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	1981535	1981535	1981535	1981535
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.14	38.14	38.14	38.14
N50	120793	120675	1150417	165472
NG50	179983	140698	1150417	291100
N75	28168	5904	311604	100510
NG75	116324	75725	186707	111243
L50	5	7	1	4
LG50	3	5	1	3
L75	12	23	2	8
LG75	7	10	3	7
# misassemblies	58	54	55	55
# misassembled contigs	11	15	4	11
Misassembled contigs length	1736208	1784888	1216269	1809056
# local misassemblies	64	54	27	65
# unaligned contigs	734 + 5 part	730 + 15 part	59 + 21 part	93 + 7 part
Unaligned length	586525	684615	348754	84577
Genome fraction (%)	81.445	81.591	53.110	87.520
Duplication ratio	1.126	1.147	1.500	1.161
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2374.56	2348.41	3595.15	2094.87
# indels per 100 kbp	64.44	63.89	84.09	55.99
Largest alignment	122175	111187	67998	149445
NA50	28168	21824	3233	30733
NGA50	35879	35717	1412	36363
NA75	-	-	-	6684
NGA75	9444	9217	-	12405
LA50	22	27	63	18
LGA50	16	17	76	16
LA75	-	-	-	49
LGA75	38	43	-	39

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

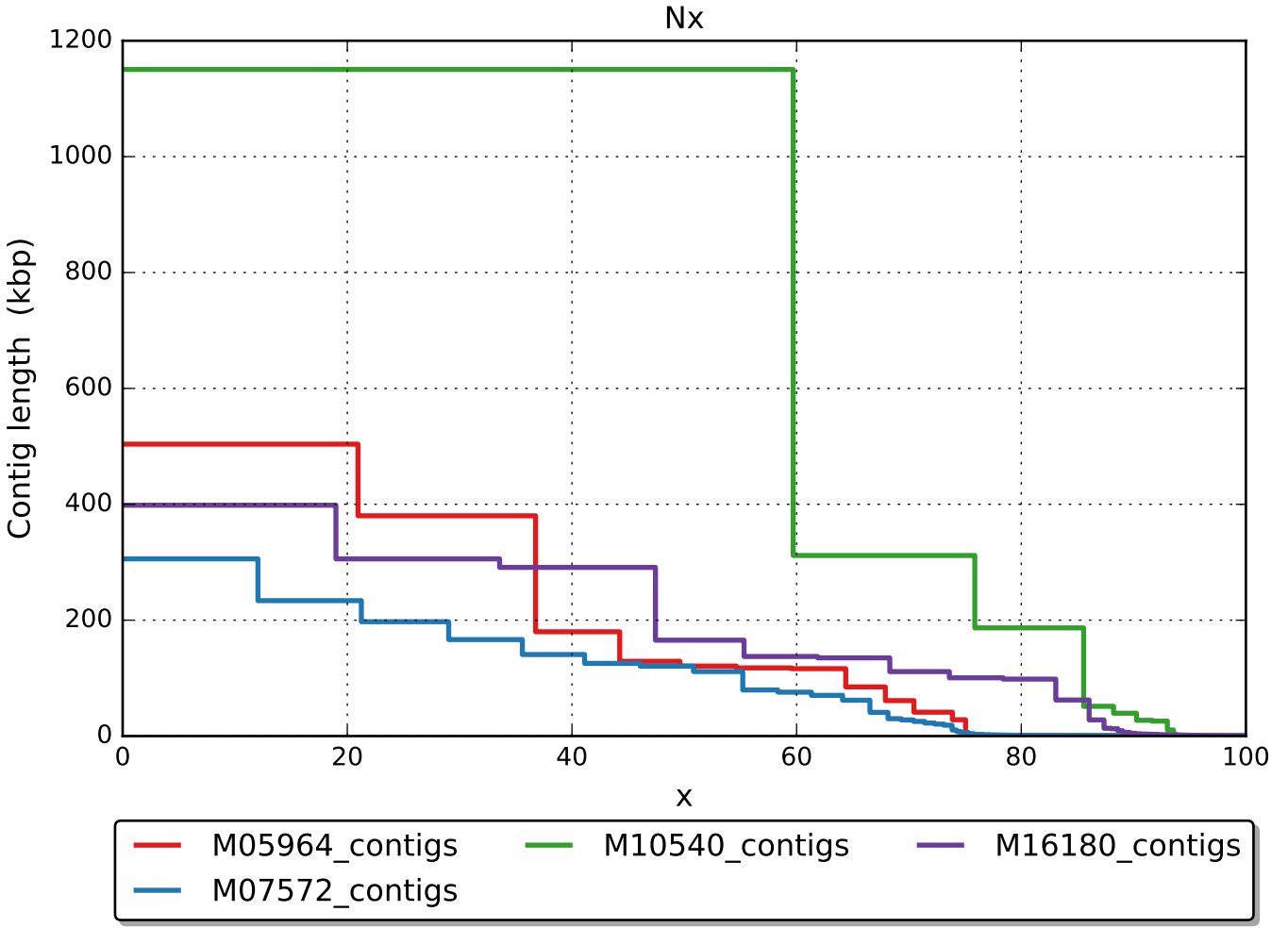
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	58	54	55	55
# relocations	58	54	55	55
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	11	15	4	11
Misassembled contigs length	1736208	1784888	1216269	1809056
# local misassemblies	64	54	27	65
# mismatches	38322	37968	37835	36330
# indels	1040	1033	885	971
# short indels	914	912	814	853
# long indels	126	121	71	118
Indels length	3377	3370	2099	3394

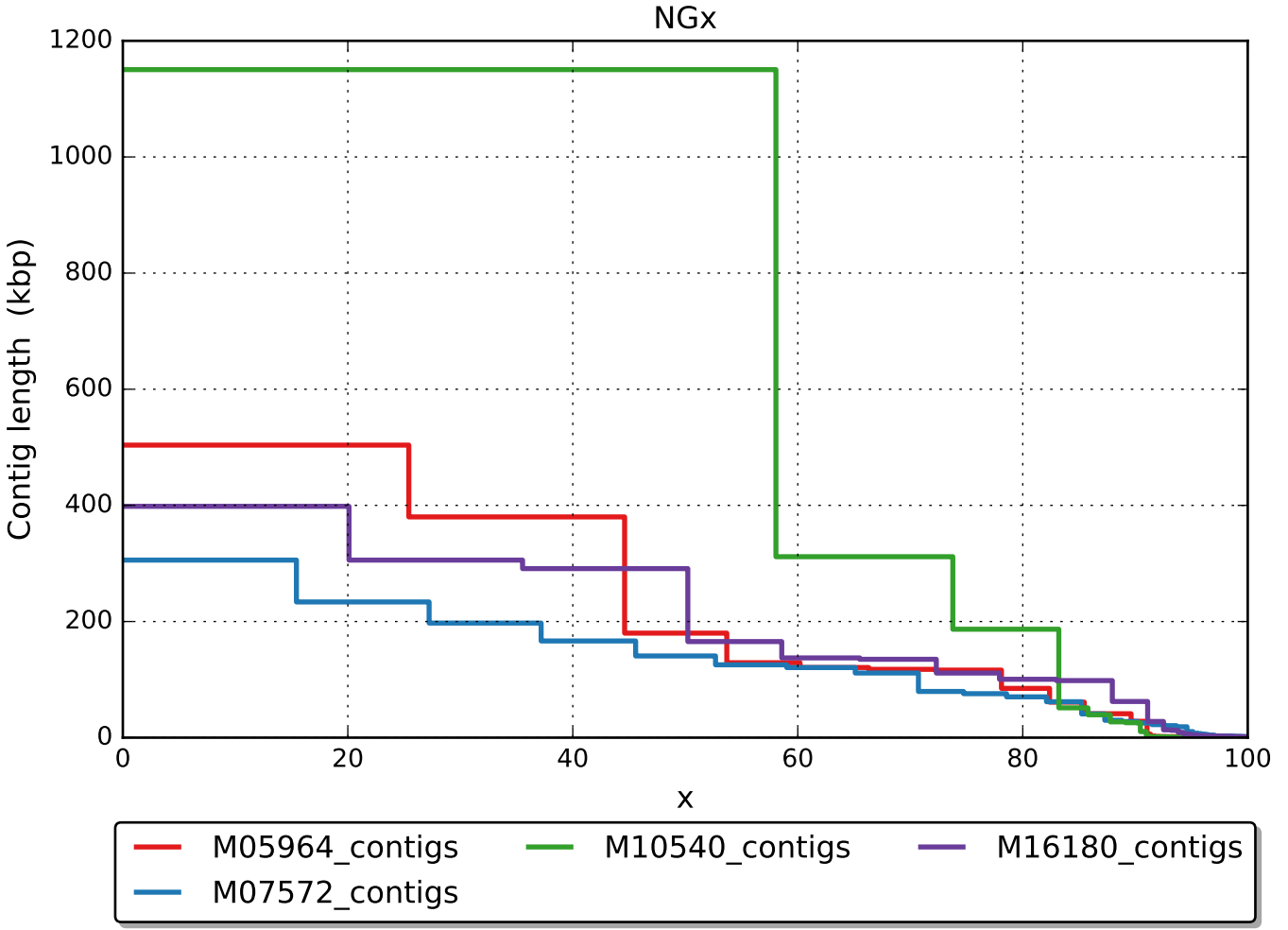
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

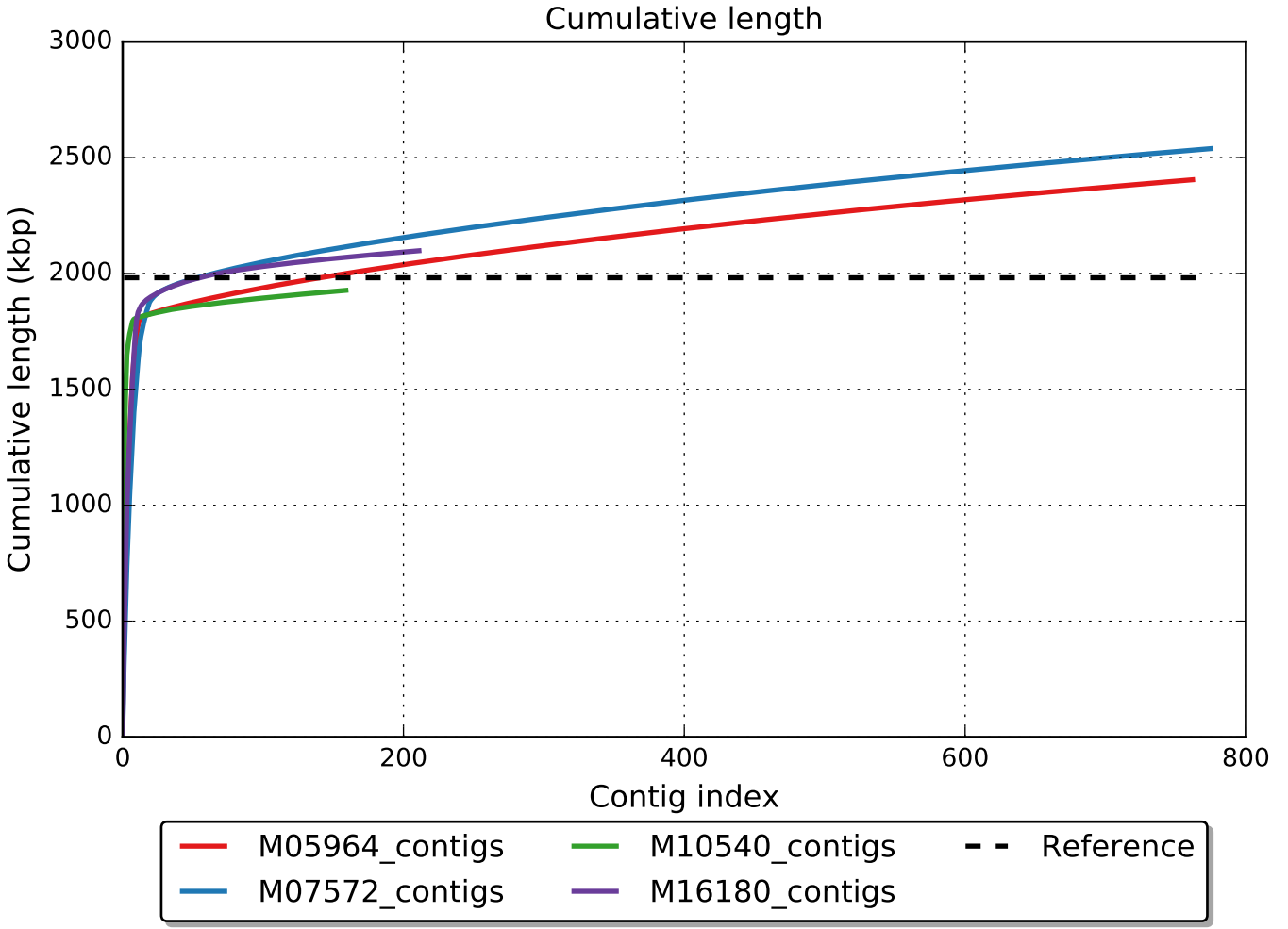
Unaligned report

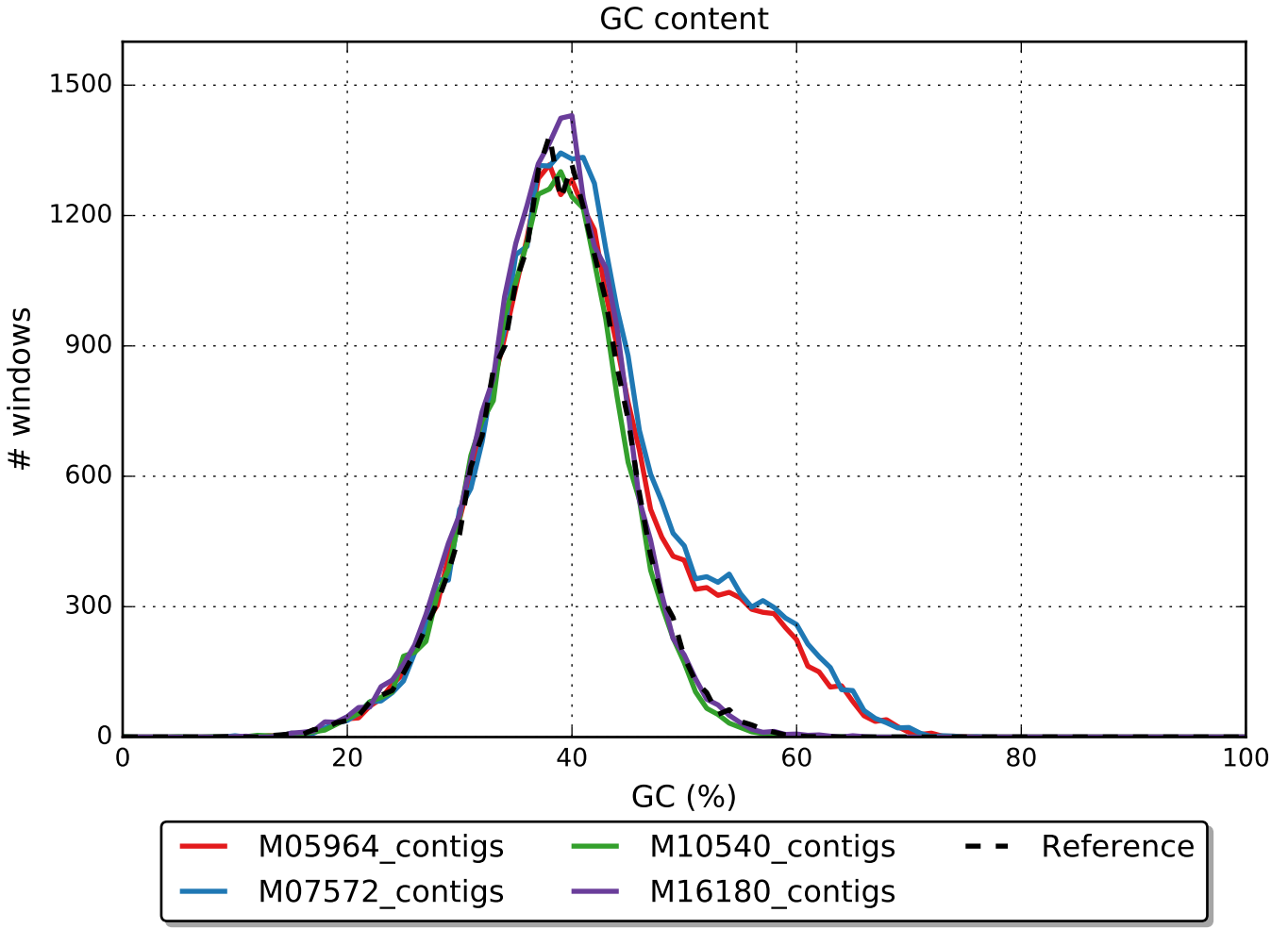
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	734	730	59	93
Fully unaligned length	585811	648504	46334	80591
# partially unaligned contigs	5	15	21	7
# with misassembly	0	4	6	1
# both parts are significant	0	6	4	2
Partially unaligned length	714	36111	302420	3986
# N's	0	0	0	0

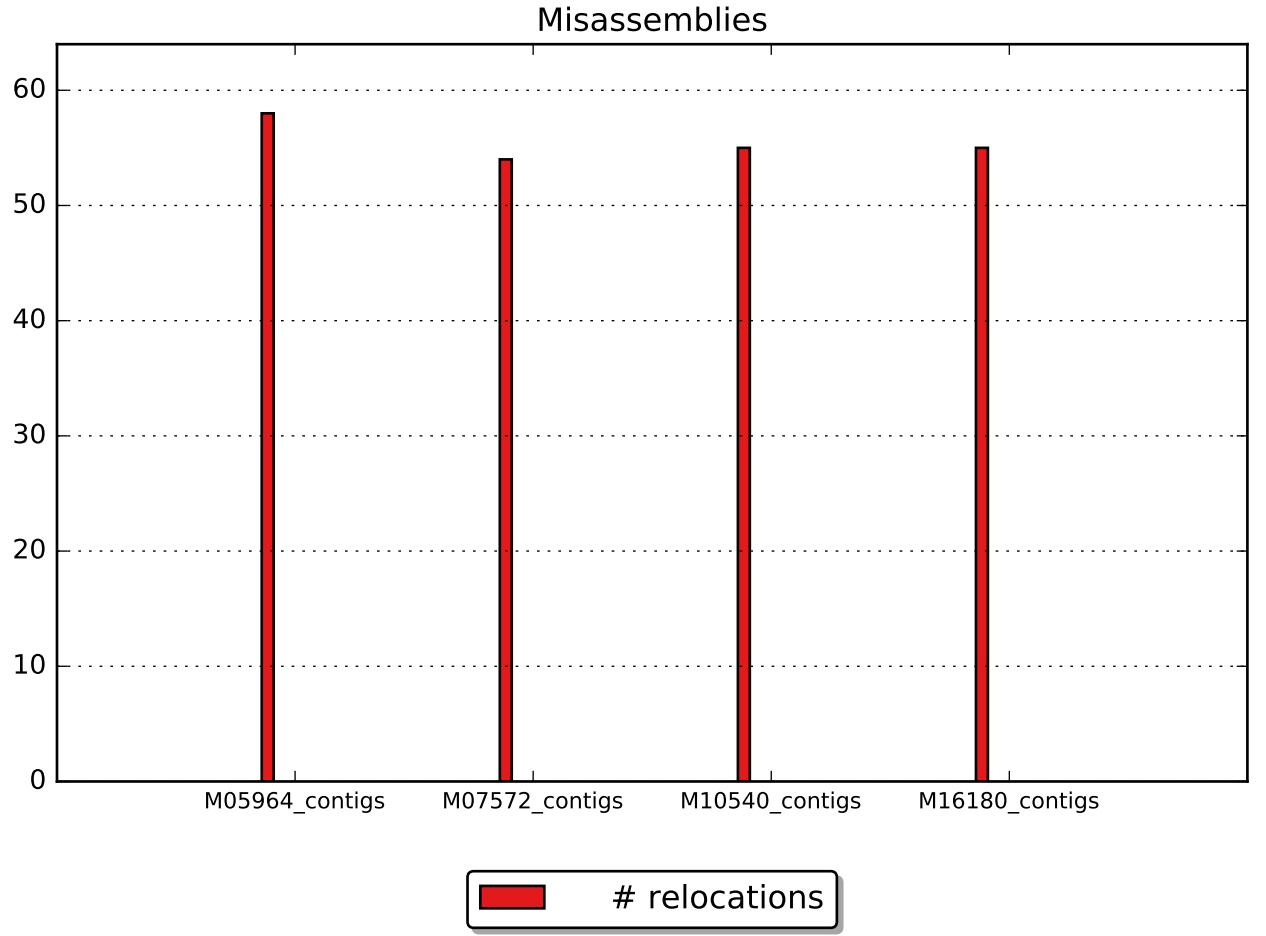
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

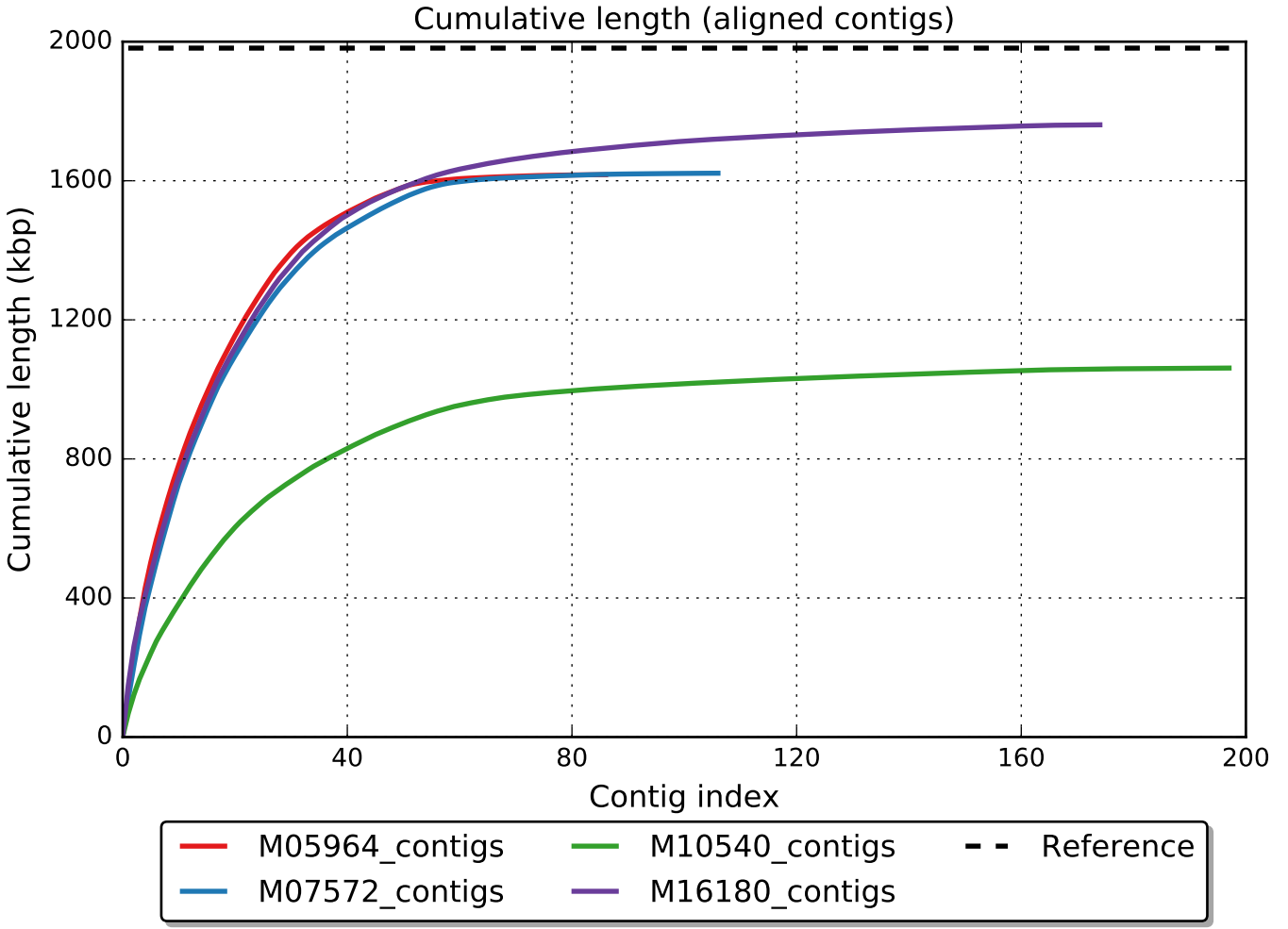

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

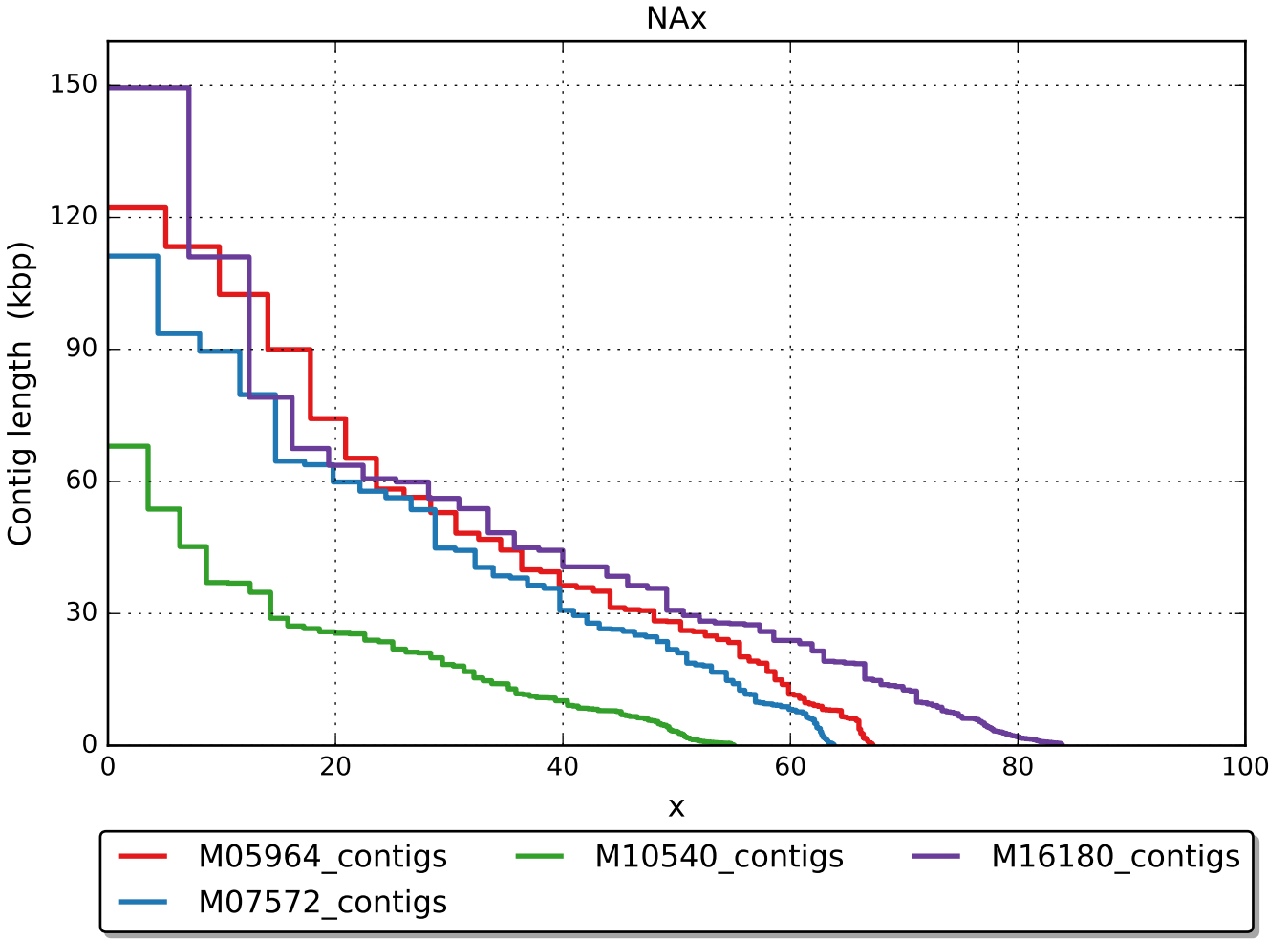

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

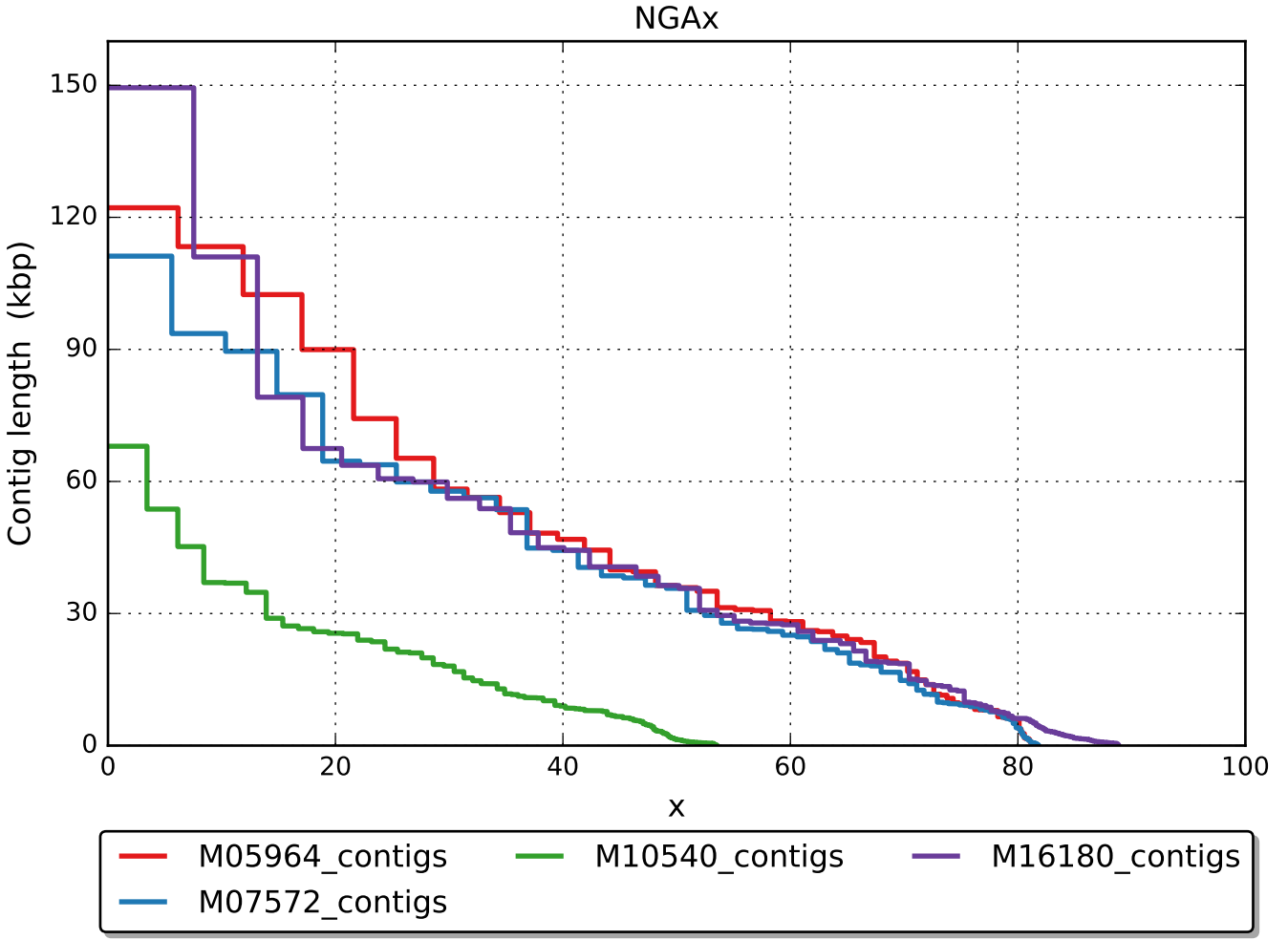

Cumulative length
Cumulative length (kbp)
Contig index
3000
2500
2000
1500
1000
500
0
0
200
400
600
800
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

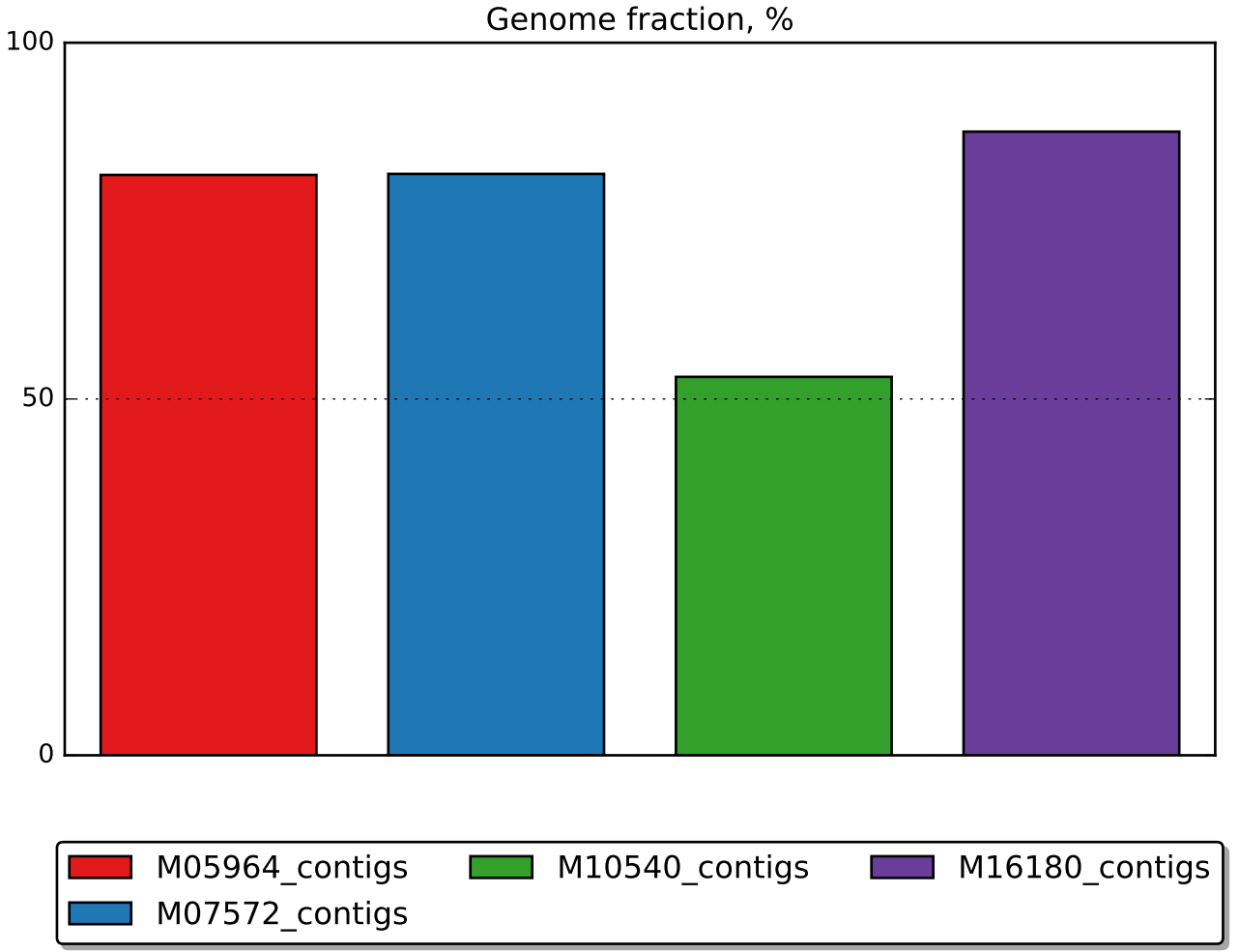

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


Misassemblies
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
40
80
120
160
200
Contig index
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs


NGAx
Contig length (kbp)
150
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