Report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# contigs (>= 0 bp)	1385	1362	372	513
# contigs (>= 1000 bp)	144	163	37	76
# contigs (>= 5000 bp)	13	24	8	17
# contigs (>= 10000 bp)	12	20	8	13
# contigs (>= 25000 bp)	12	16	7	11
# contigs (>= 50000 bp)	9	12	4	10
Total length (>= 0 bp)	2661212	2781649	2014929	2219994
Total length (>= 1000 bp)	1985203	2119498	1846809	2009011
Total length (>= 5000 bp)	1810246	1910923	1802832	1886087
Total length (>= 10000 bp)	1804199	1884981	1802832	1859159
Total length (>= 25000 bp)	1804199	1812728	1792394	1833107
Total length (>= 50000 bp)	1693662	1688852	1700071	1805243
# contigs	762	775	159	211
Largest contig	503758	305777	1150417	398369
Total length	2404236	2538580	1927120	2098123
Reference length	1887620	1887620	1887620	1887620
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.23	38.23	38.23	38.23
N50	120793	120675	1150417	165472
NG50	179983	140698	1150417	291100
N75	28168	5904	311604	100510
NG75	117636	79549	311604	134943
L50	5	7	1	4
LG50	3	5	1	3
L75	12	23	2	8
LG75	6	9	2	6
# misassemblies	40	17	80	28
# misassembled contigs	12	9	8	8
Misassembled contigs length	1777375	890581	1742756	1631751
# local misassemblies	64	36	45	40
# unaligned contigs	714 + 6 part	731 + 6 part	84 + 18 part	144 + 23 part
Unaligned length	569961	634087	111323	215638
Genome fraction (%)	84.226	94.043	61.095	88.717
Duplication ratio	1.154	1.073	1.575	1.124
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2341.96	1198.54	3508.55	1853.42
# indels per 100 kbp	63.02	31.15	82.03	51.12
Largest alignment	202939	283582	61112	221430
NA50	28168	61015	8526	62249
NGA50	41226	110255	8787	92095
NA75	-	-	-	13834
NGA75	16715	52197	-	27864
LA50	19	11	42	9
LGA50	12	6	40	8
LA75	-	-	-	26
LGA75	29	13	-	18

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

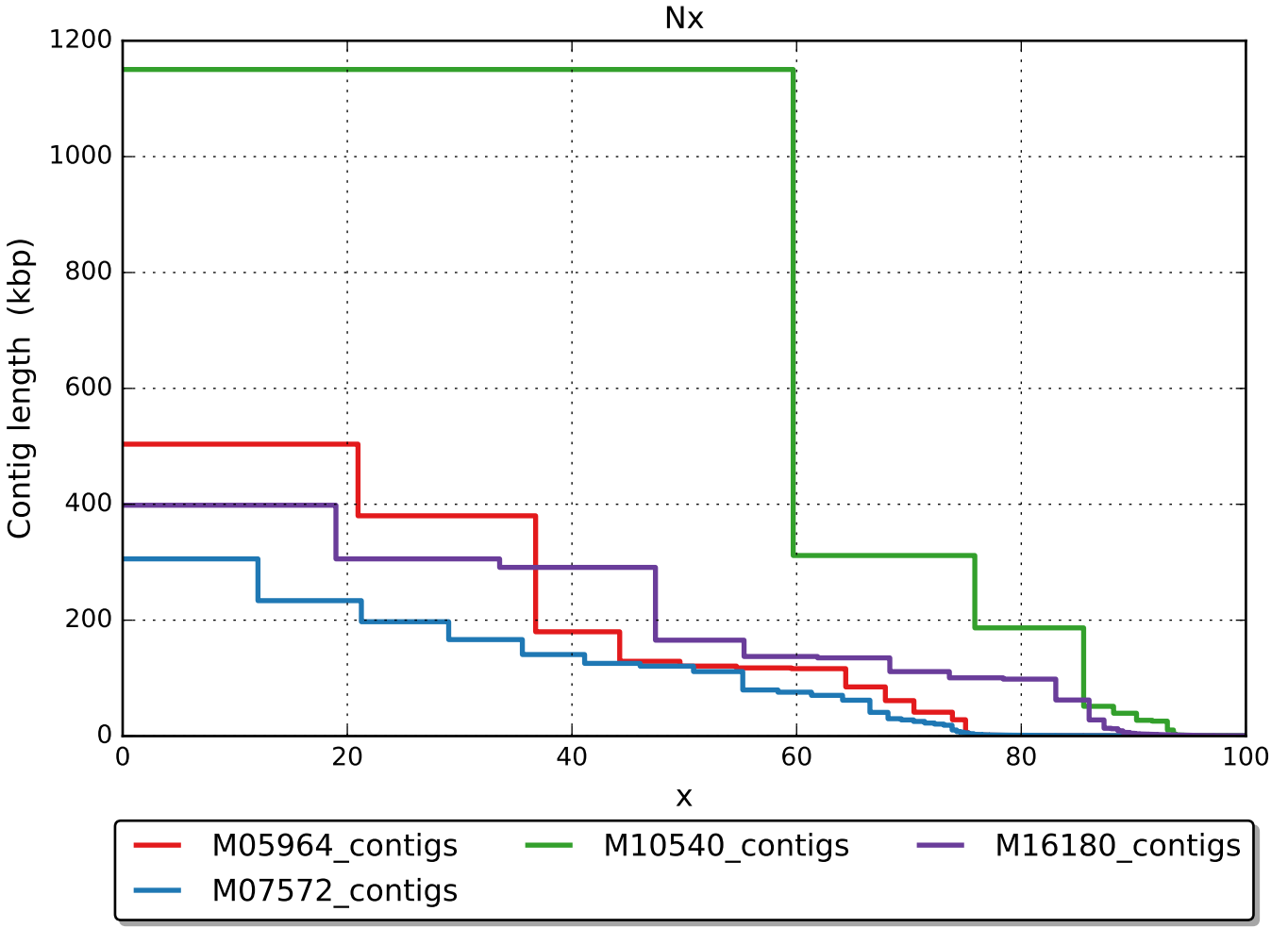
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	40	17	80	28
# relocations	39	17	79	28
# translocations	0	0	0	0
# inversions	1	0	1	0
# misassembled contigs	12	9	8	8
Misassembled contigs length	1777375	890581	1742756	1631751
# local misassemblies	64	36	45	40
# mismatches	37234	21276	40462	31038
# indels	1002	553	946	856
# short indels	895	479	846	764
# long indels	107	74	100	92
Indels length	2973	2029	2477	2491

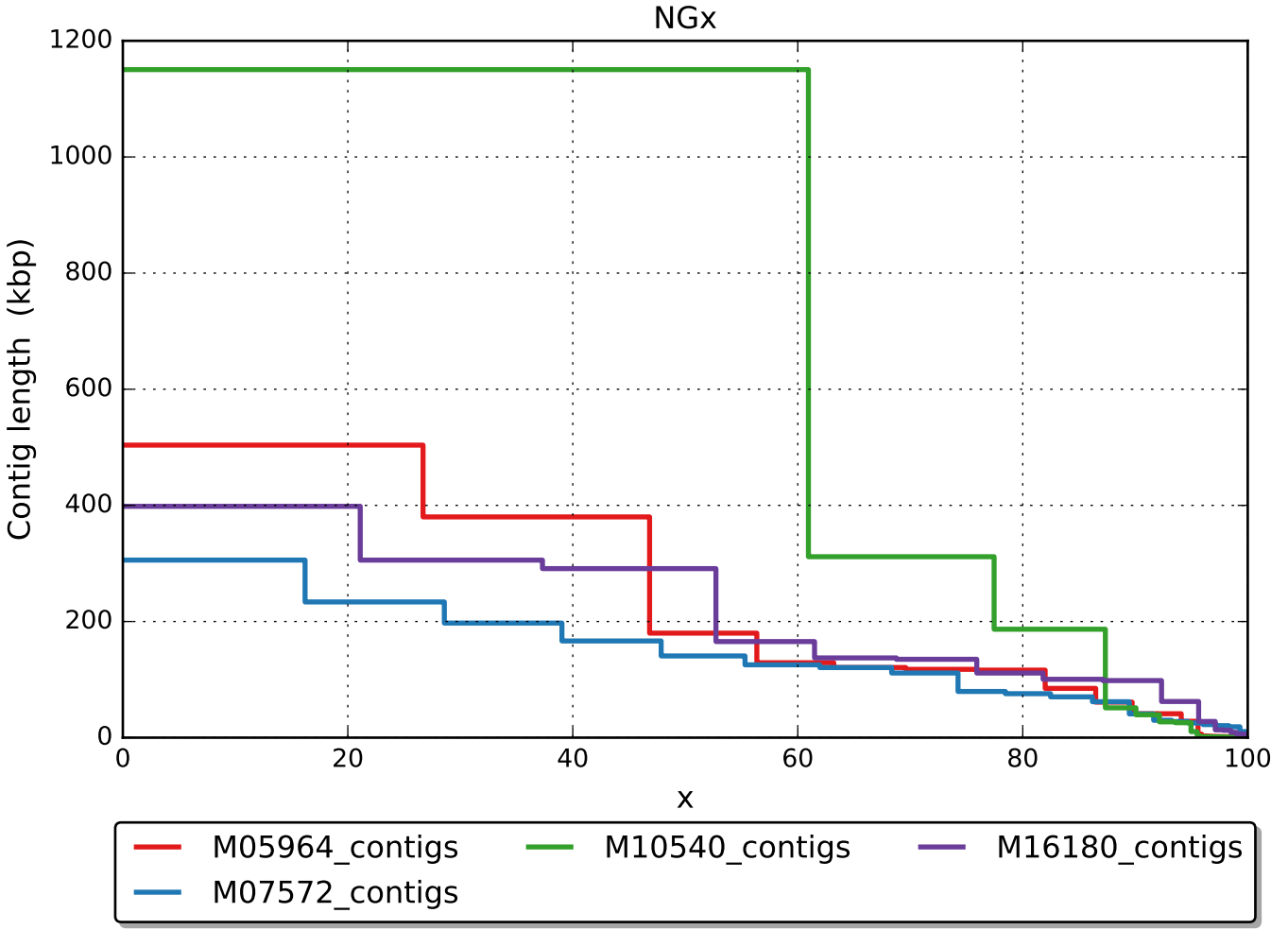
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

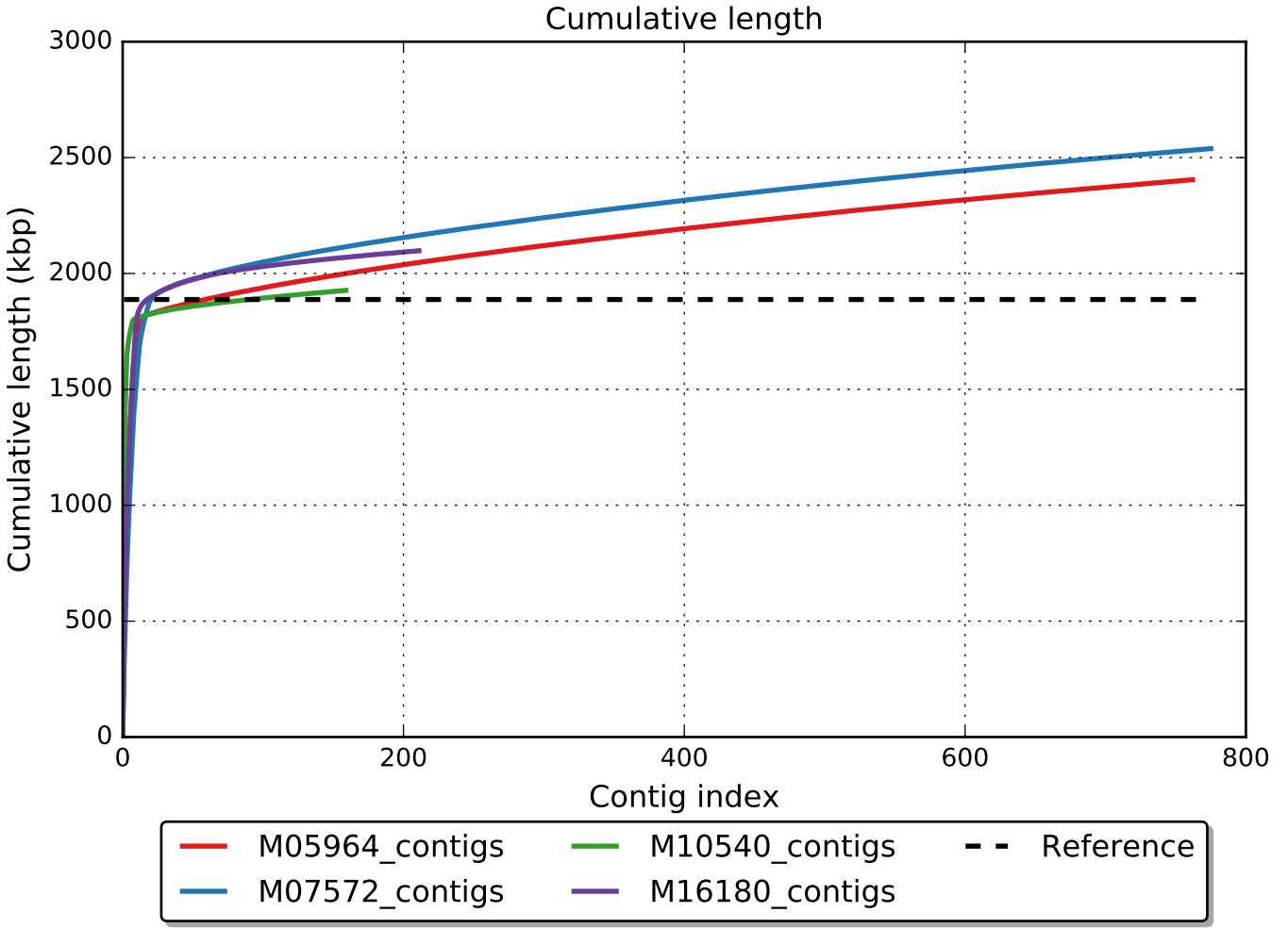
Unaligned report

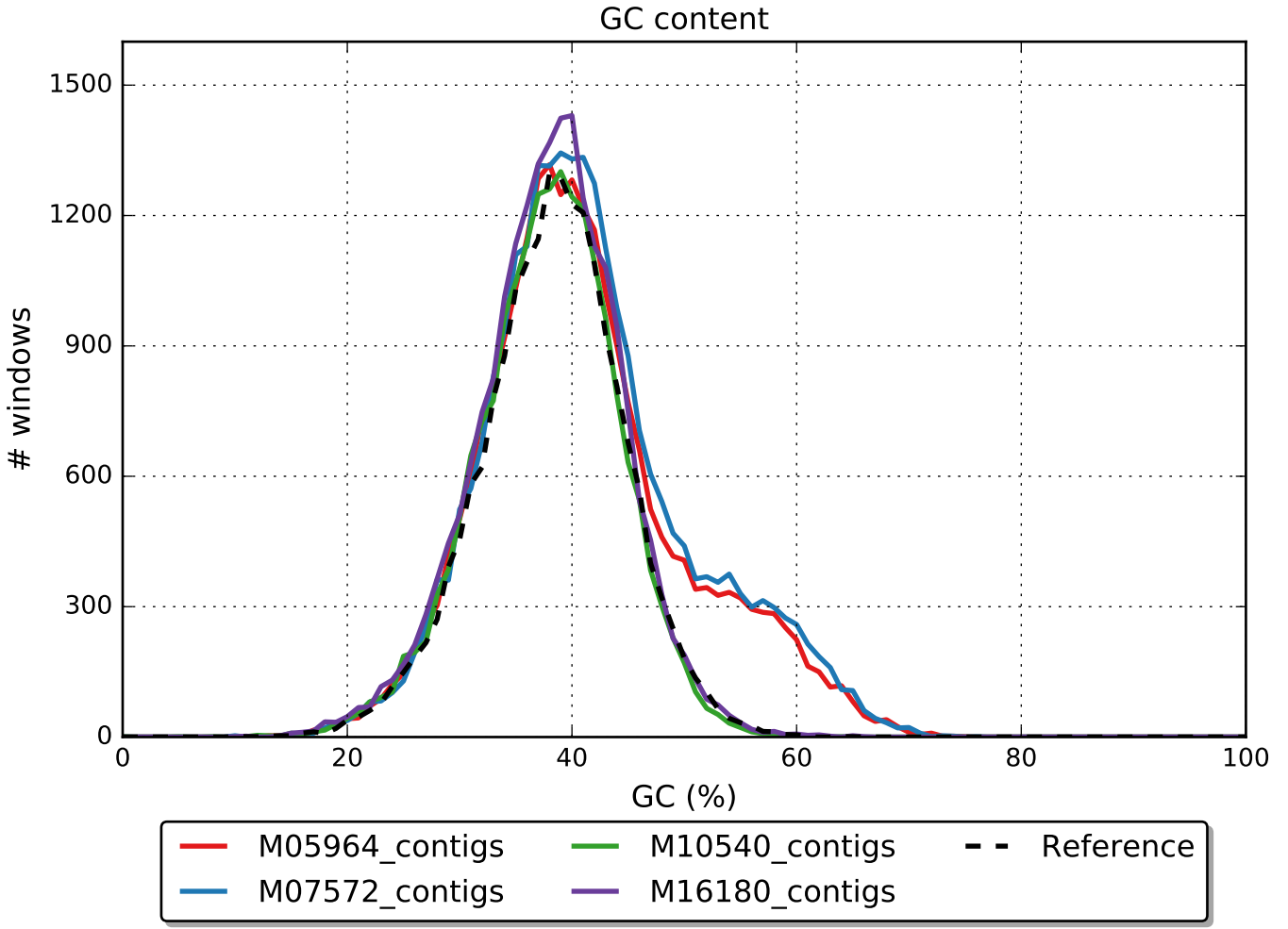
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	714	731	84	144
Fully unaligned length	563645	599495	68696	181542
# partially unaligned contigs	6	6	18	23
# with misassembly	0	1	4	2
# both parts are significant	1	2	2	2
Partially unaligned length	6316	34592	42627	34096
# N's	0	0	0	0

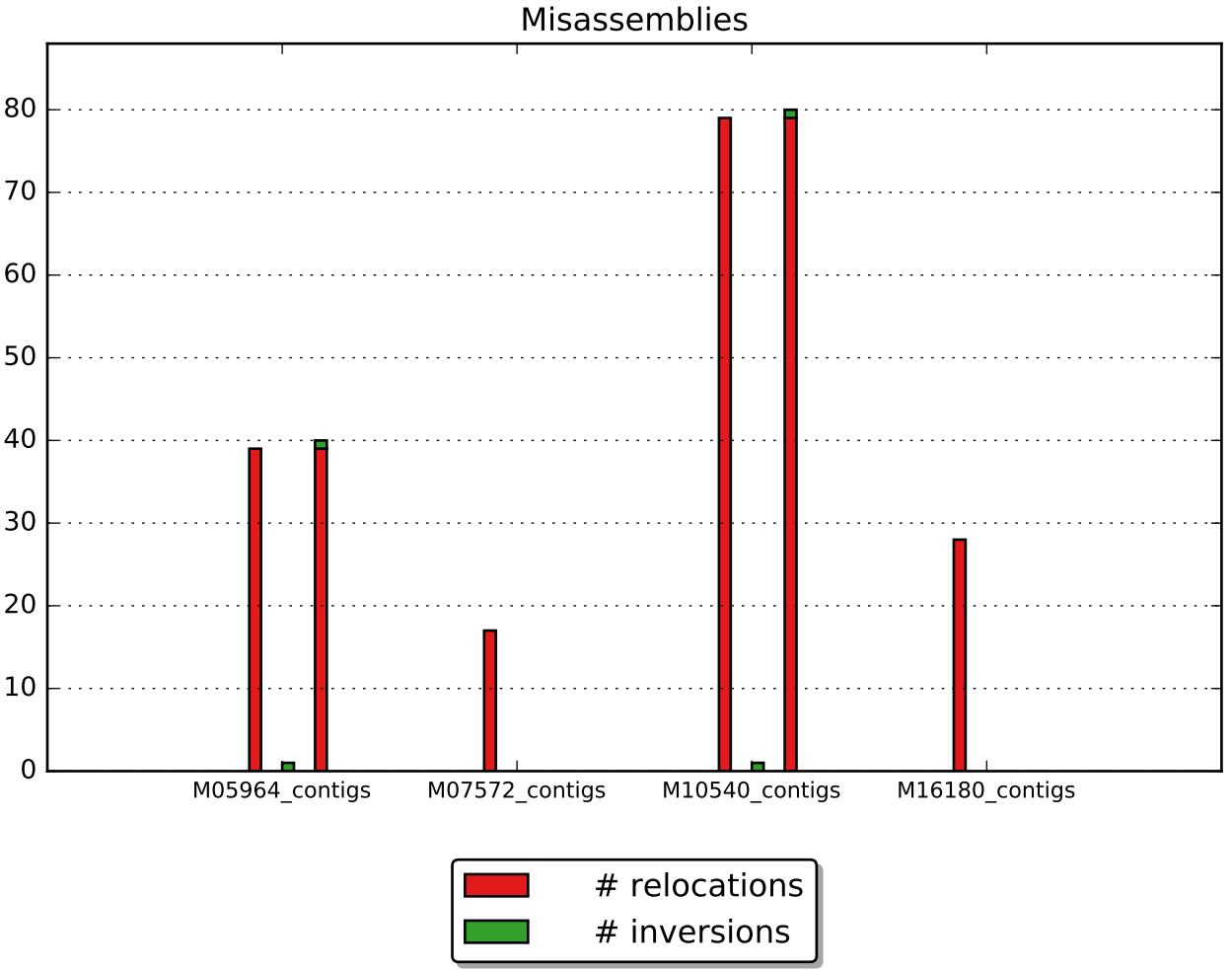
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

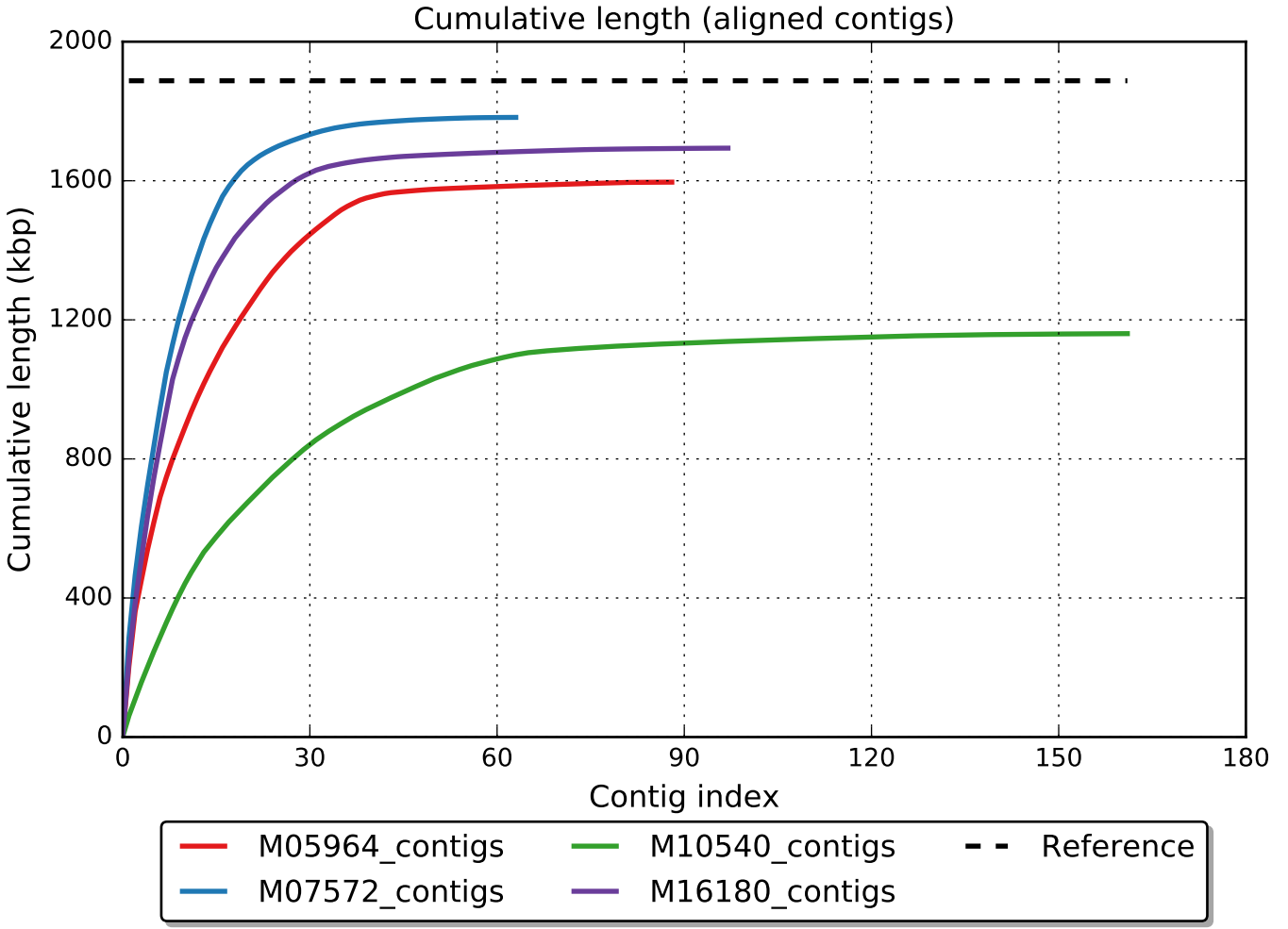

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

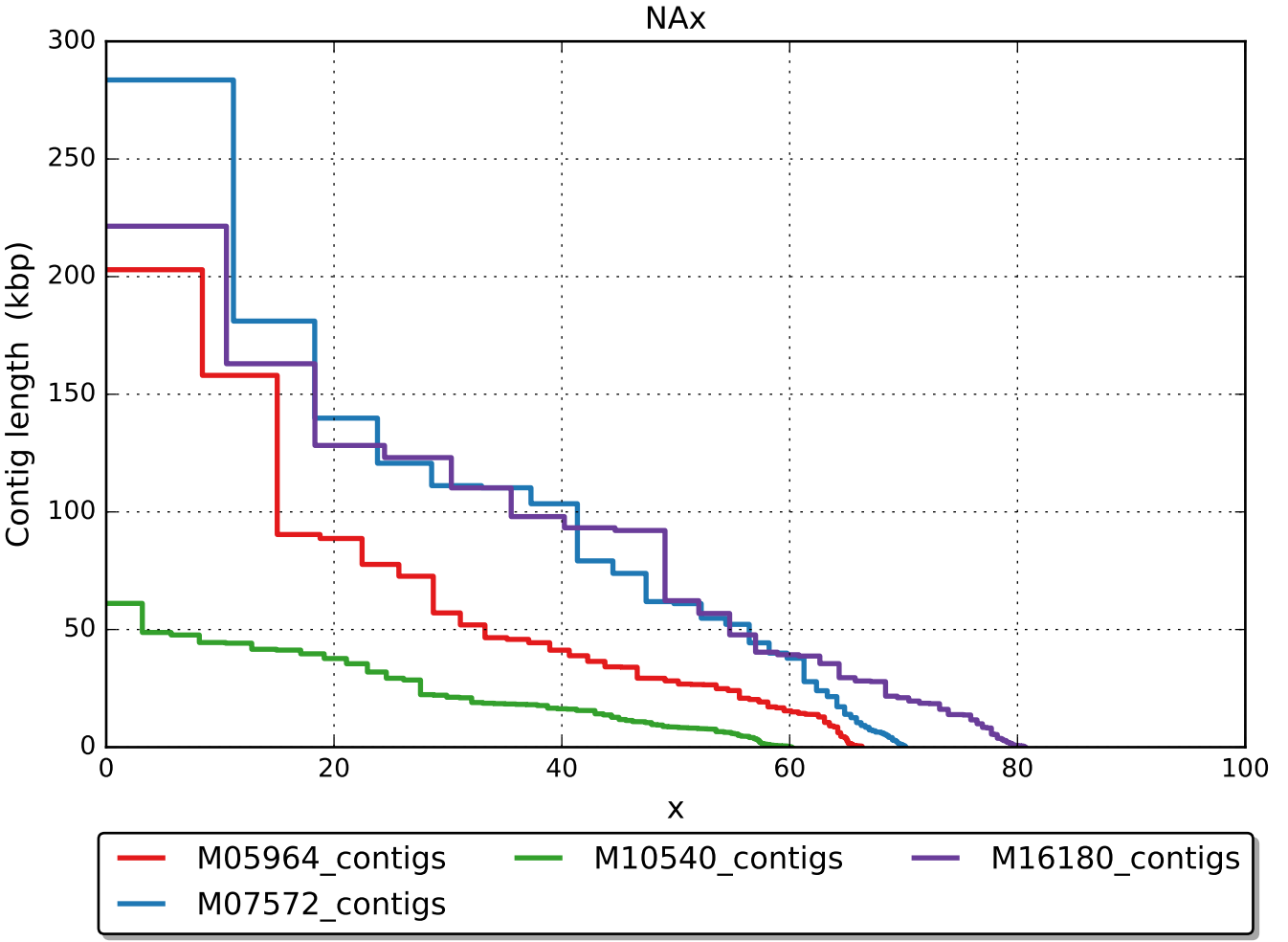

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

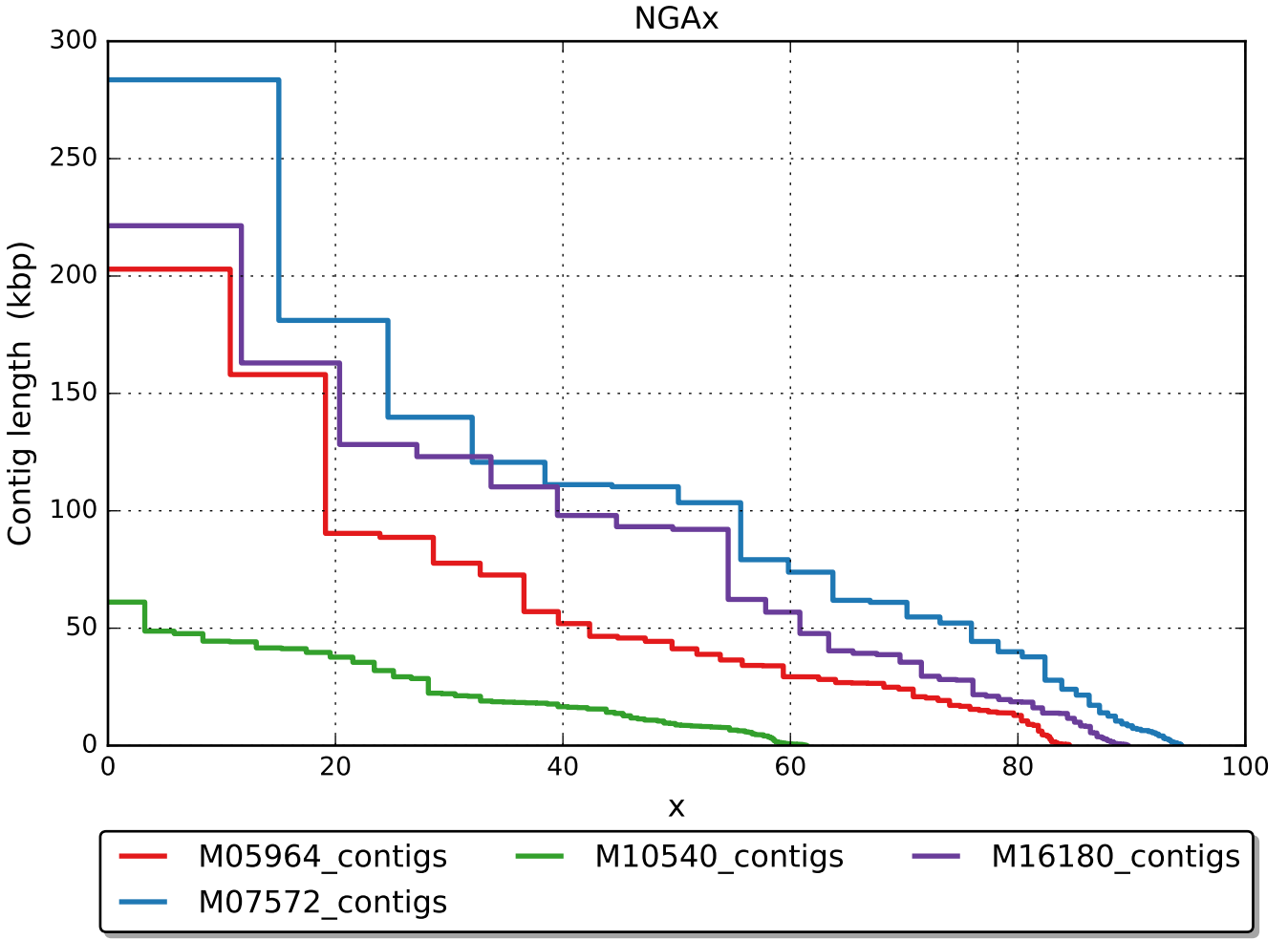

Cumulative length
Cumulative length (kbp)
Contig index
0
500
1000
1500
2000
2500
3000
0
200
400
600
800
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

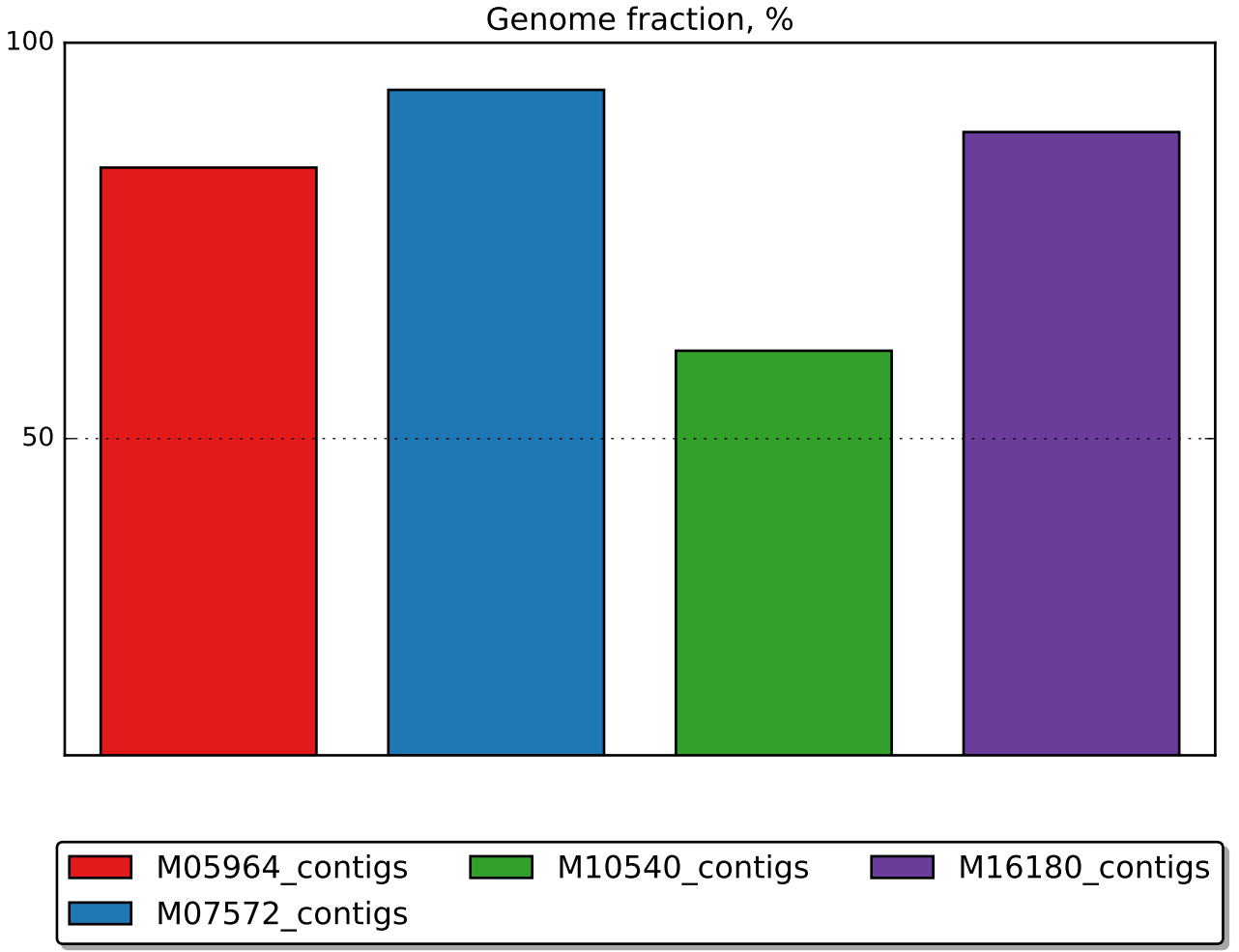

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


Misassemblies
80
70
60
50
40
30
20
10
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
30
60
90
120
150
180
Contig index
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


NAx
Contig length (kbp)
300
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)
300
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
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs