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	1914490	1914490	1914490	1914490
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.16	38.16	38.16	38.16
N50	120793	120675	1150417	165472
NG50	179983	140698	1150417	291100
N75	28168	5904	311604	100510
NG75	116324	79549	311604	111243
L50	5	7	1	4
LG50	3	5	1	3
L75	12	23	2	8
LG75	7	9	2	7
# misassemblies	40	18	83	28
# misassembled contigs	12	11	7	7
Misassembled contigs length	1777375	1166436	1741781	1494429
# local misassemblies	66	26	42	45
# unaligned contigs	719 + 4 part	739 + 5 part	83 + 18 part	155 + 19 part
Unaligned length	572290	681958	120185	226510
Genome fraction (%)	85.207	89.918	56.454	88.626
Duplication ratio	1.123	1.079	1.672	1.103
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2130.67	1124.85	3459.63	1667.09
# indels per 100 kbp	57.99	35.84	82.99	46.32
Largest alignment	157990	222814	64661	269379
NA50	33976	53711	6313	93858
NGA50	45816	111326	6591	103594
NA75	-	-	-	17976
NGA75	19190	44262	-	28137
LA50	18	11	51	7
LGA50	12	6	50	6
LA75	-	-	-	23
LGA75	27	14	-	16

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

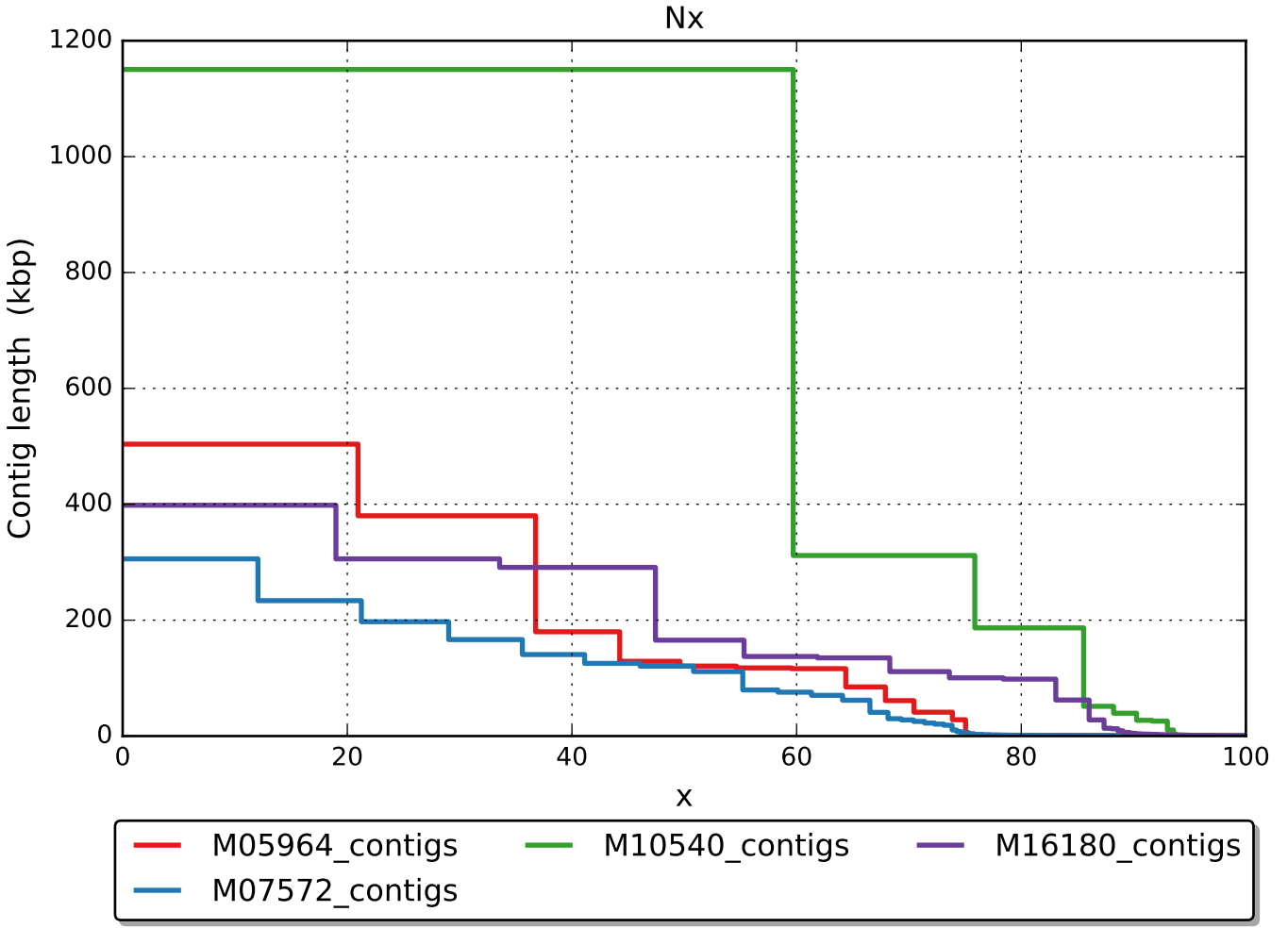
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	40	18	83	28
# relocations	40	18	81	28
# translocations	0	0	0	0
# inversions	0	0	2	0
# misassembled contigs	12	11	7	7
Misassembled contigs length	1777375	1166436	1741781	1494429
# local misassemblies	66	26	42	45
# mismatches	34757	19364	37392	28286
# indels	946	617	897	786
# short indels	828	543	816	694
# long indels	118	74	81	92
Indels length	3162	2300	2208	2392

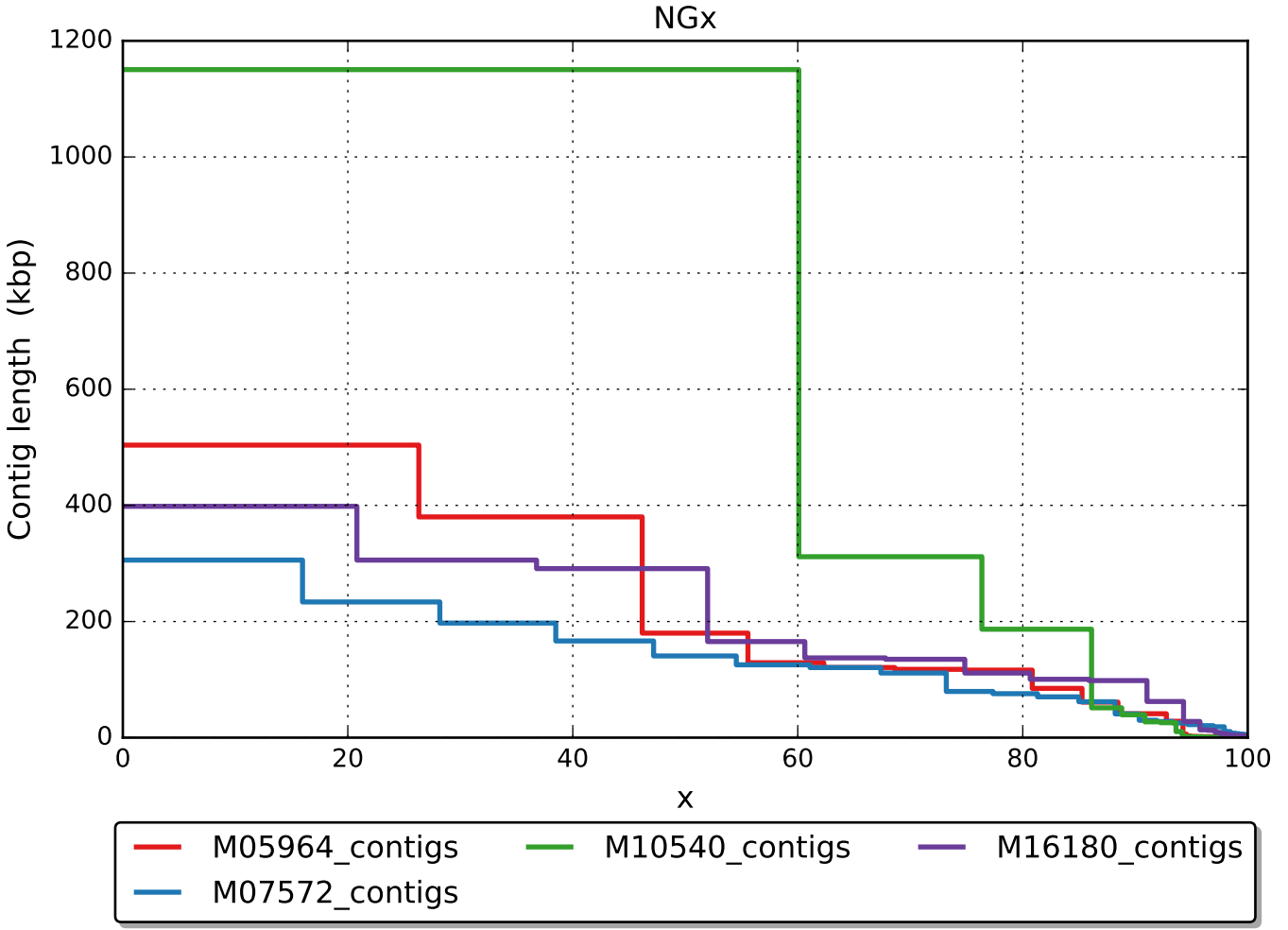
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

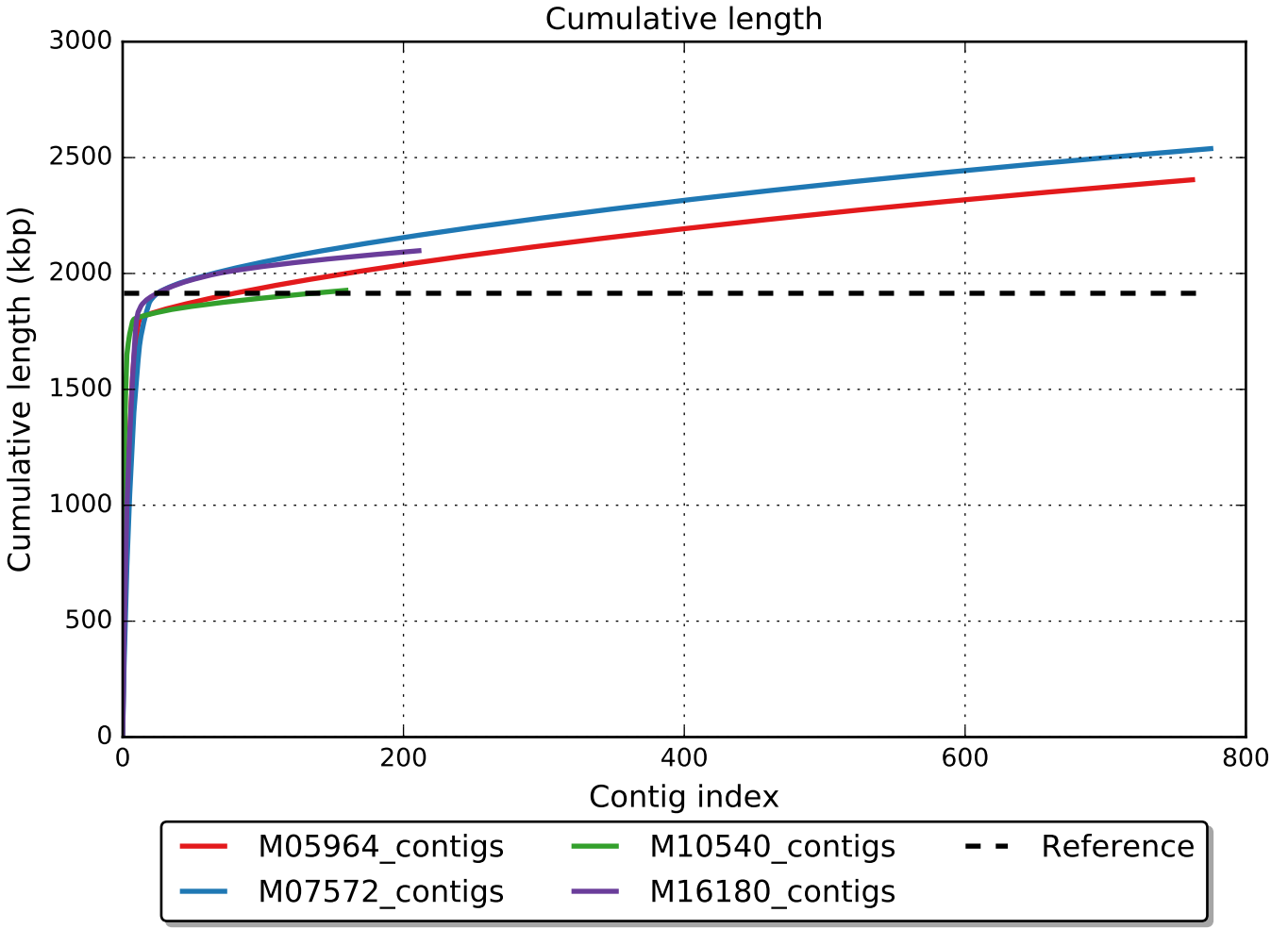
Unaligned report

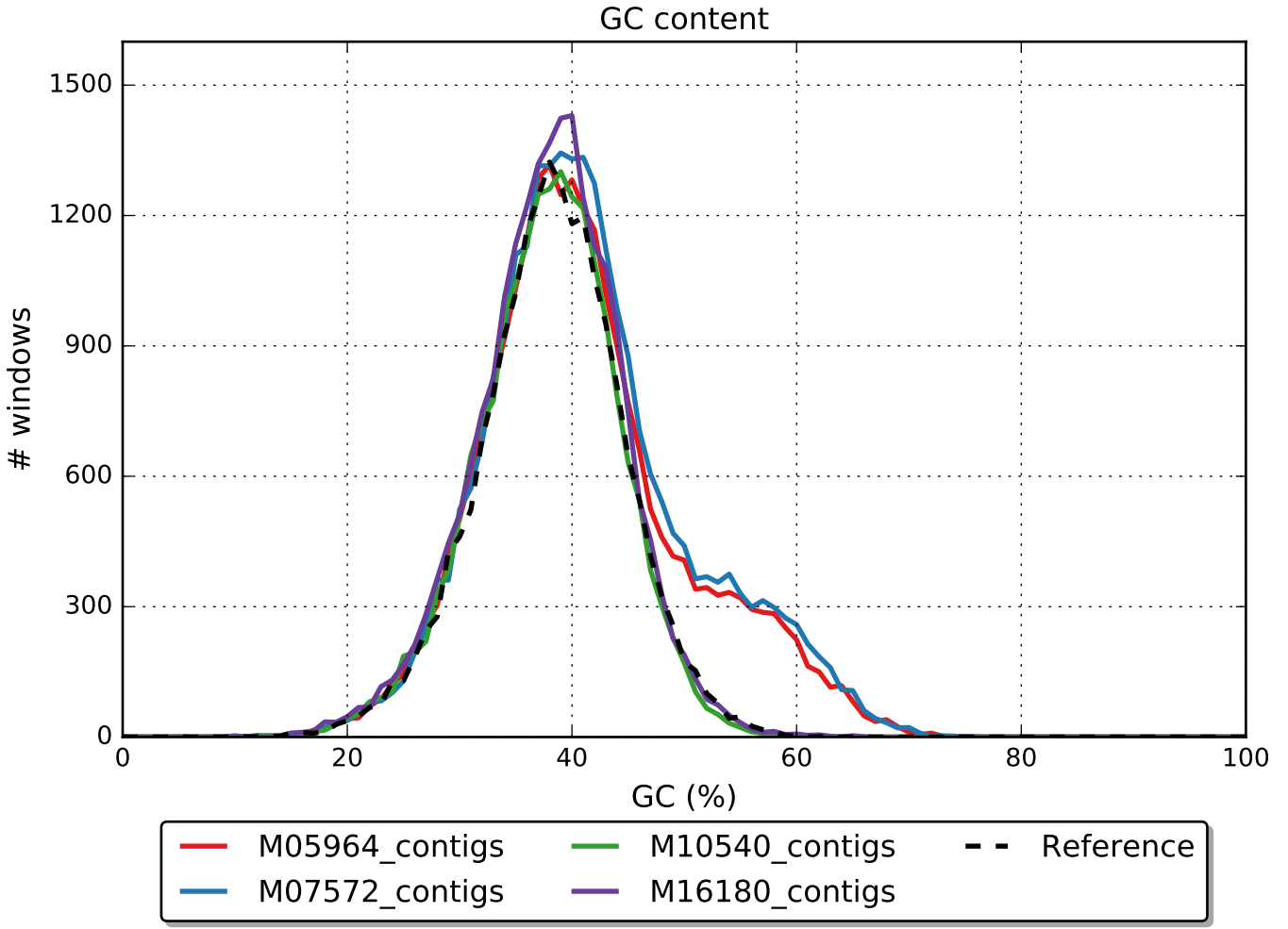
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	719	739	83	155
Fully unaligned length	569397	636339	67236	192541
# partially unaligned contigs	4	5	18	19
# with misassembly	0	1	4	2
# both parts are significant	1	2	2	2
Partially unaligned length	2893	45619	52949	33969
# N's	0	0	0	0

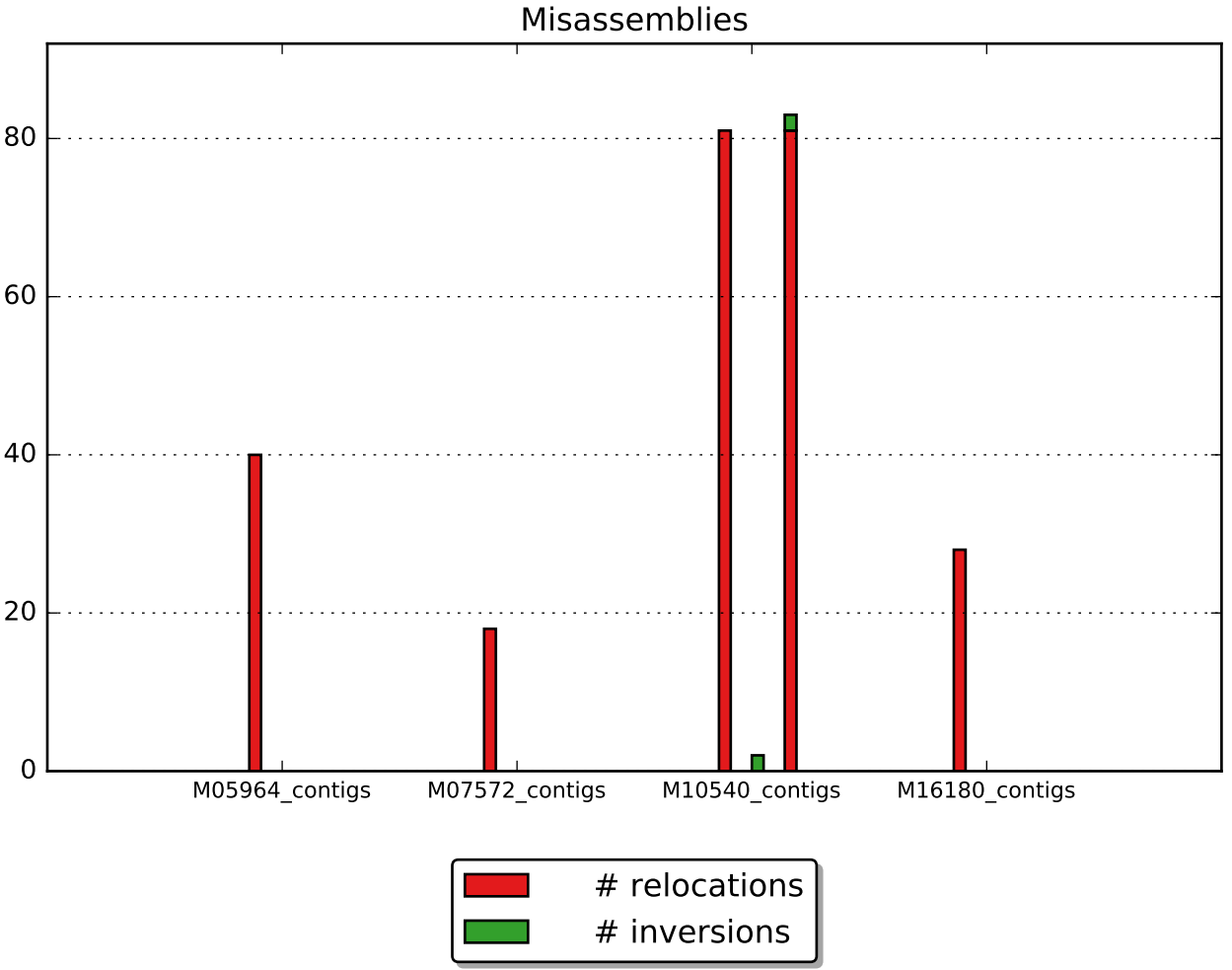
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

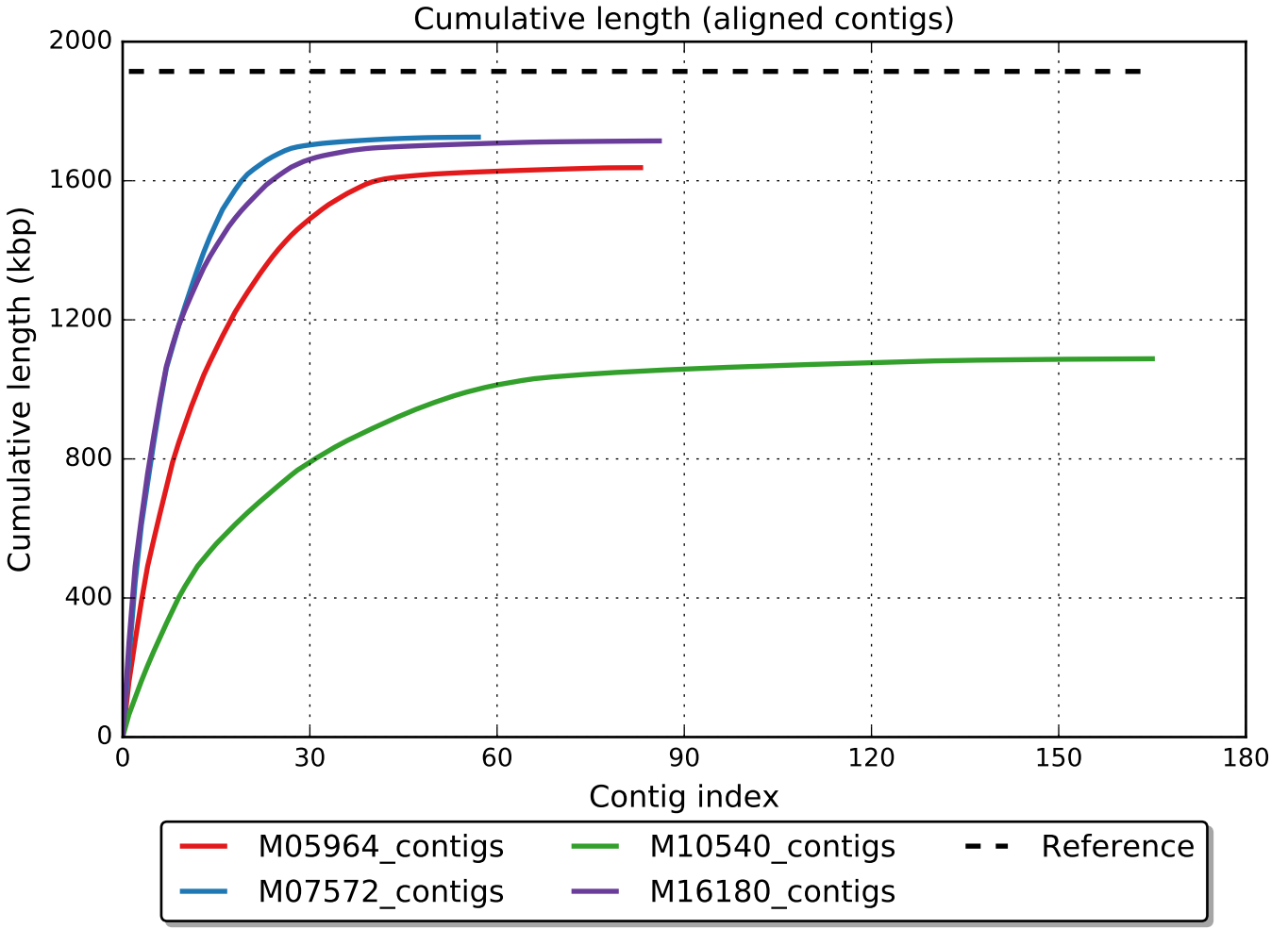

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

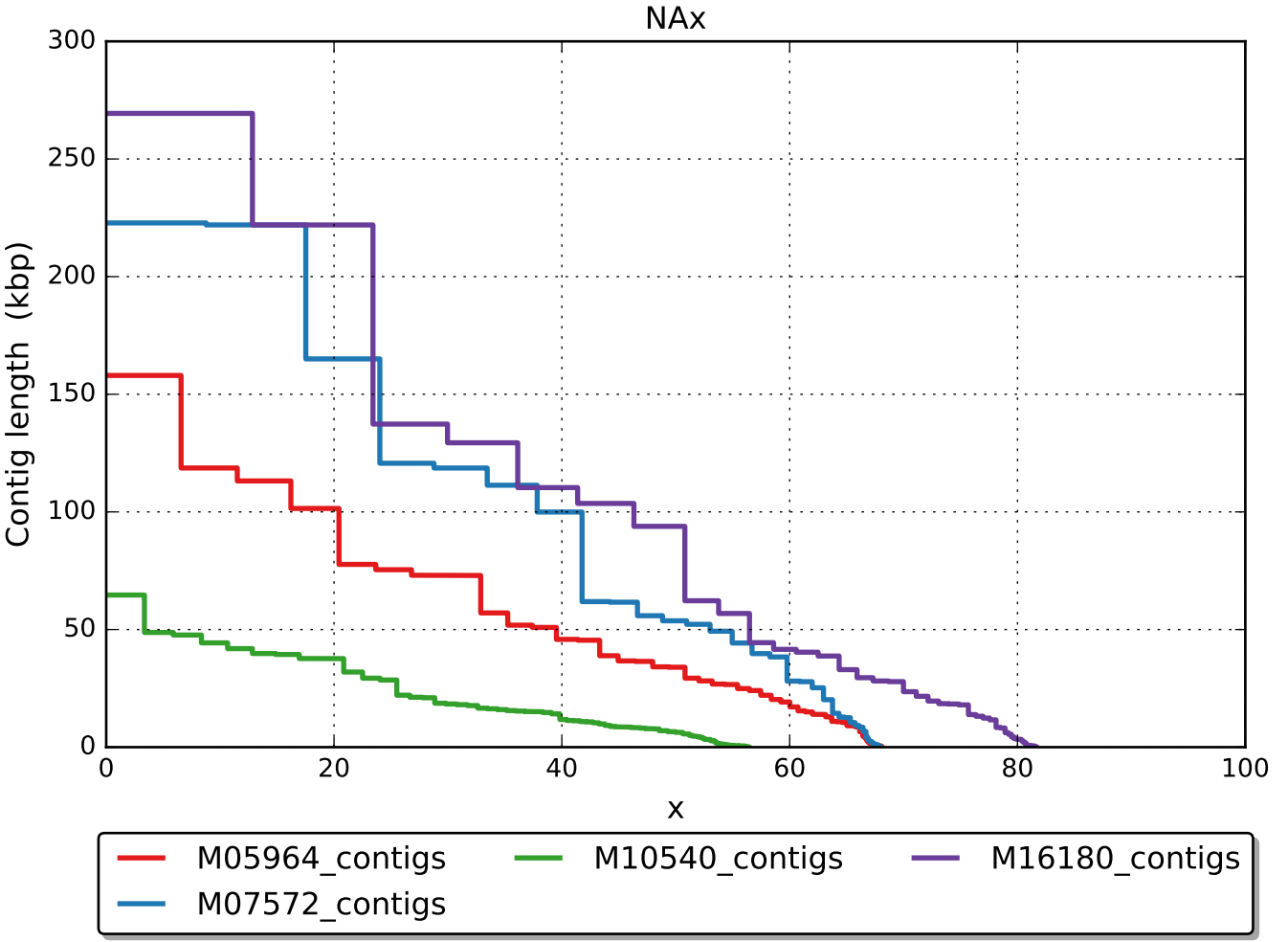

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

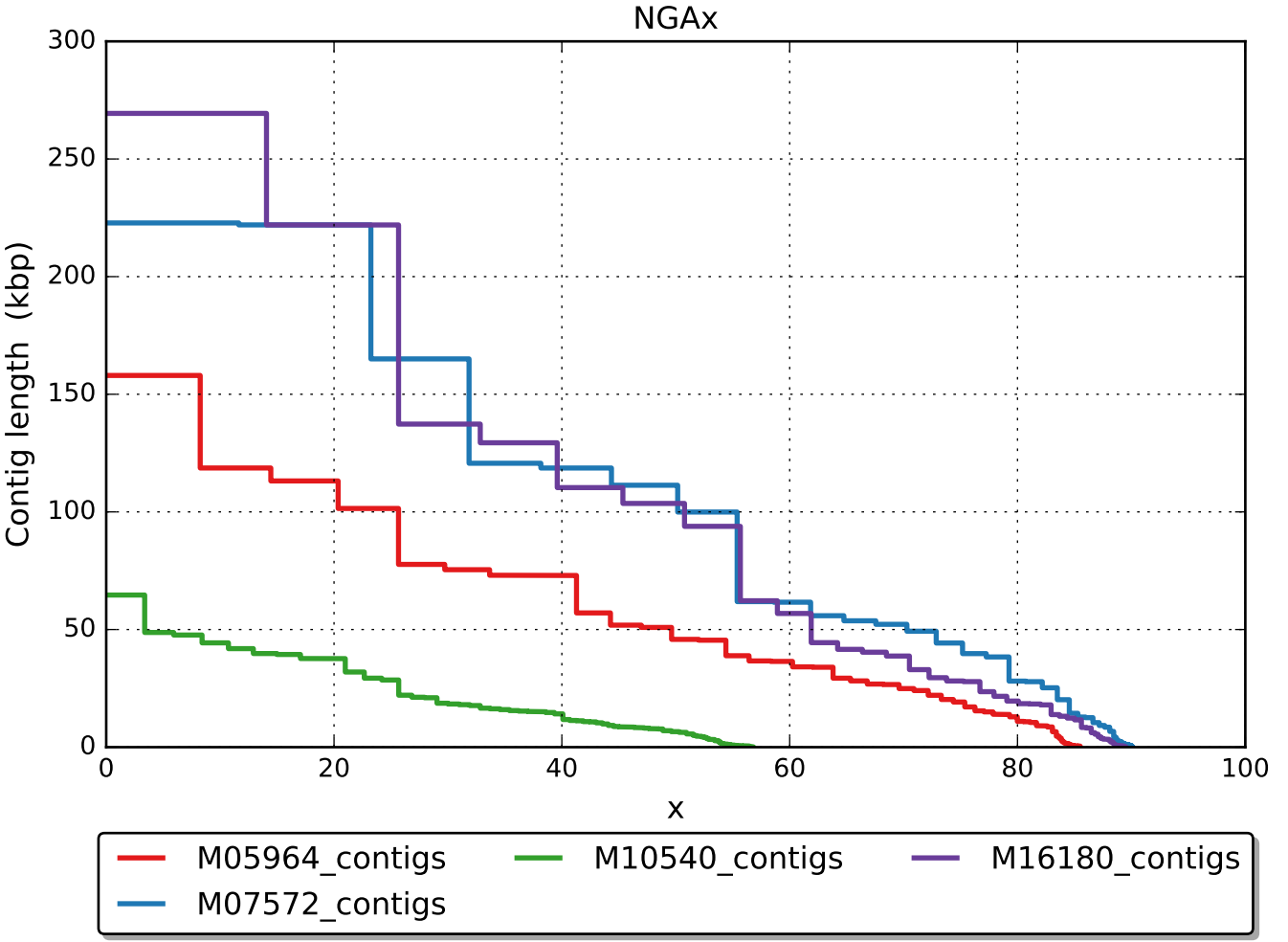

Cumulative length
Cumulative length (kbp)
Contig index
0
500
1000
1500
2000
2500
3000
0
200
400
600
800
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

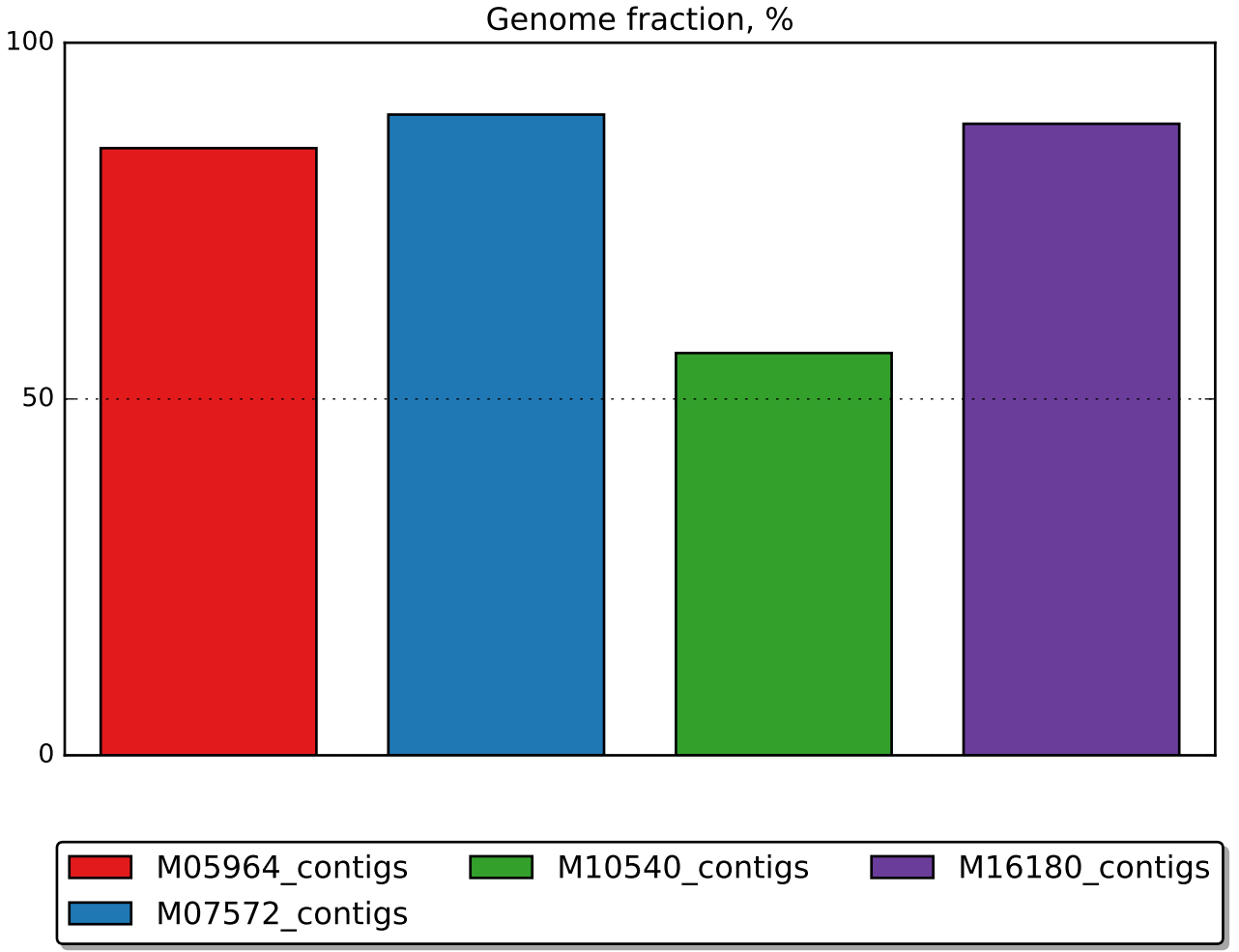

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


Misassemblies
80
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
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
0
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs