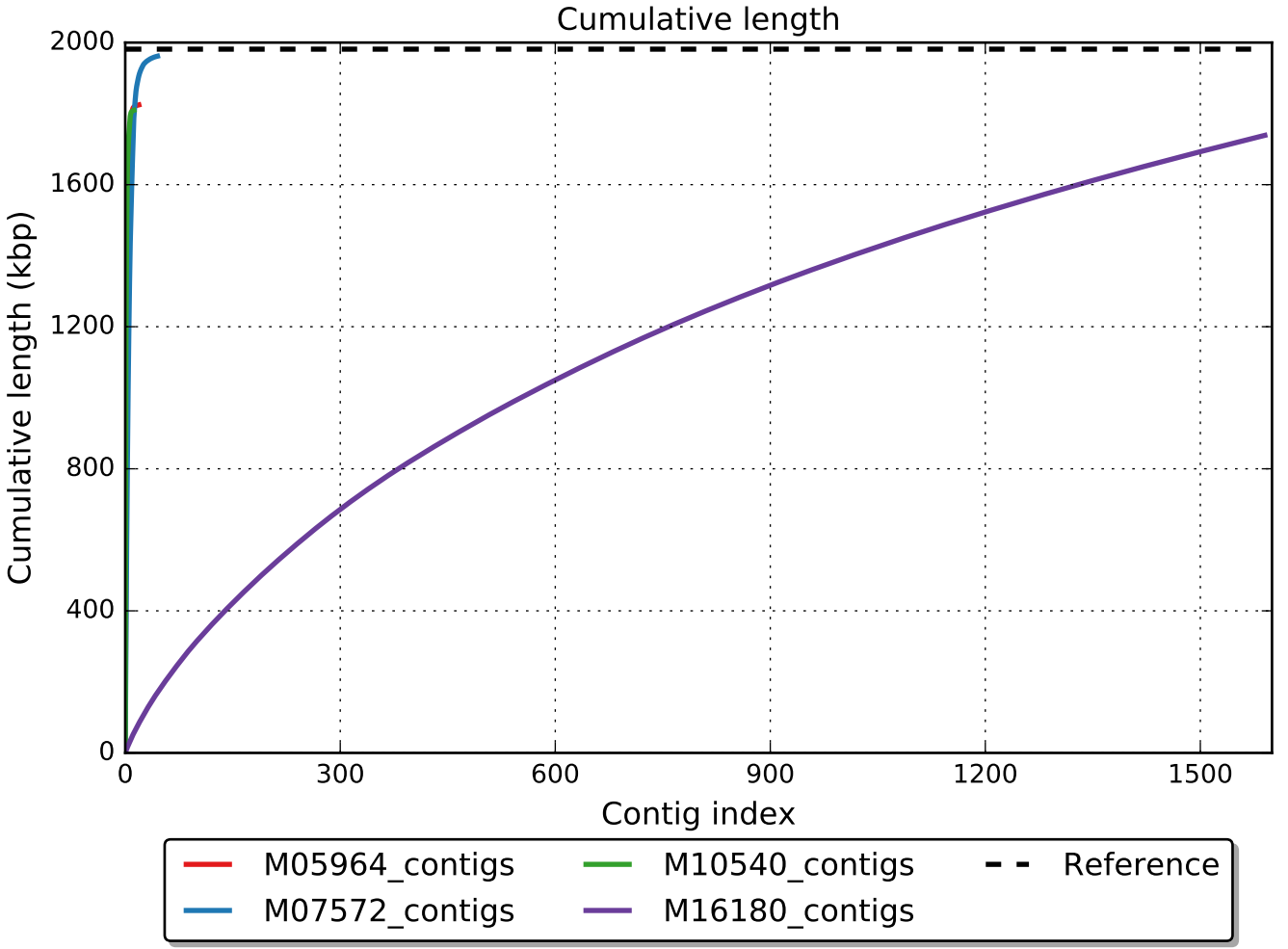
Unaligned report

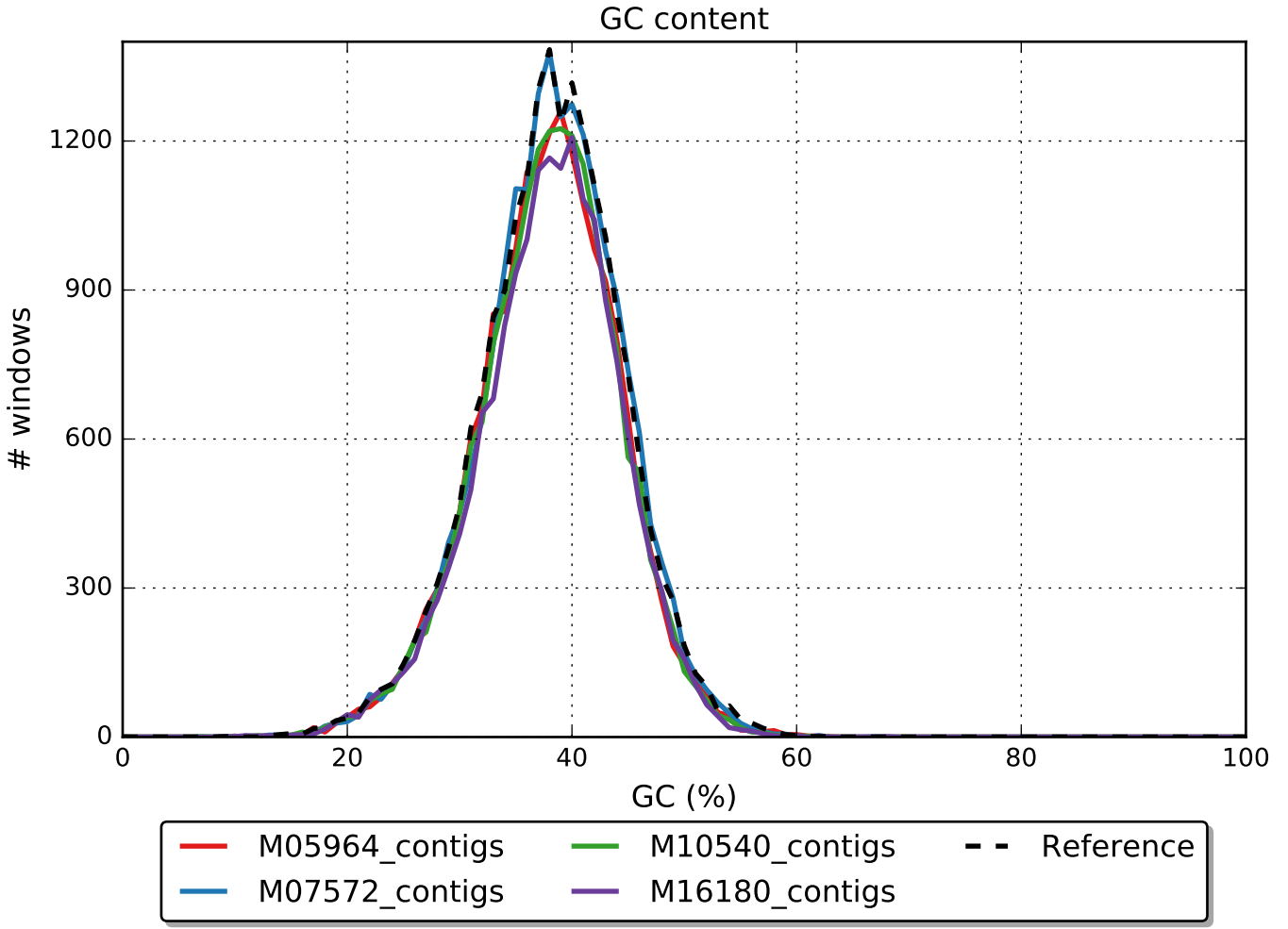
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	2	13	0	226
Fully unaligned length	8340	55309	0	274777
# partially unaligned contigs	0	8	6	106
# with misassembly	0	4	4	3
# both parts are significant	0	5	3	21
Partially unaligned length	0	64960	294954	70669
# N's	1086	1127	693	1471

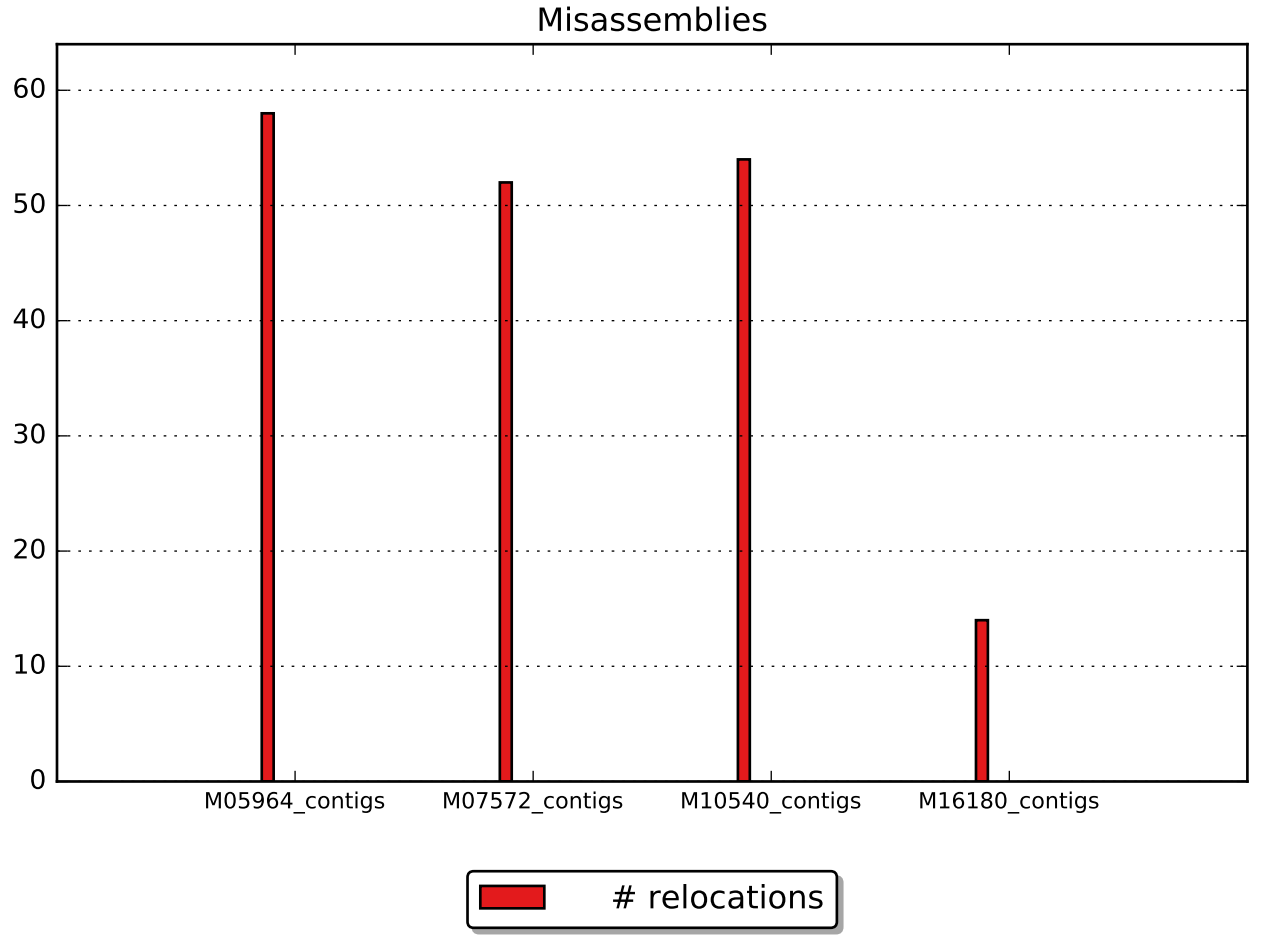
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

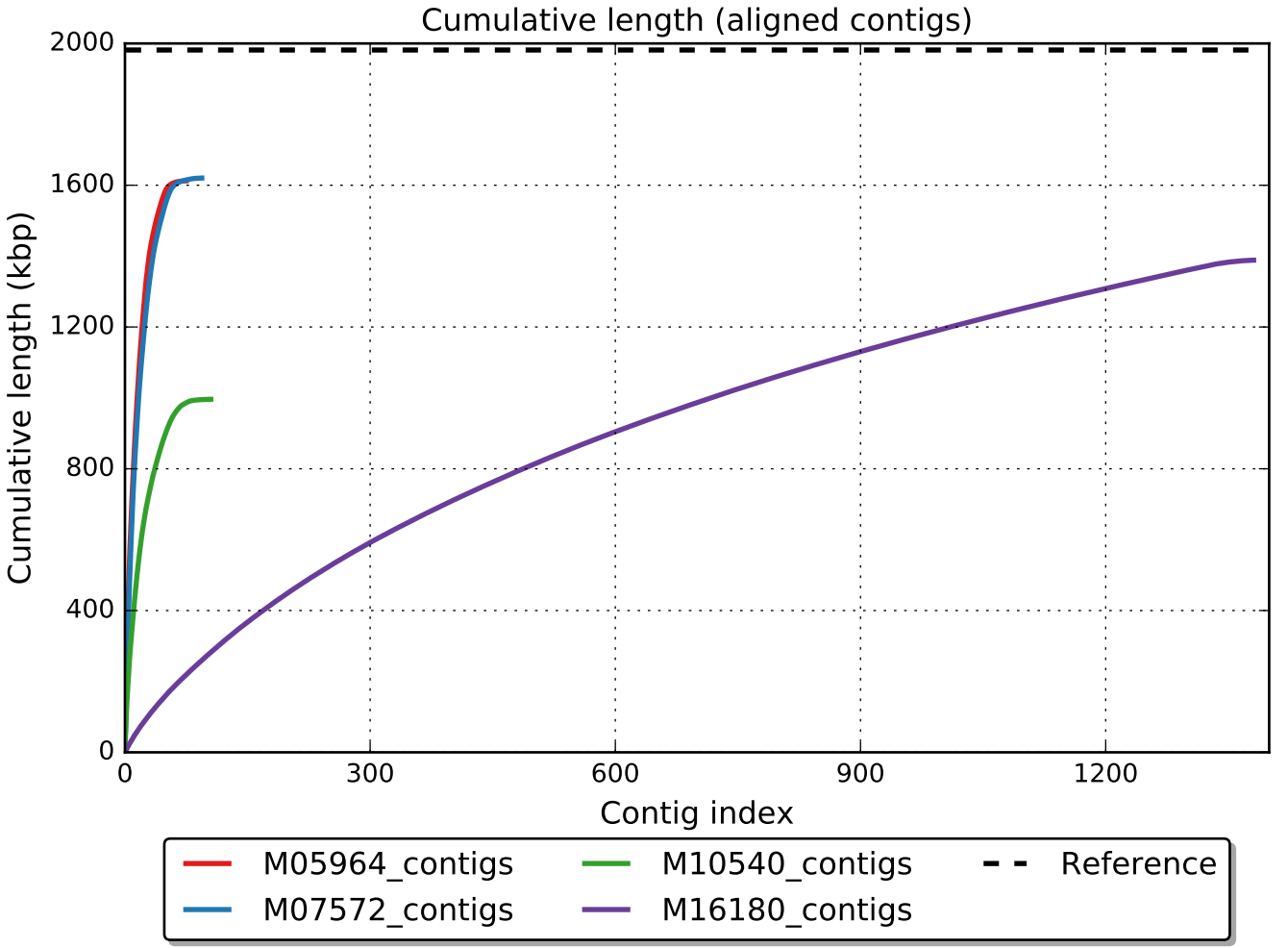

Nx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

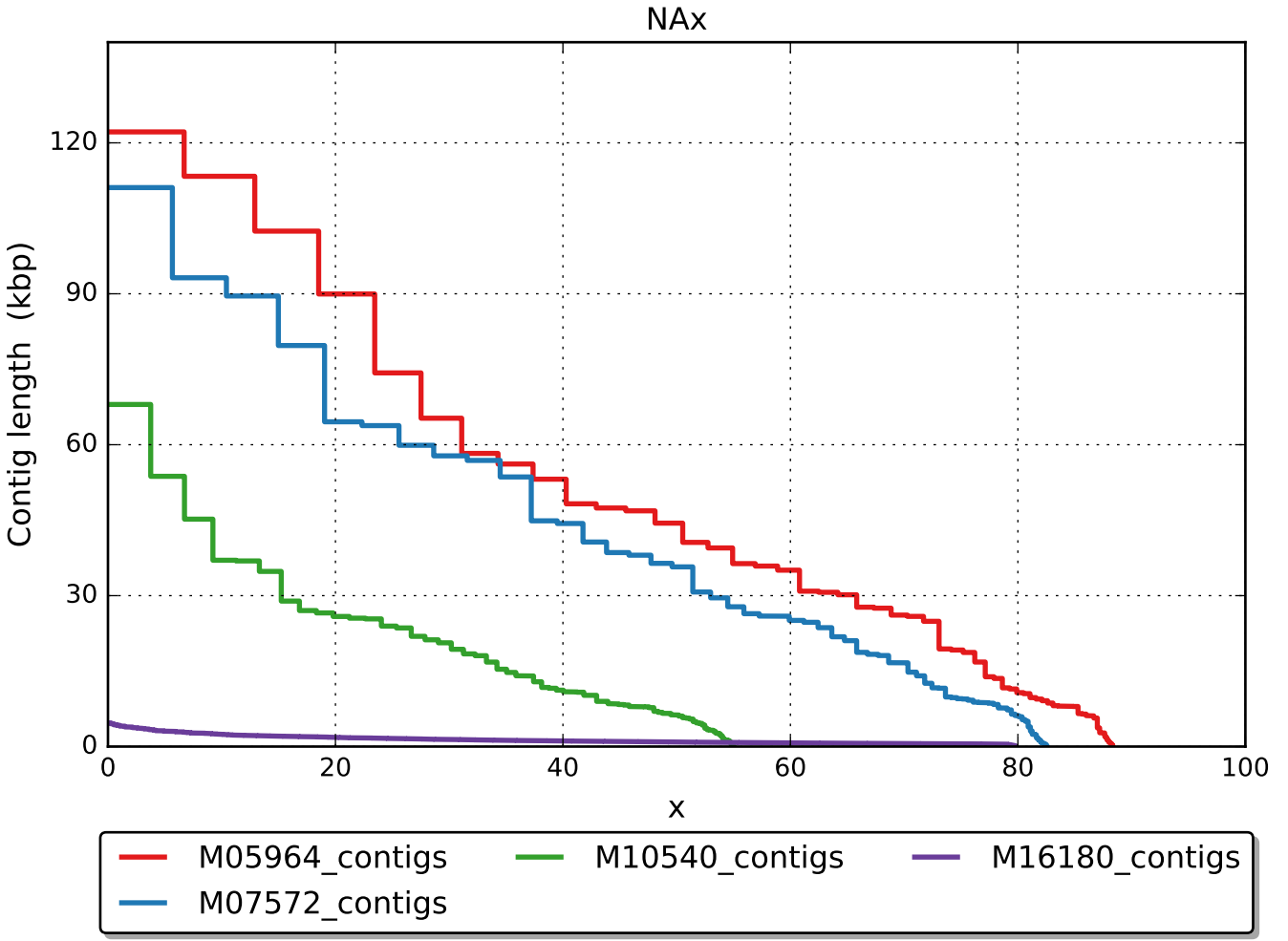

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

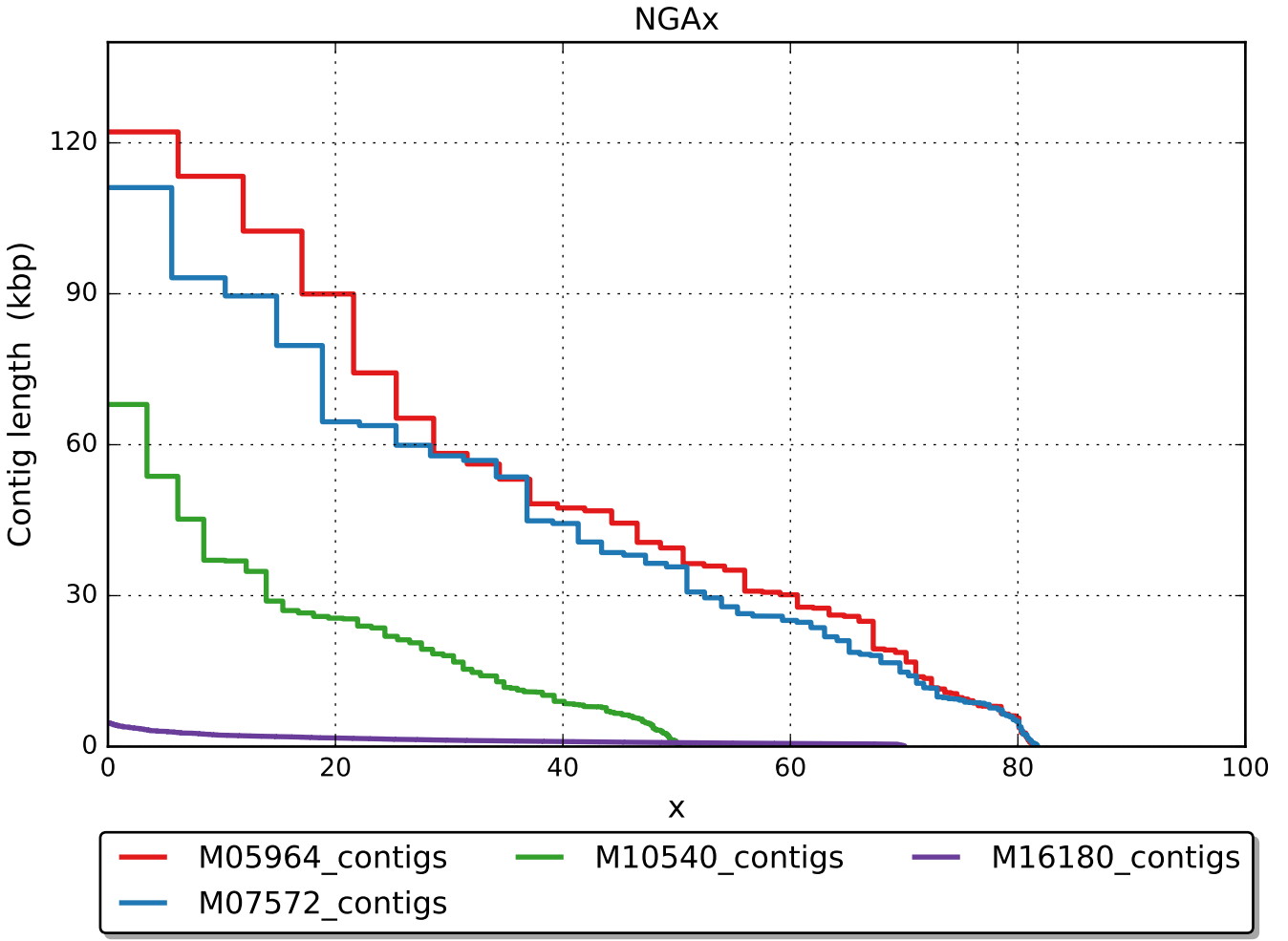

Cumulative length
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
300
600
900
1200
1500
Contig index
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

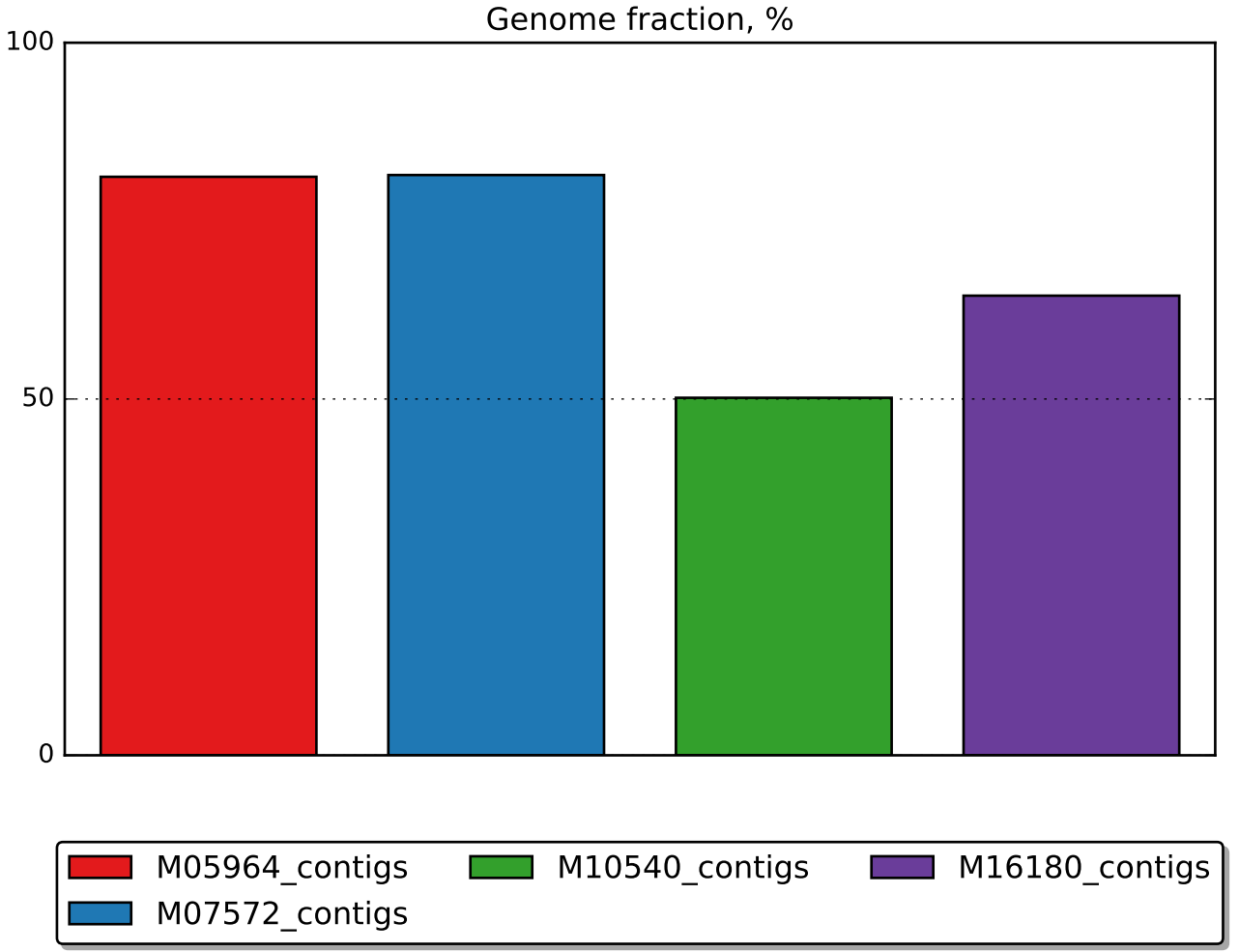

GC content
windows
GC (%)
0
300
600
900
1200
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


Misassemblies
60
50
40
30
20
10
0
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
300
600
900
1200
Contig index
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


NAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs


NGAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs


Genome fraction, %
100
50
0
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs