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	1985832	1985832	1985832	1985832
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.22	38.22	38.22	38.22
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	68	76	21	75
# misassembled contigs	11	16	4	11
Misassembled contigs length	1776031	1759573	340337	1806170
# local misassemblies	54	75	9	74
# unaligned contigs	730 + 4 part	737 + 9 part	85 + 22 part	131 + 31 part
Unaligned length	583665	687227	869574	201321
Genome fraction (%)	75.048	79.176	45.013	80.347
Duplication ratio	1.222	1.177	1.183	1.189
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2711.40	2603.01	3770.30	2501.69
# indels per 100 kbp	74.41	69.90	90.28	67.75
Largest alignment	110247	121627	52175	74294
NA50	16473	16914	-	27864
NGA50	24858	28222	-	29586
NA75	-	-	-	1396
NGA75	519	5962	-	6261
LA50	32	32	-	23
LGA50	22	20	-	21
LA75	-	-	-	80
LGA75	84	53	-	49

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

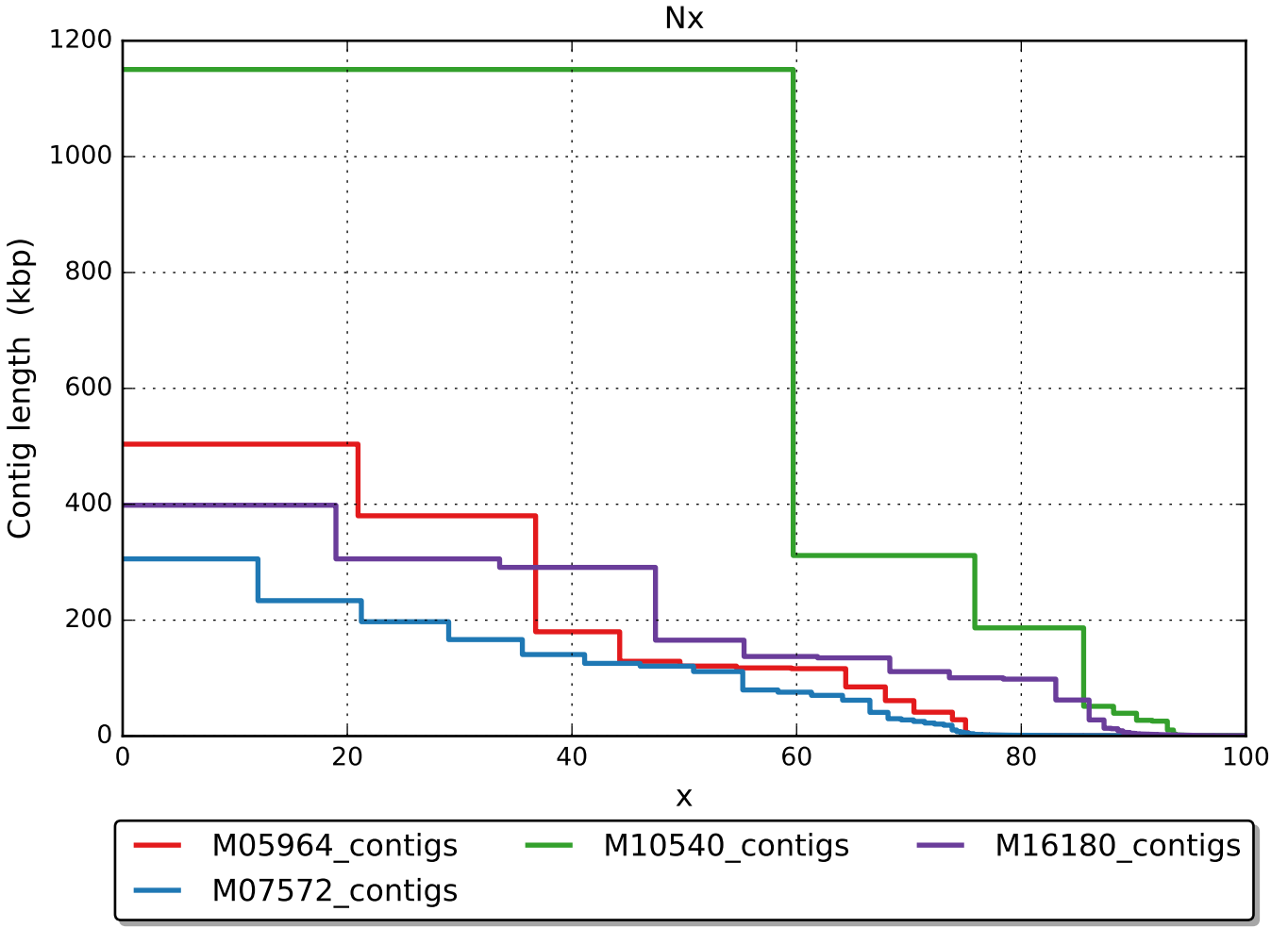
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	68	76	21	75
# relocations	68	75	21	75
# translocations	0	0	0	0
# inversions	0	1	0	0
# misassembled contigs	11	16	4	11
Misassembled contigs length	1776031	1759573	340337	1806170
# local misassemblies	54	75	9	74
# mismatches	40409	40927	33702	39916
# indels	1109	1099	807	1081
# short indels	980	983	735	954
# long indels	129	116	72	127
Indels length	3583	3383	1910	3483

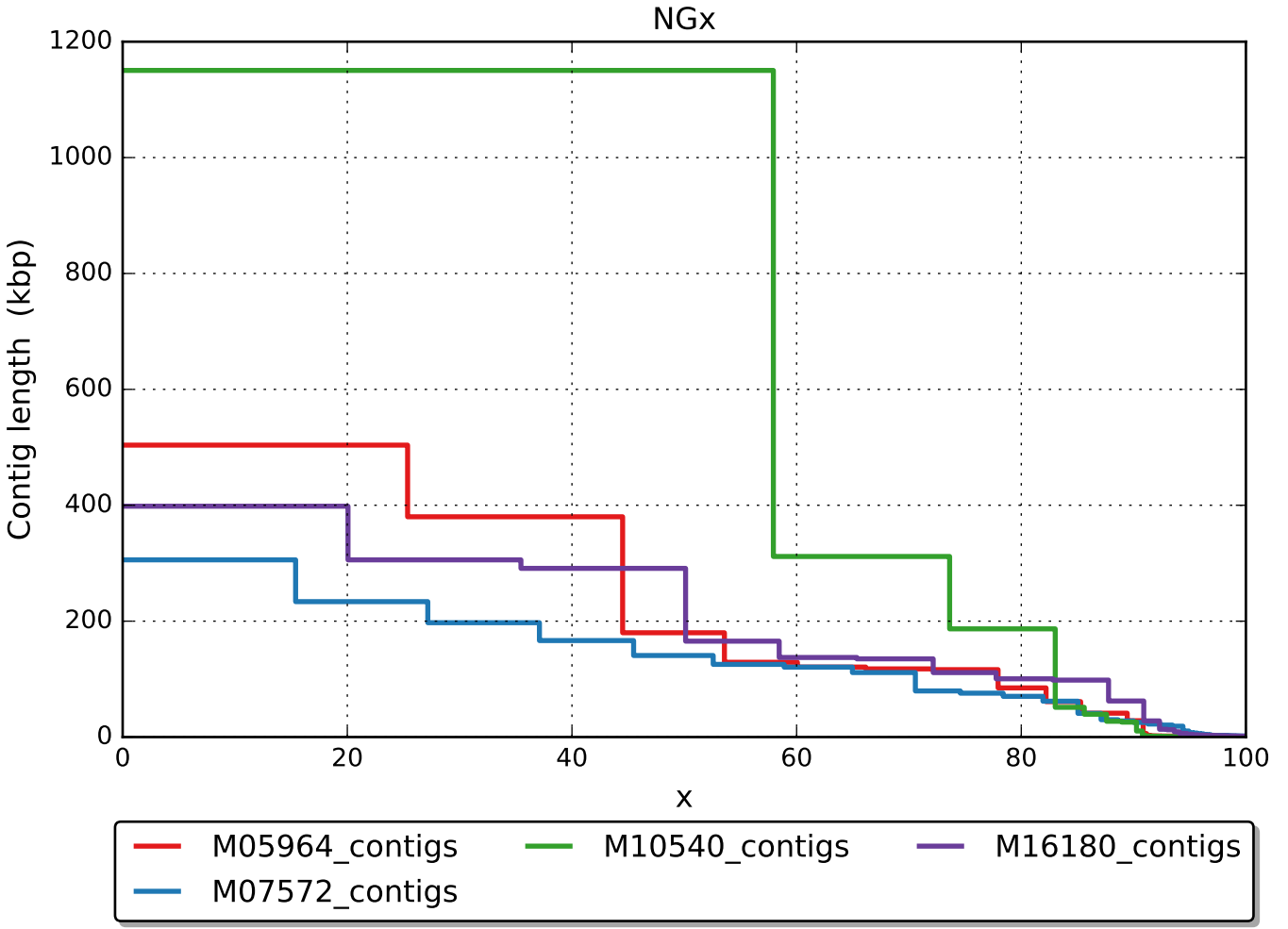
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

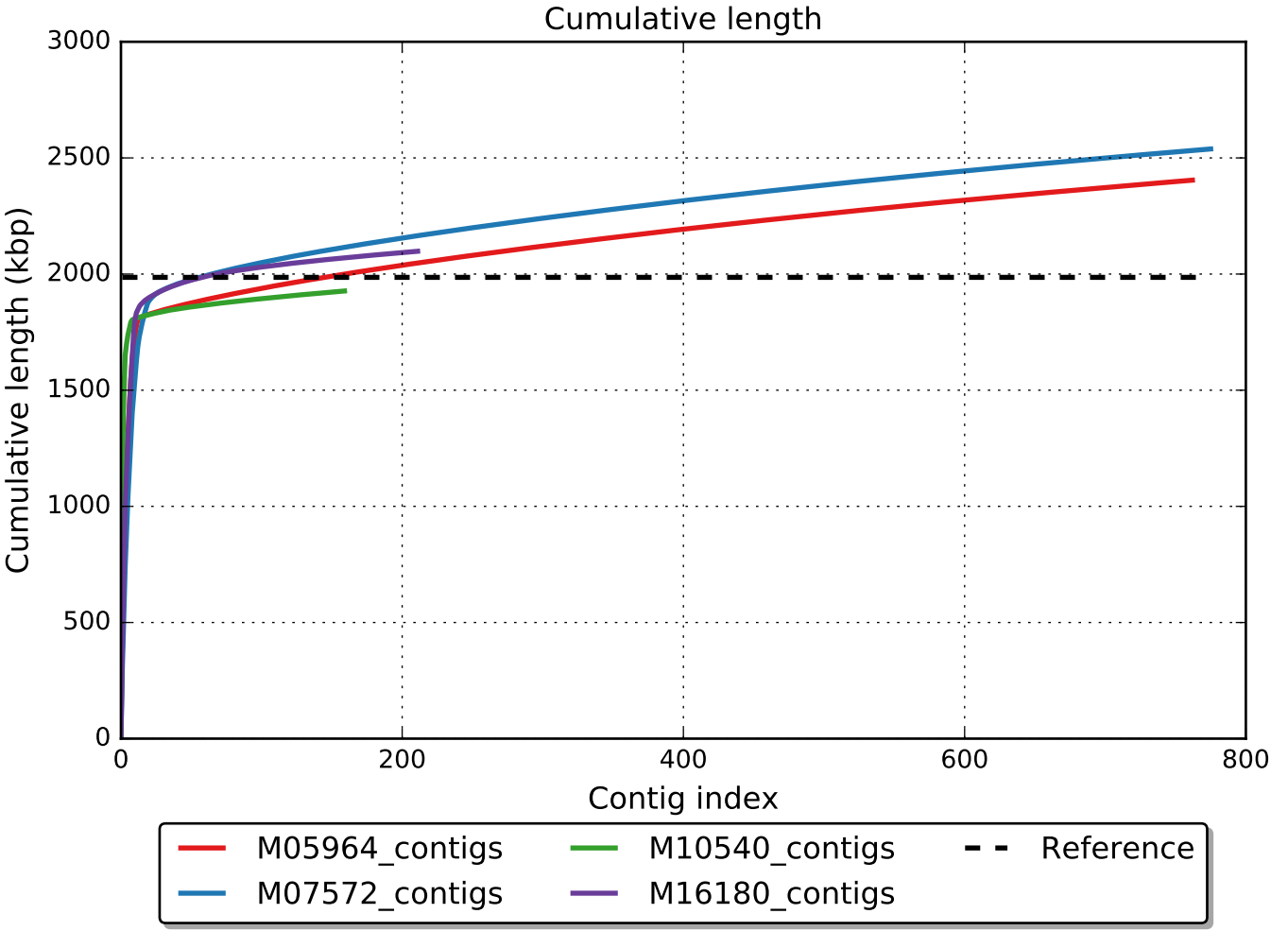
Unaligned report

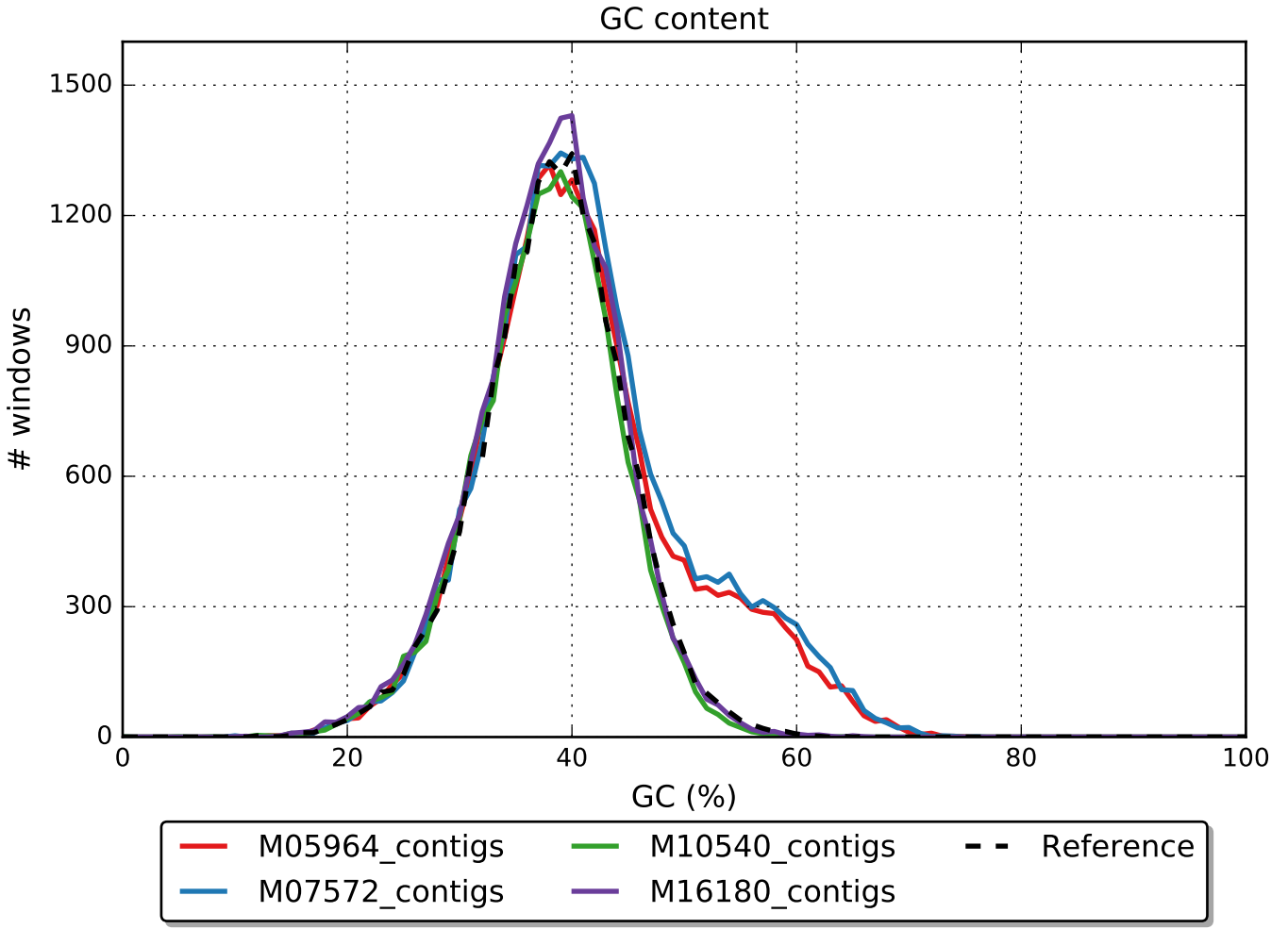
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	730	737	85	131
Fully unaligned length	582620	613650	69903	142642
# partially unaligned contigs	4	9	22	31
# with misassembly	0	4	8	4
# both parts are significant	0	5	5	7
Partially unaligned length	1045	73577	799671	58679
# N's	0	0	0	0

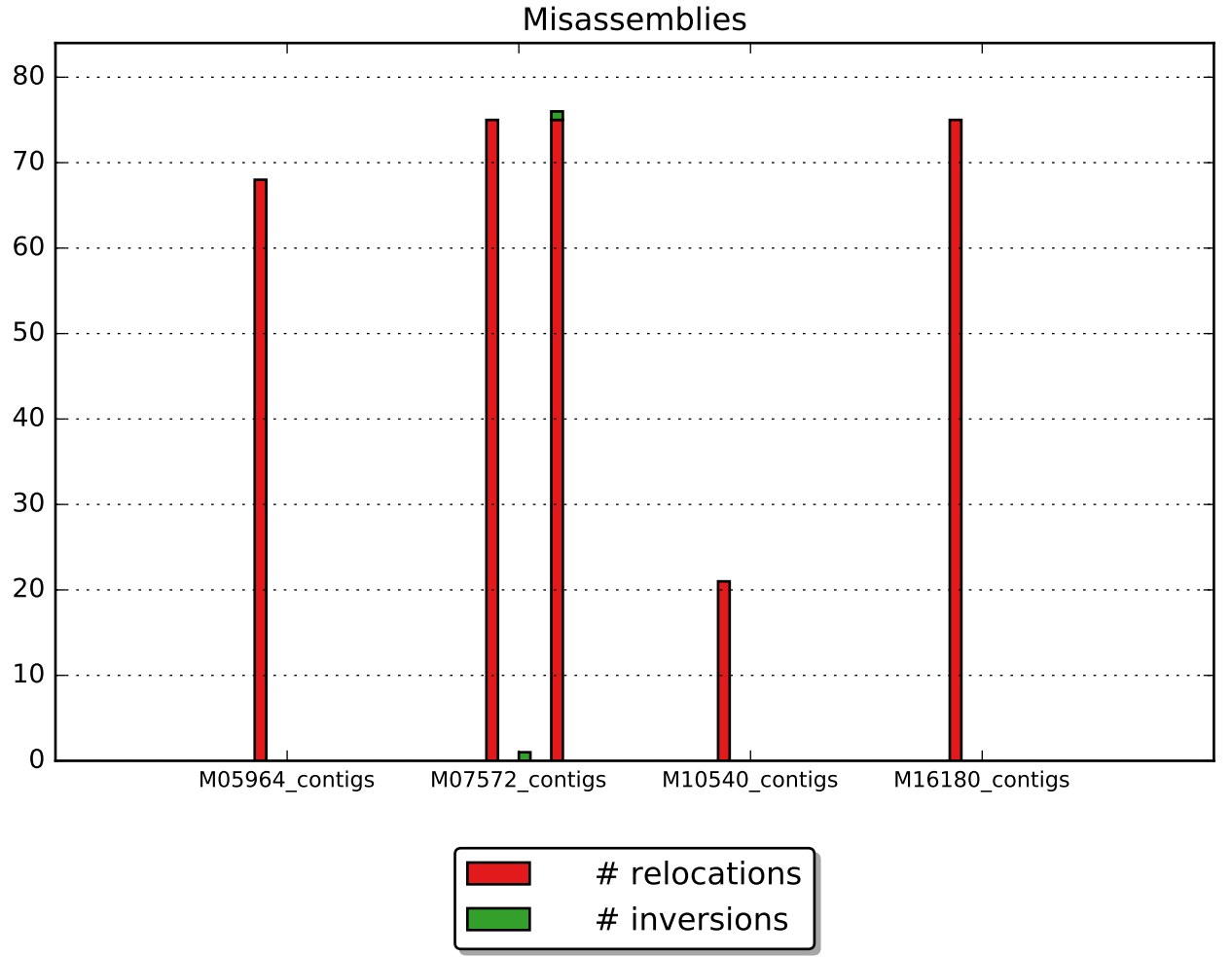
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

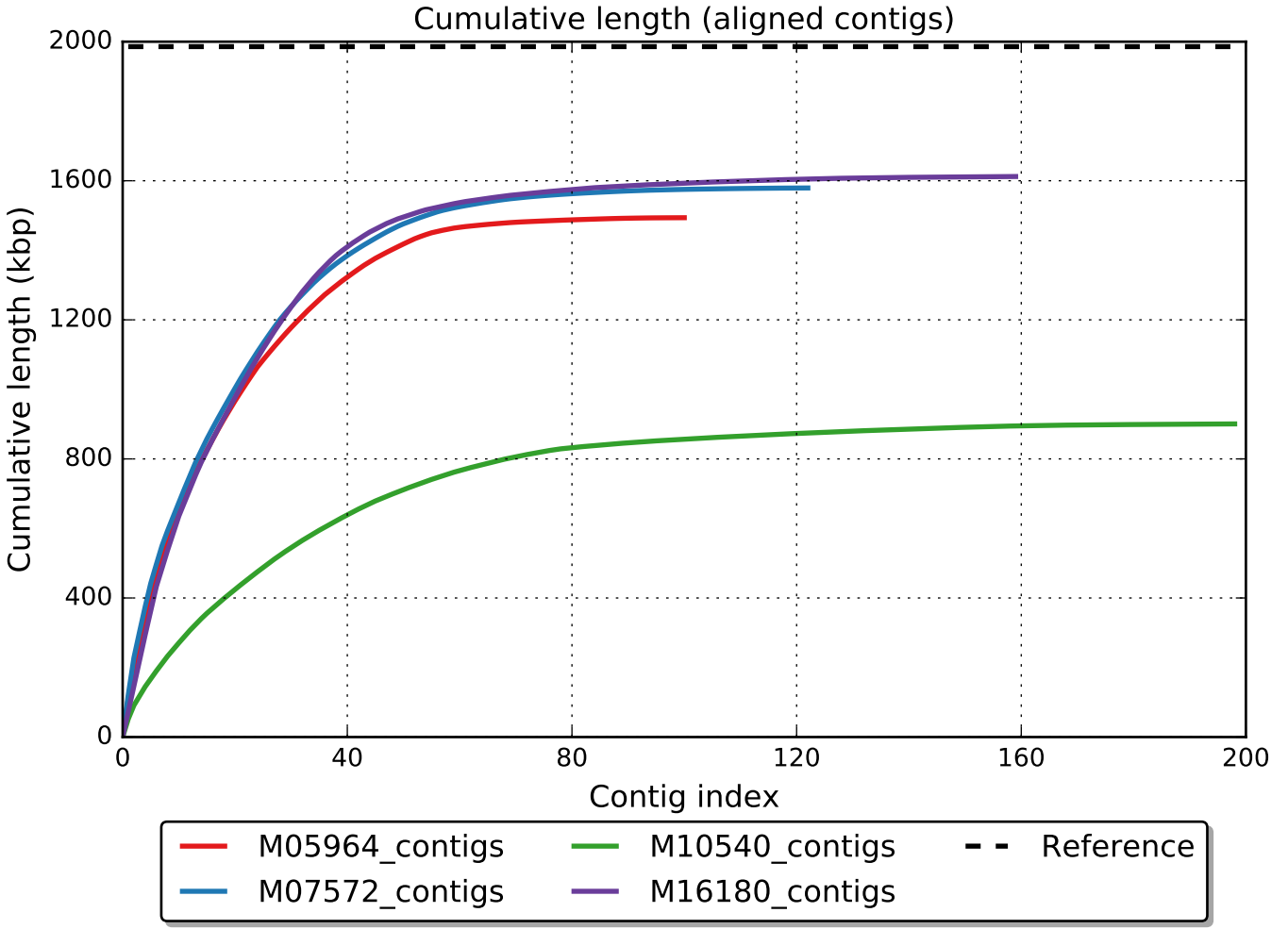

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

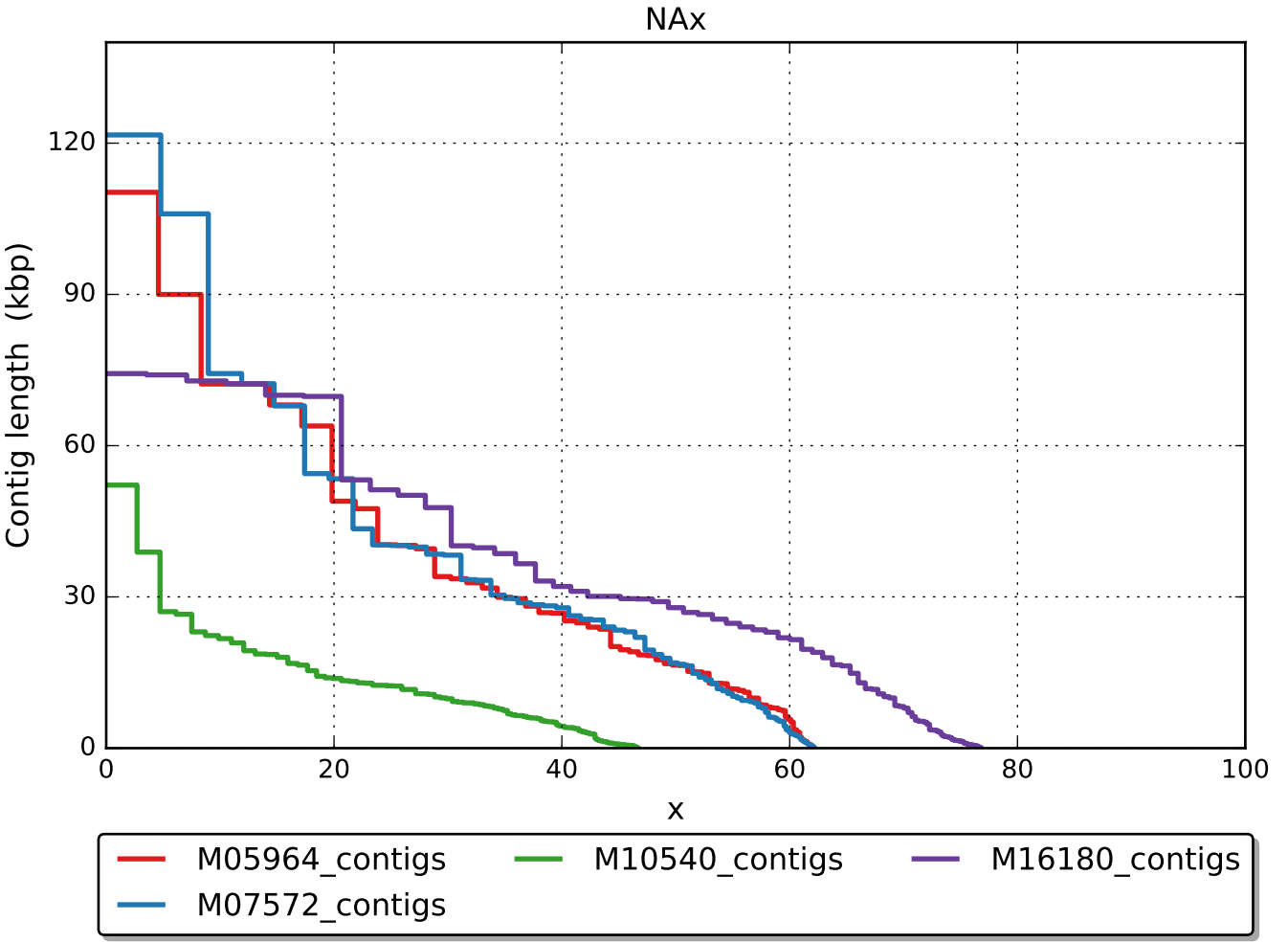

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

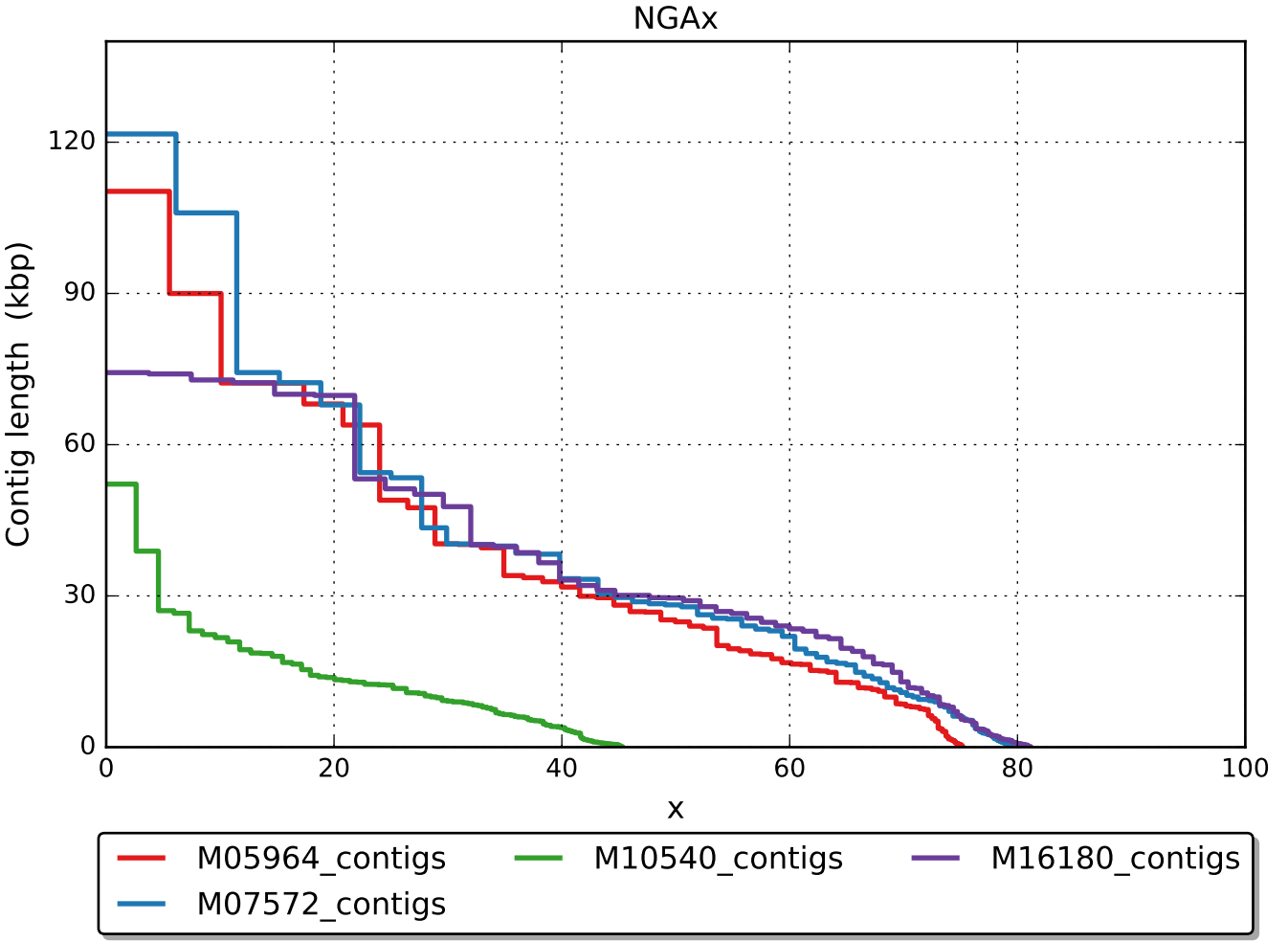

Cumulative length
Cumulative length (kbp)
Contig index
3000
2500
2000
1500
1000
500
0
0
200
400
600
800
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

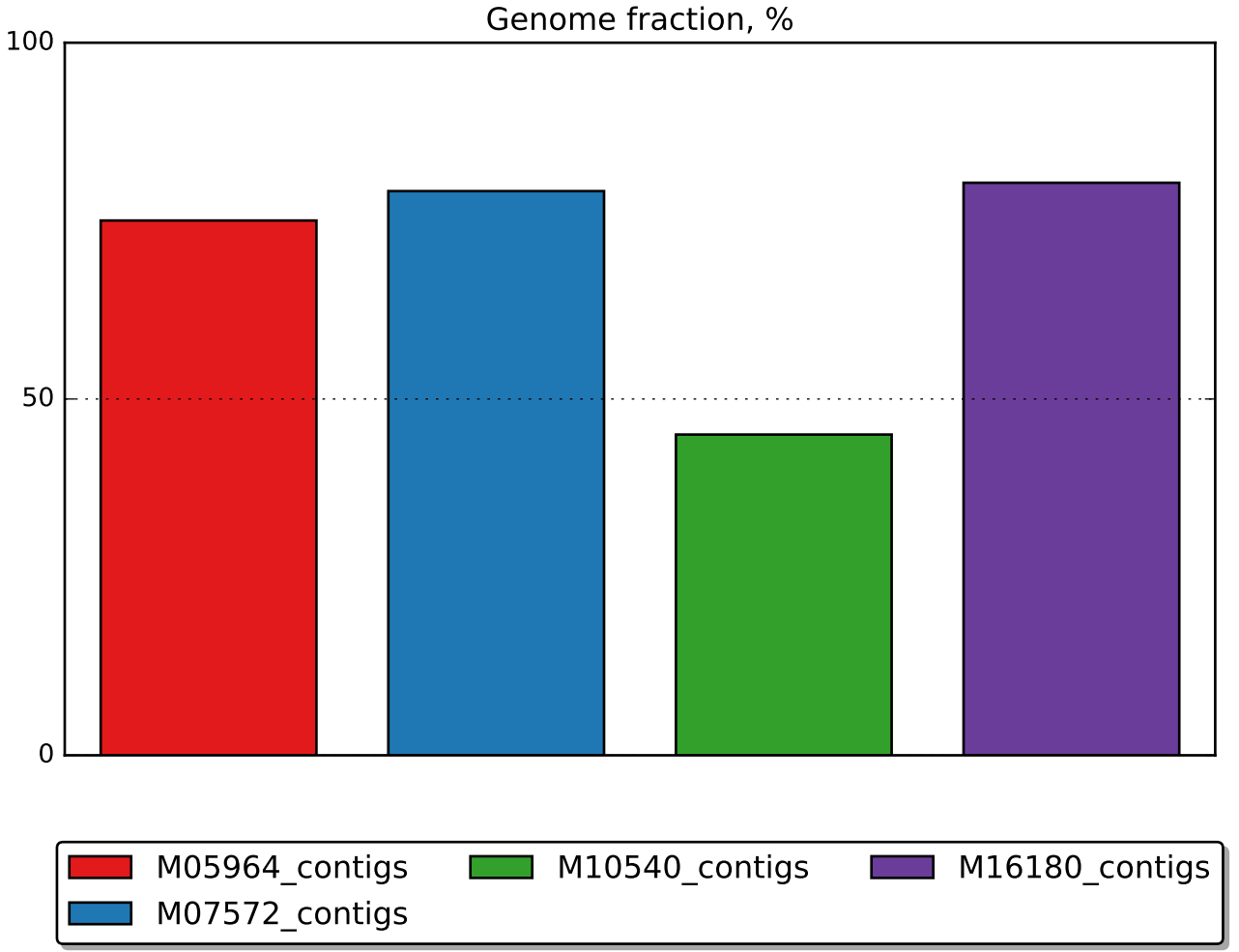

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


Misassemblies
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
40
80
120
160
200
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