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	1890645	1890645	1890645	1890645
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.23	38.23	38.23	38.23
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1127
N75	179754	79547	311459	786
NG75	179754	112073	311459	690
L50	2	4	1	437
LG50	2	4	1	502
L75	4	8	2	884
LG75	4	7	2	1040
# misassemblies	51	11	83	4
# misassembled contigs	9	8	6	4
Misassembled contigs length	1782615	1333263	1741348	4077
# local misassemblies	64	20	44	7
# unaligned contigs	1 + 1 part	2 + 4 part	0 + 3 part	296 + 87 part
Unaligned length	3658	45755	34736	354539
Genome fraction (%)	84.719	95.921	58.172	67.751
Duplication ratio	1.137	1.056	1.614	1.081
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2413.18	685.68	3564.77	1395.46
# indels per 100 kbp	60.37	23.60	79.65	27.64
Largest alignment	150890	244345	47680	5936
NA50	40709	111087	10803	968
NGA50	40709	111087	8646	870
NA75	19190	44112	-	543
NGA75	14892	47096	-	-
LA50	13	5	40	519
LGA50	13	5	44	602
LA75	28	13	-	1128
LGA75	31	12	-	-

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

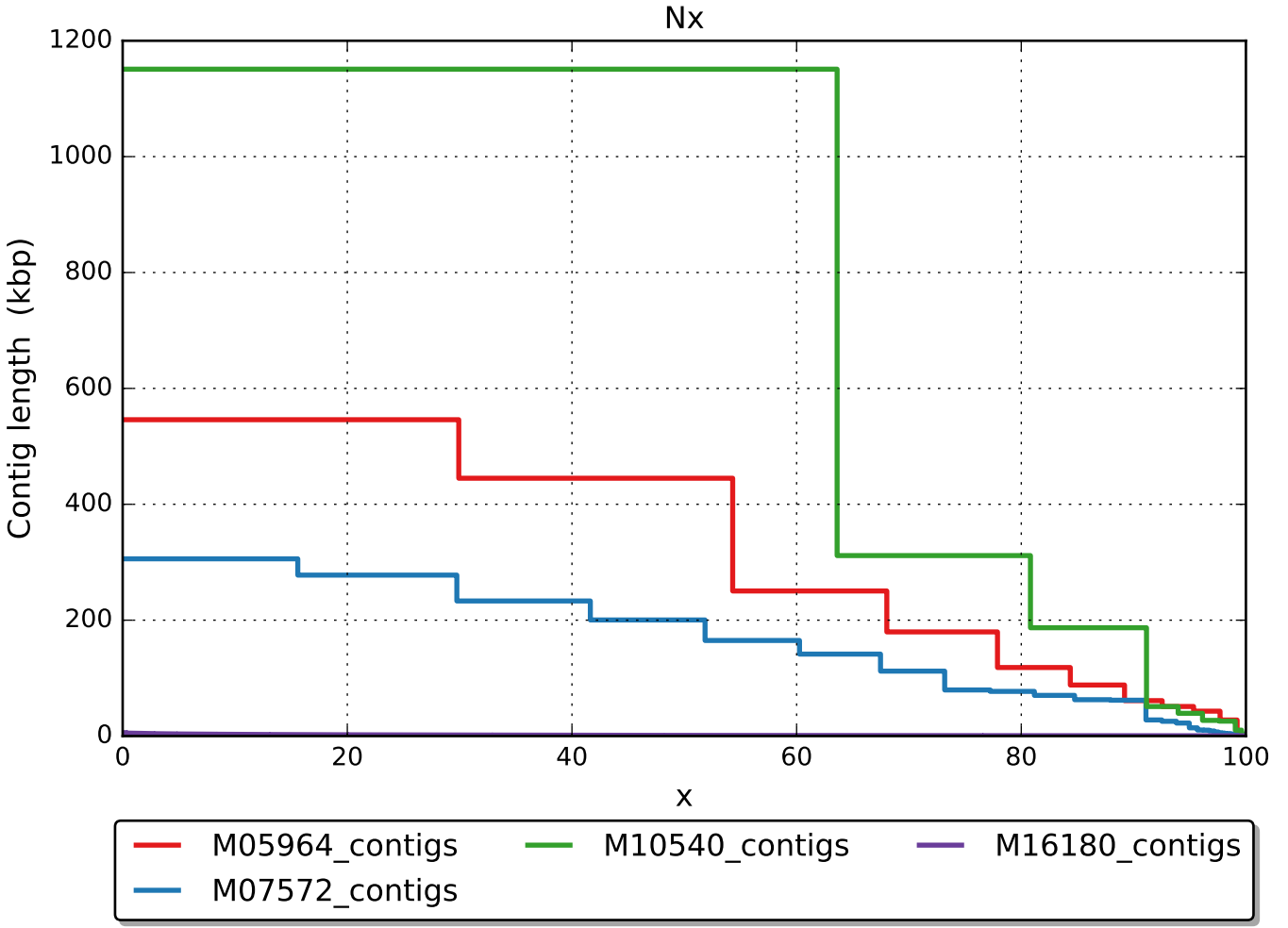
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	51	11	83	4
# relocations	50	11	83	4
# translocations	0	0	0	0
# inversions	1	0	0	0
# misassembled contigs	9	8	6	4
Misassembled contigs length	1782615	1333263	1741348	4077
# local misassemblies	64	20	44	7
# mismatches	38653	12435	39206	17875
# indels	967	428	876	354
# short indels	854	360	787	317
# long indels	113	68	89	37
Indels length	3100	2049	2195	1073

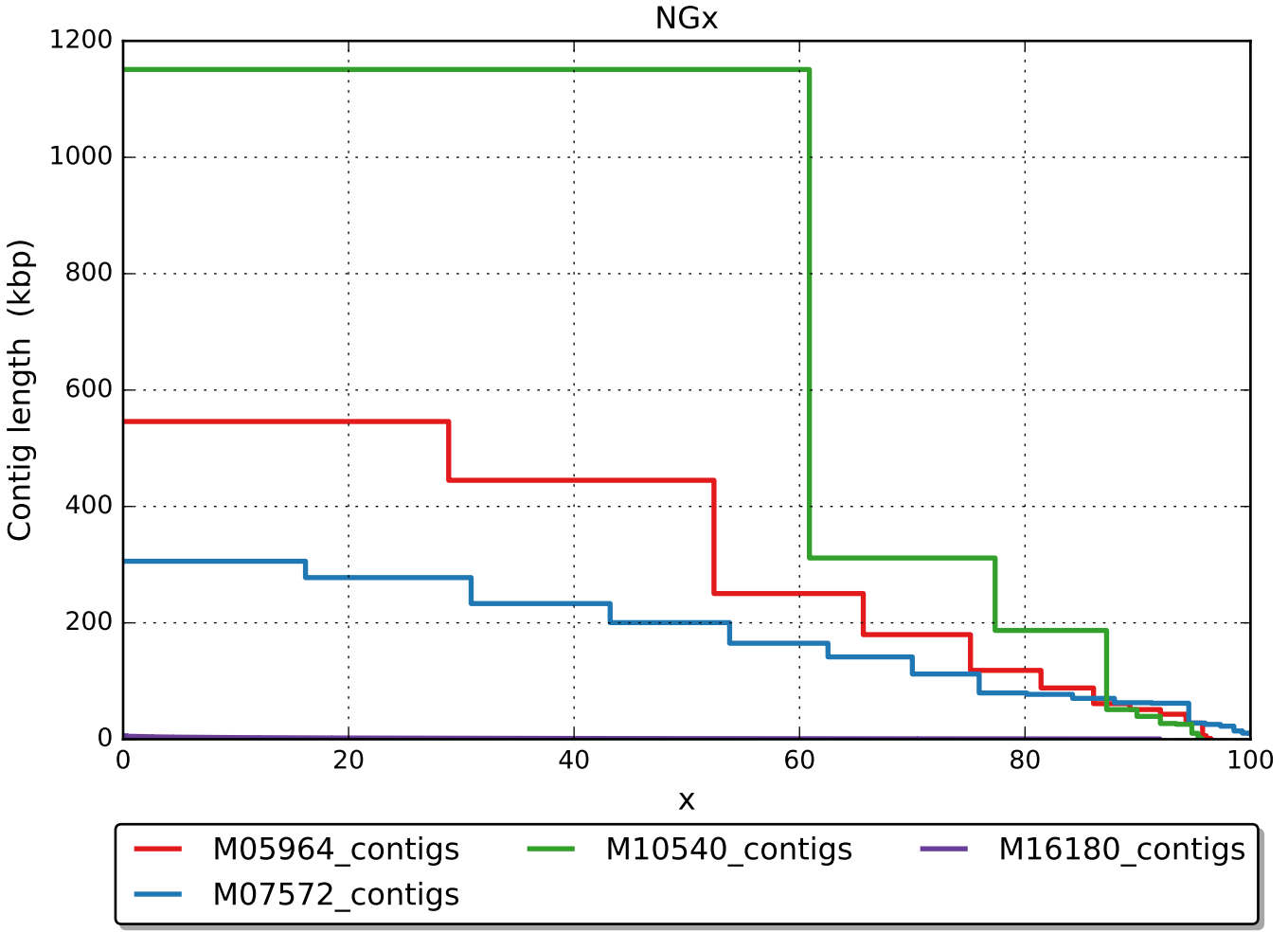
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

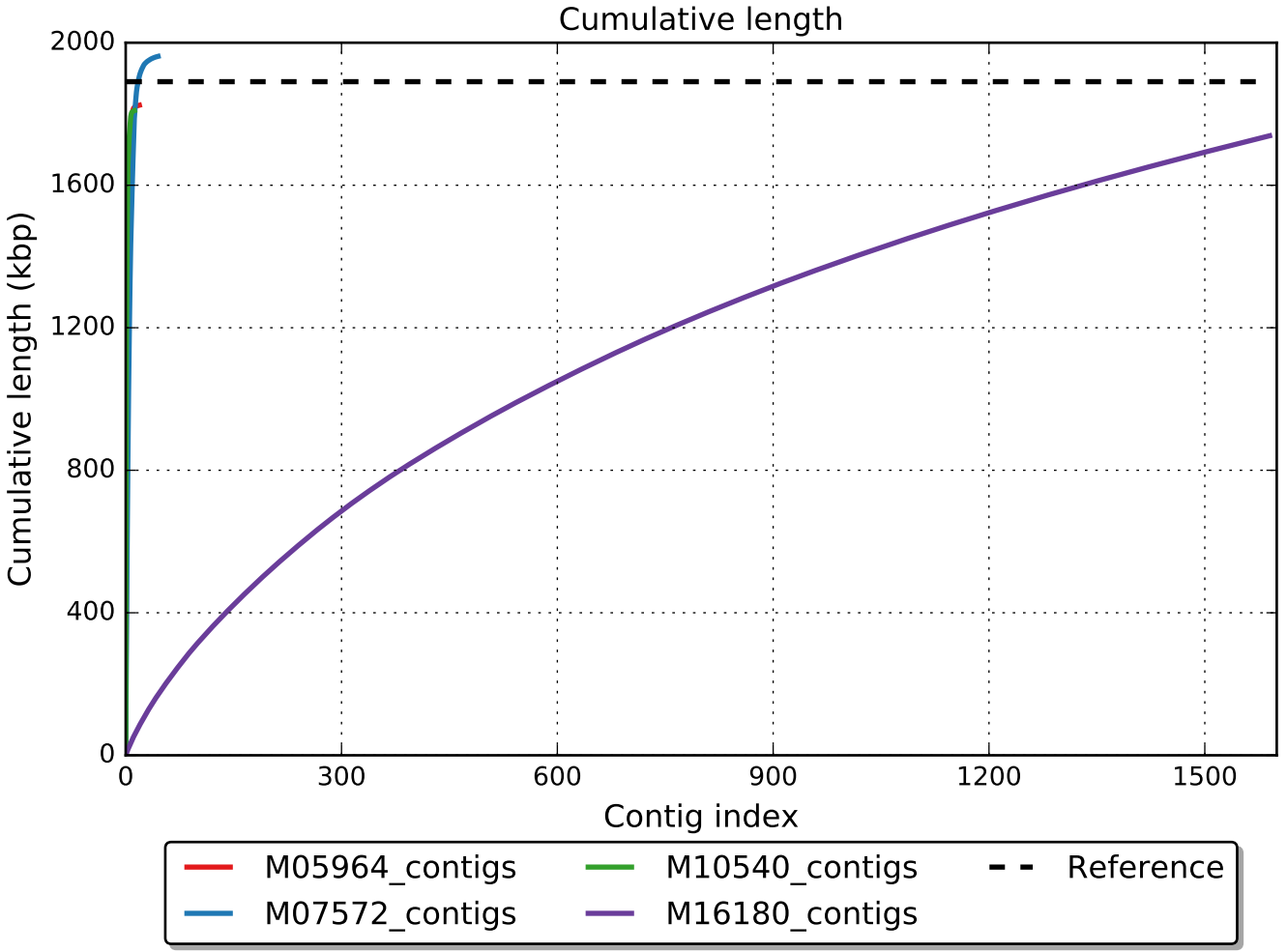
Unaligned report

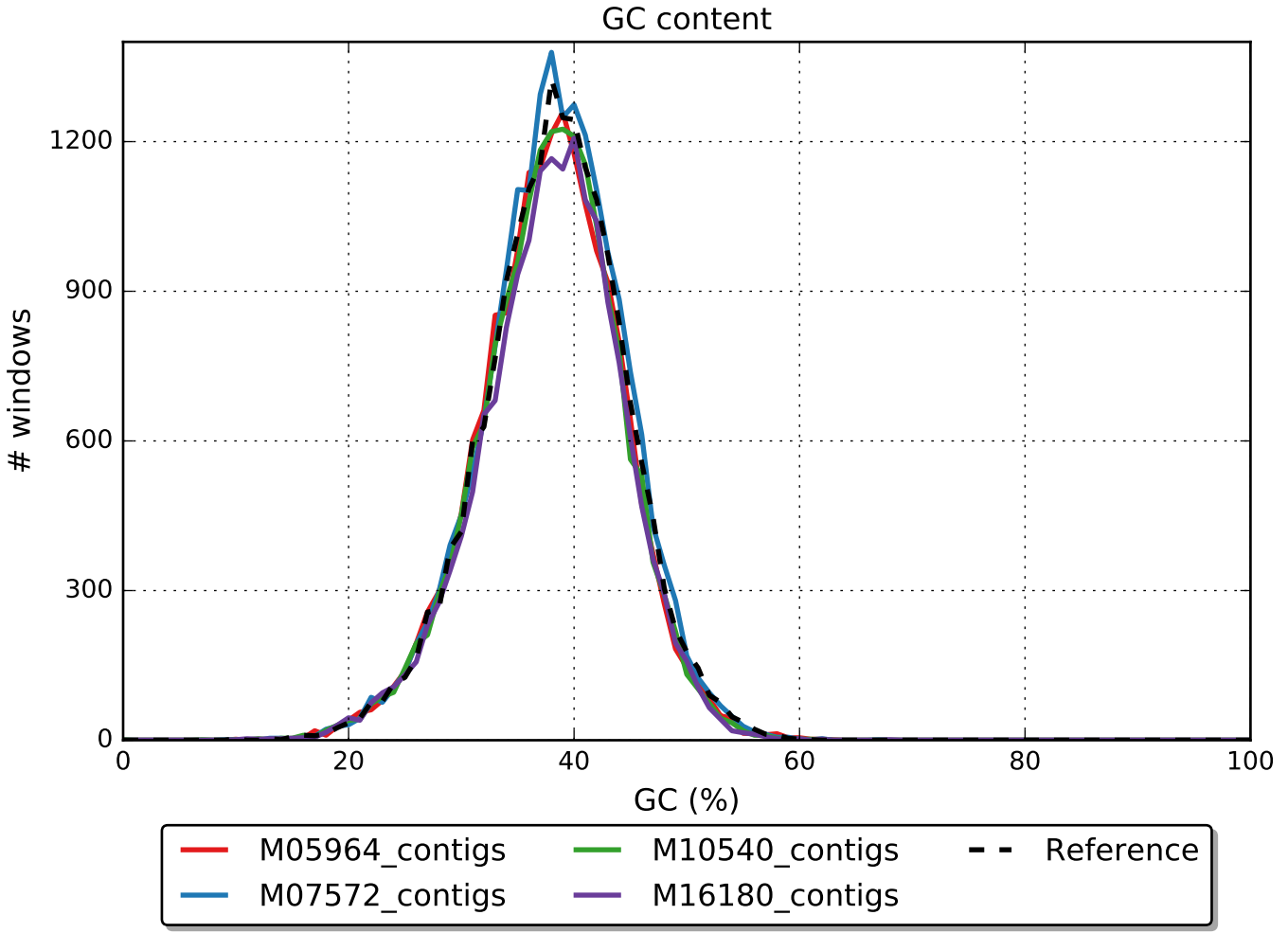
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	1	2	0	296
Fully unaligned length	2293	6857	0	304695
# partially unaligned contigs	1	4	3	87
# with misassembly	0	2	2	1
# both parts are significant	1	2	1	13
Partially unaligned length	1365	38898	34736	49844
# N's	1086	1127	693	1471

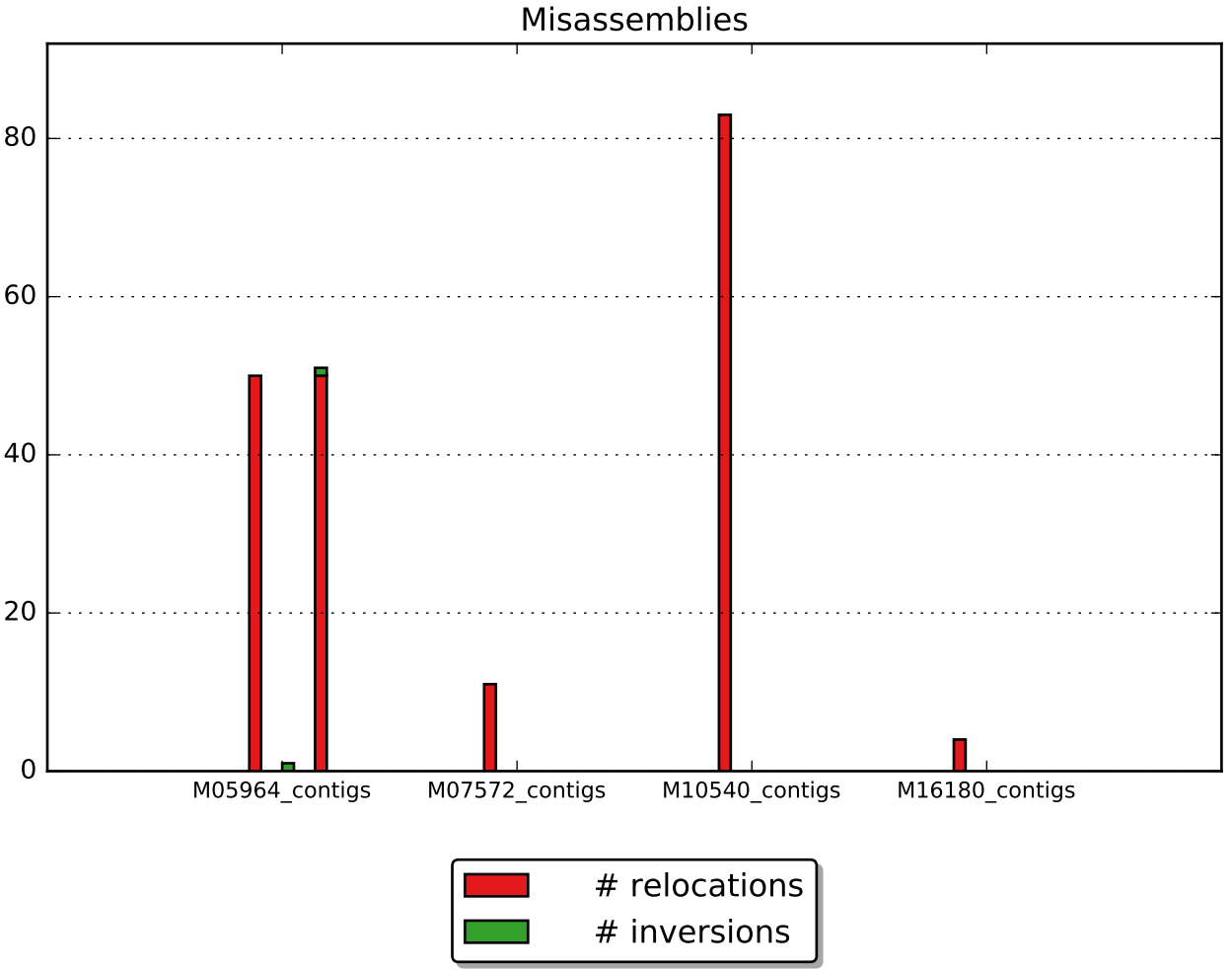
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

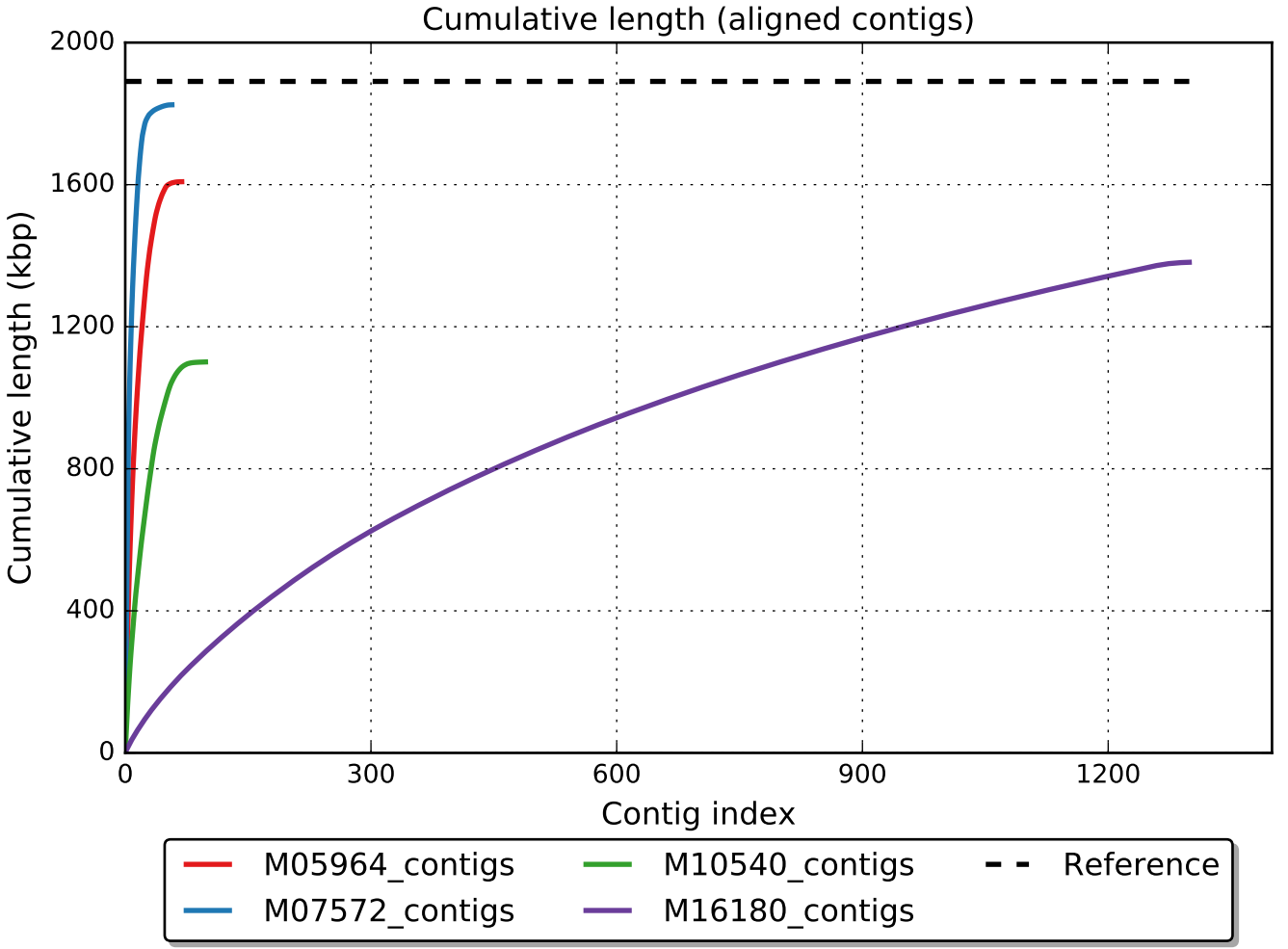

Nx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

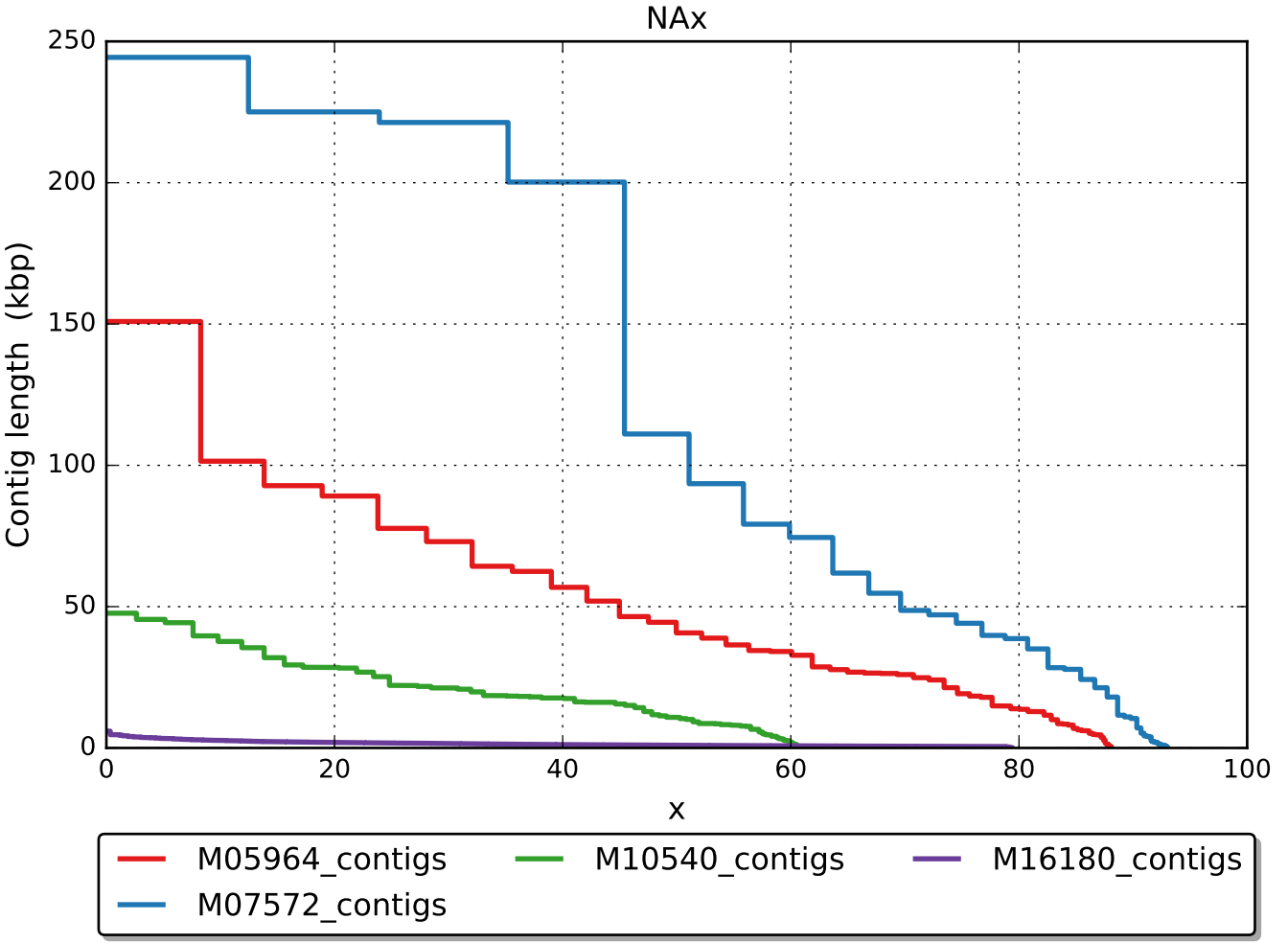

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

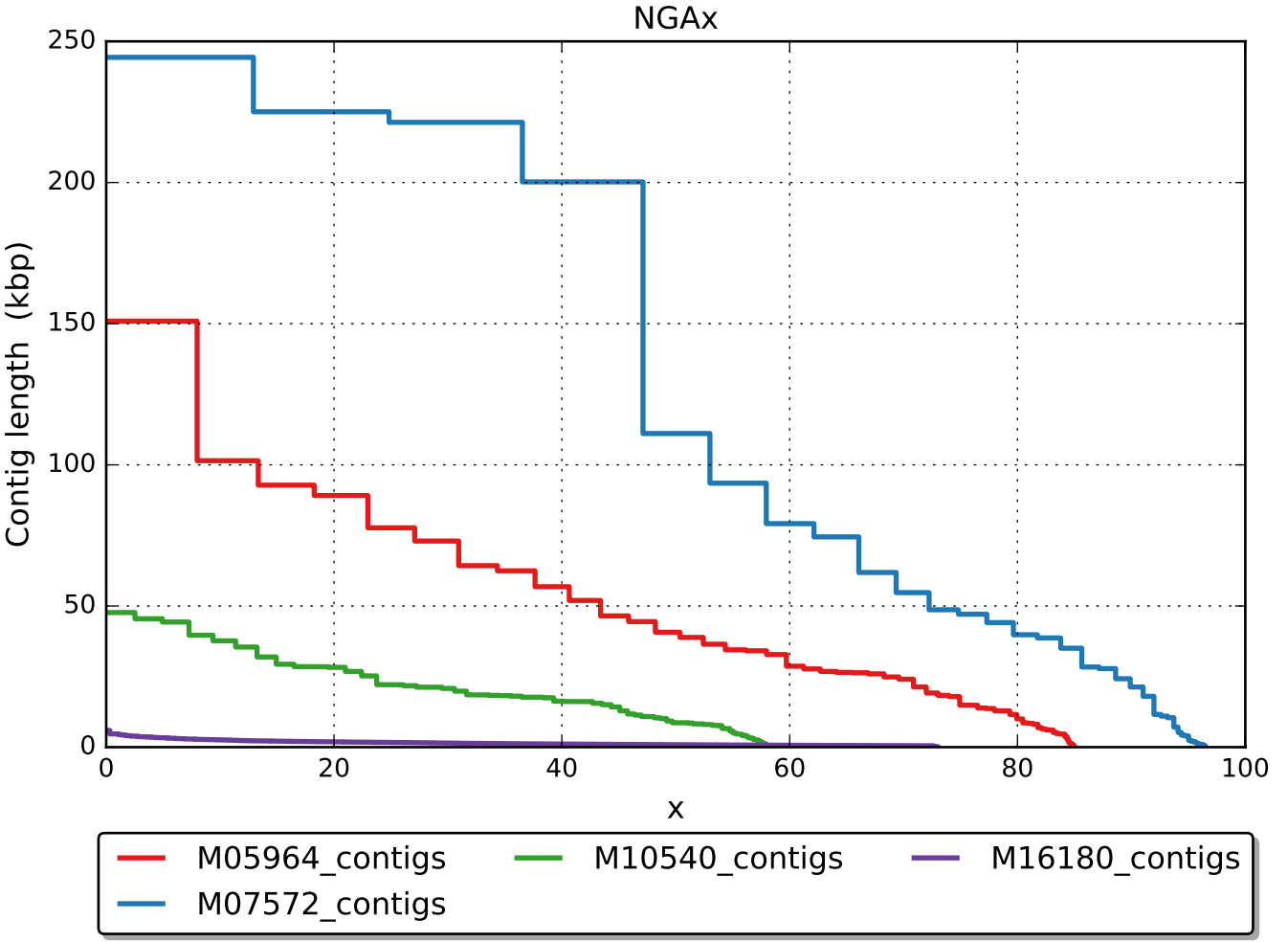

Cumulative length
Cumulative length (kbp)
2000
1600
1200
800
400
0
0
300
600
900
1200
1500
Contig index
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

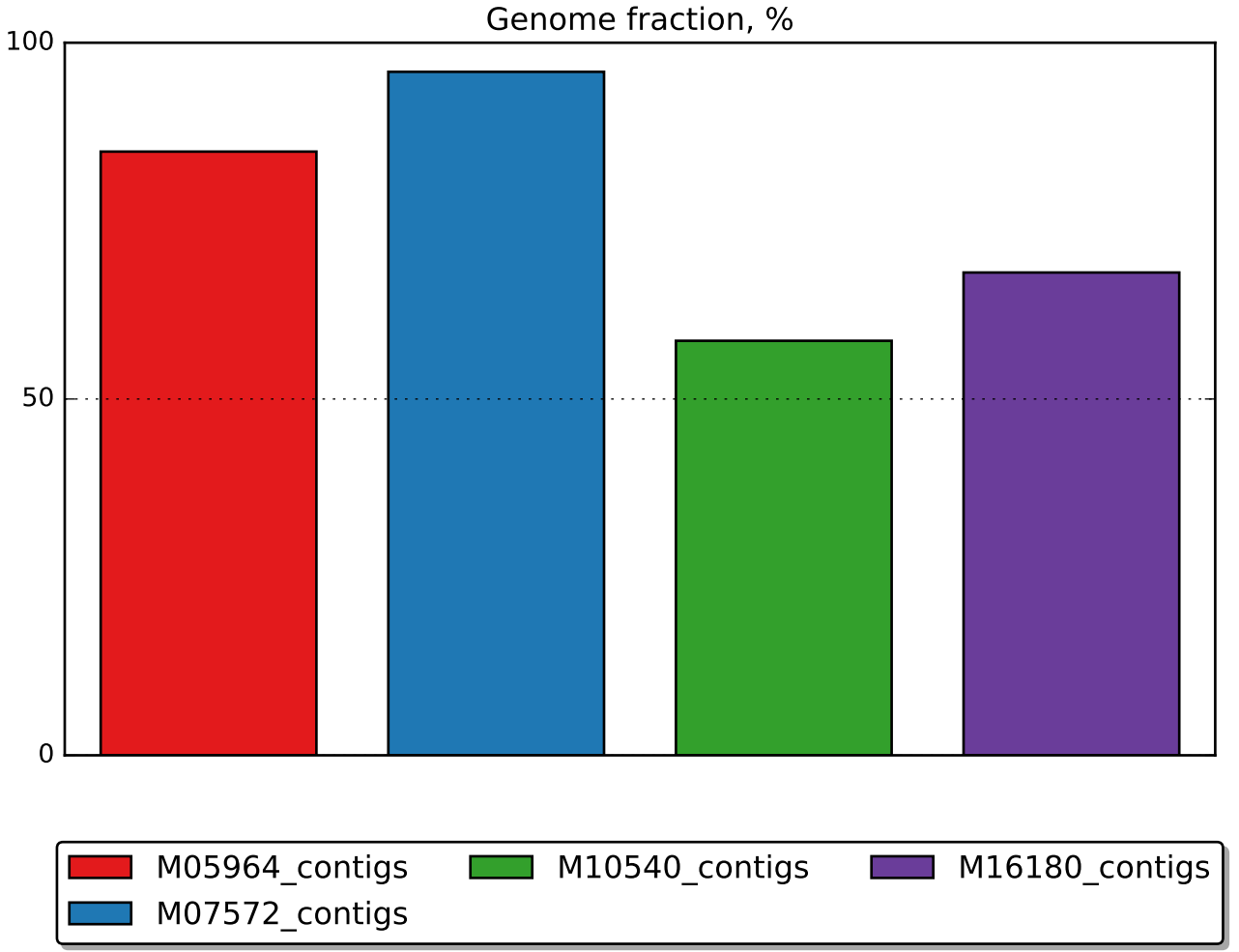

GC content
windows
GC (%)
0
300
600
900
1200
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


Misassemblies
80
60
40
20
0
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
relocations
inversions


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)
250
200
150
100
50
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs


NGAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs


Genome fraction, %
100
50
0
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs