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	2007018	2007018	2007018	2007018
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	165472
N75	28168	5904	311604	100510
NG75	116324	75725	186707	111243
L50	5	7	1	4
LG50	3	5	1	4
L75	12	23	2	8
LG75	7	10	3	7
# misassemblies	65	71	13	75
# misassembled contigs	12	17	5	12
Misassembled contigs length	1689219	1746346	216230	1839613
# local misassemblies	60	68	7	69
# unaligned contigs	728 + 6 part	735 + 10 part	78 + 26 part	135 + 31 part
Unaligned length	651073	706250	1028572	198165
Genome fraction (%)	75.360	78.973	39.884	80.774
Duplication ratio	1.159	1.156	1.123	1.172
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2649.21	2538.35	3753.39	2591.20
# indels per 100 kbp	75.70	75.96	90.70	76.80
Largest alignment	125362	120766	30386	122949
NA50	17327	16774	-	26504
NGA50	21161	27402	-	27418
NA75	-	-	-	2741
NGA75	764	6882	-	7628
LA50	31	33	-	21
LGA50	21	20	-	20
LA75	-	-	-	66
LGA75	77	53	-	52

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

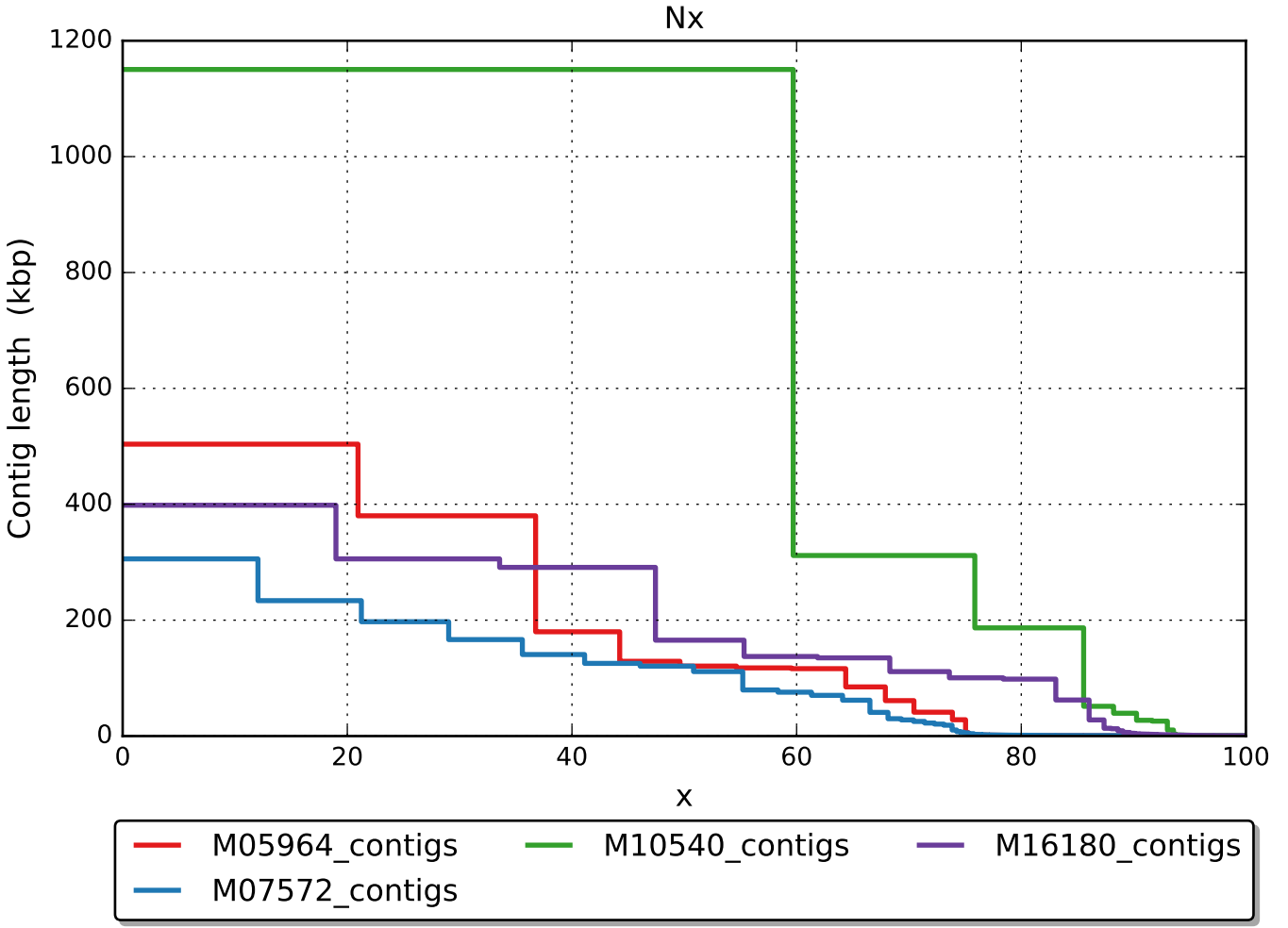
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	65	71	13	75
# relocations	64	70	13	75
# translocations	0	0	0	0
# inversions	1	1	0	0
# misassembled contigs	12	17	5	12
Misassembled contigs length	1689219	1746346	216230	1839613
# local misassemblies	60	68	7	69
# mismatches	40069	40233	30045	42007
# indels	1145	1204	726	1245
# short indels	1010	1062	667	1101
# long indels	135	142	59	144
Indels length	3736	3915	1783	3978

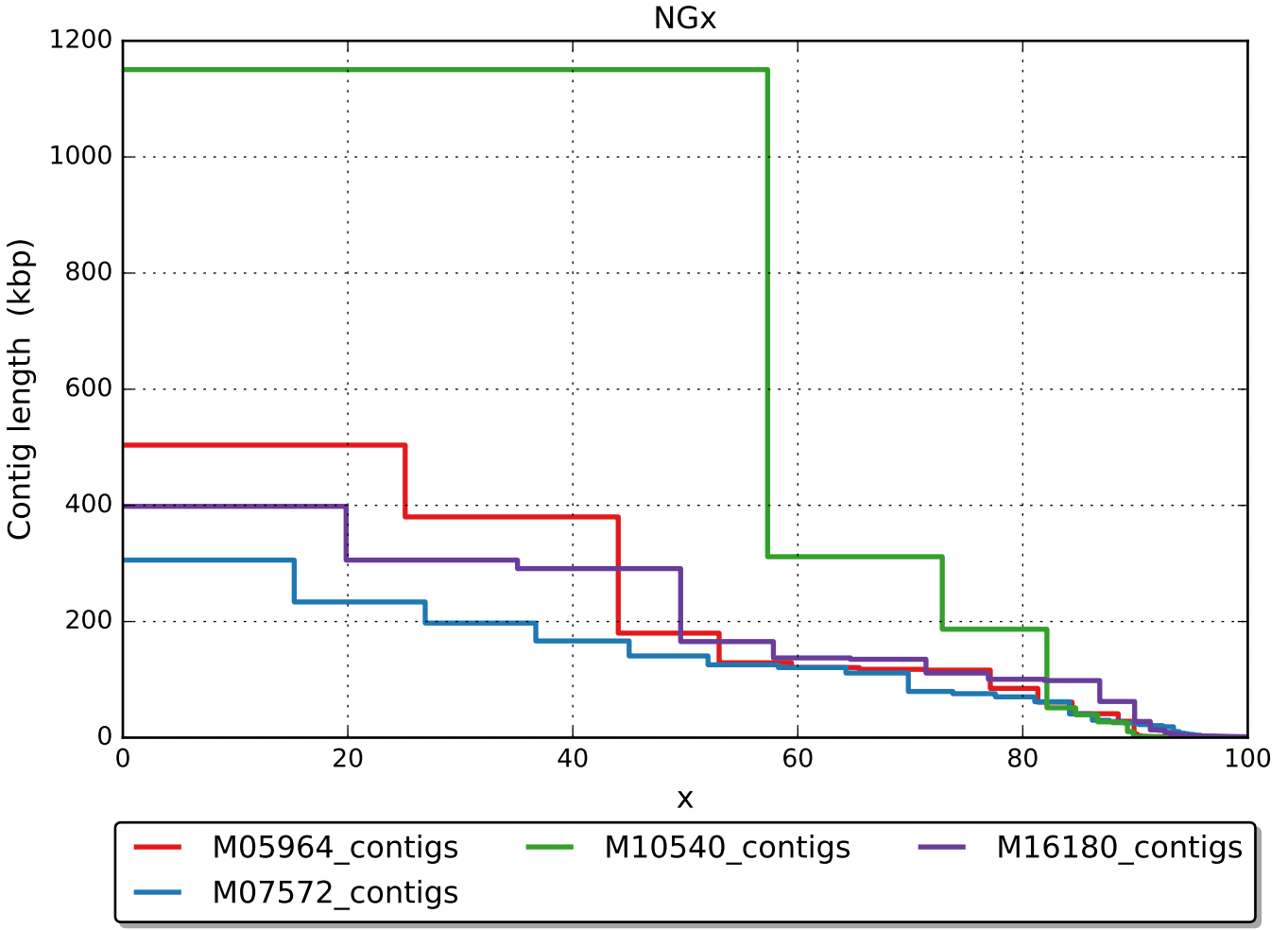
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

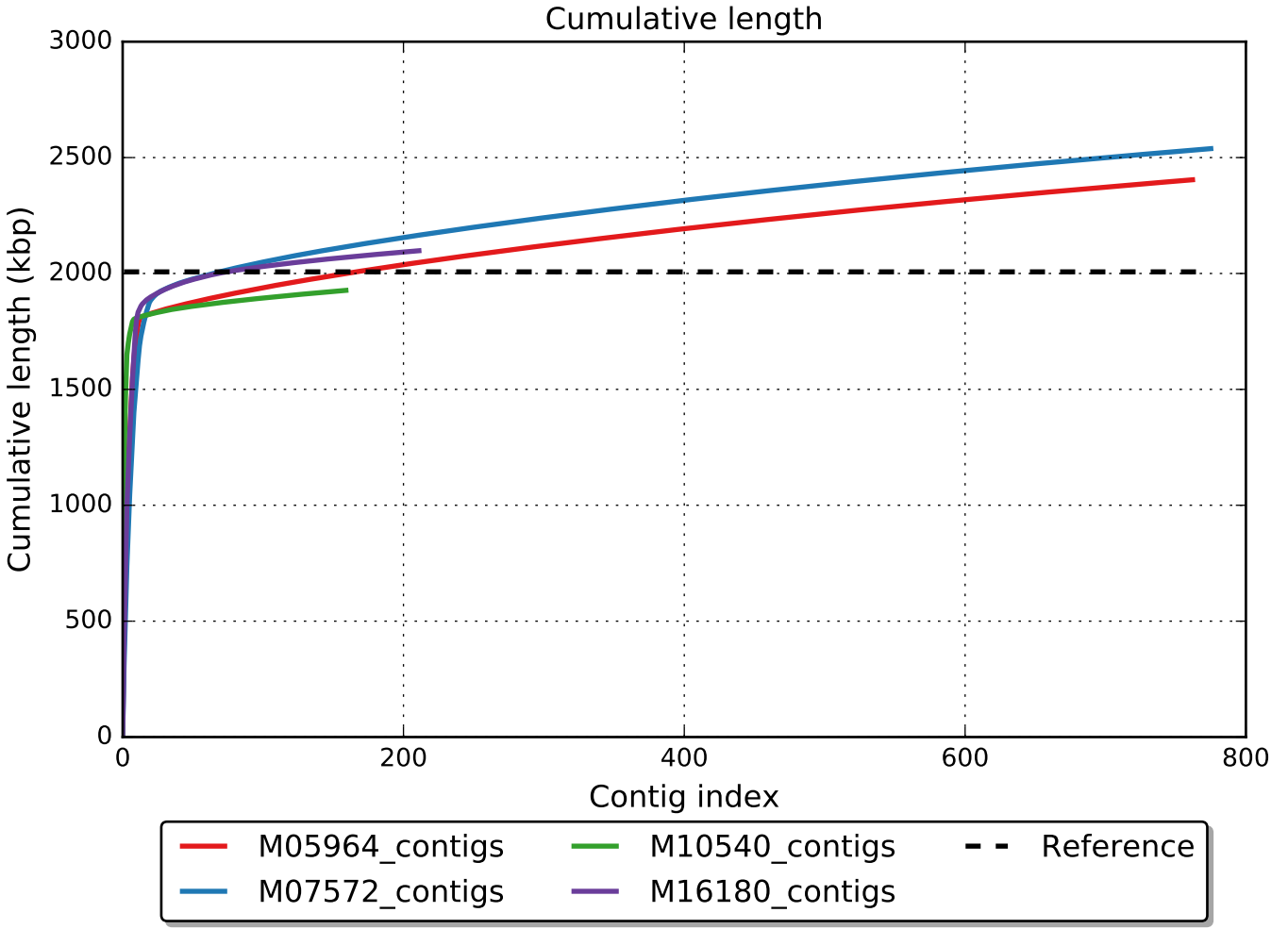
Unaligned report

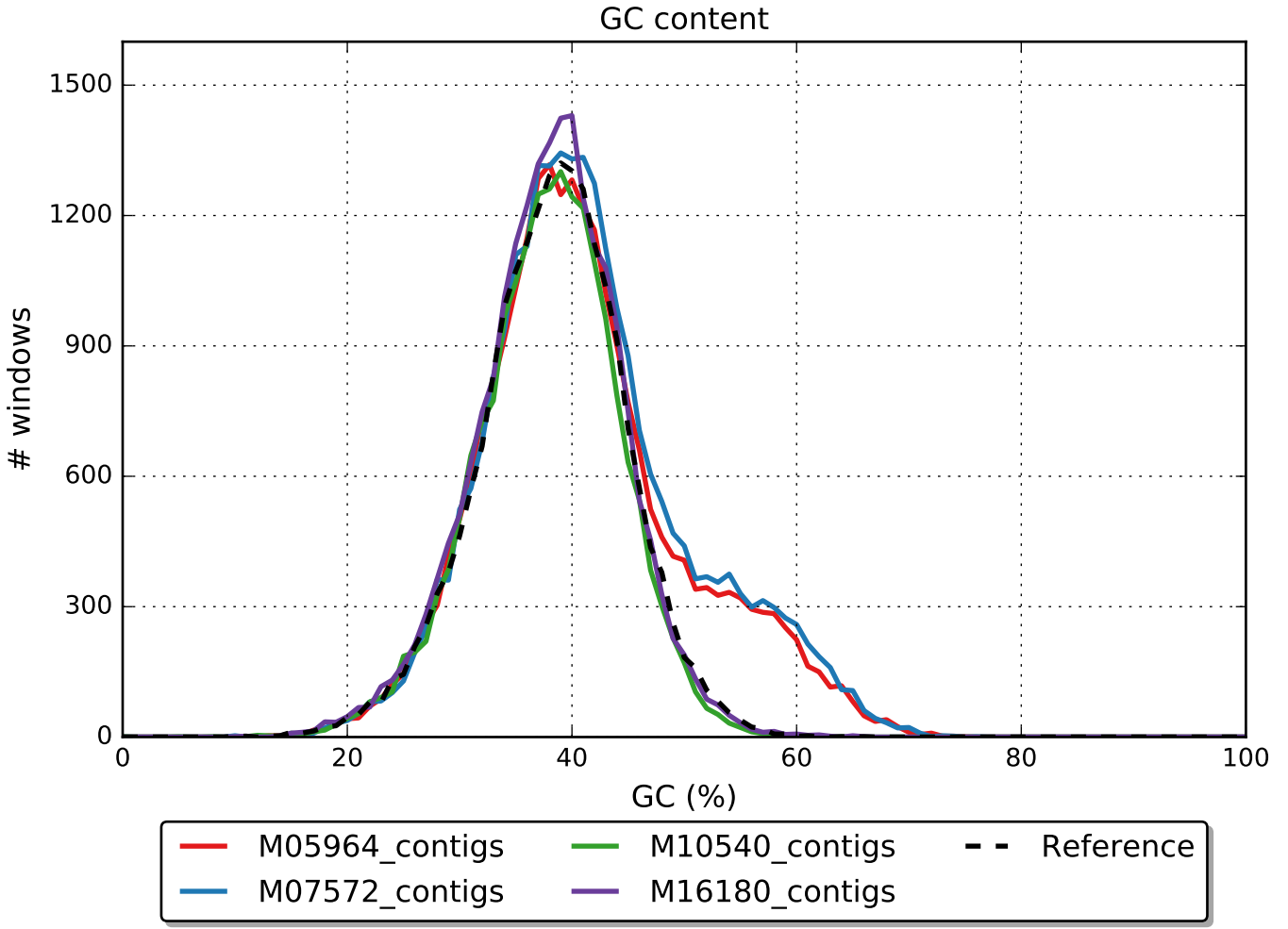
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	728	735	78	135
Fully unaligned length	580717	623772	65467	160426
# partially unaligned contigs	6	10	26	31
# with misassembly	1	4	7	3
# both parts are significant	1	5	6	8
Partially unaligned length	70356	82478	963105	37739
# N's	0	0	0	0

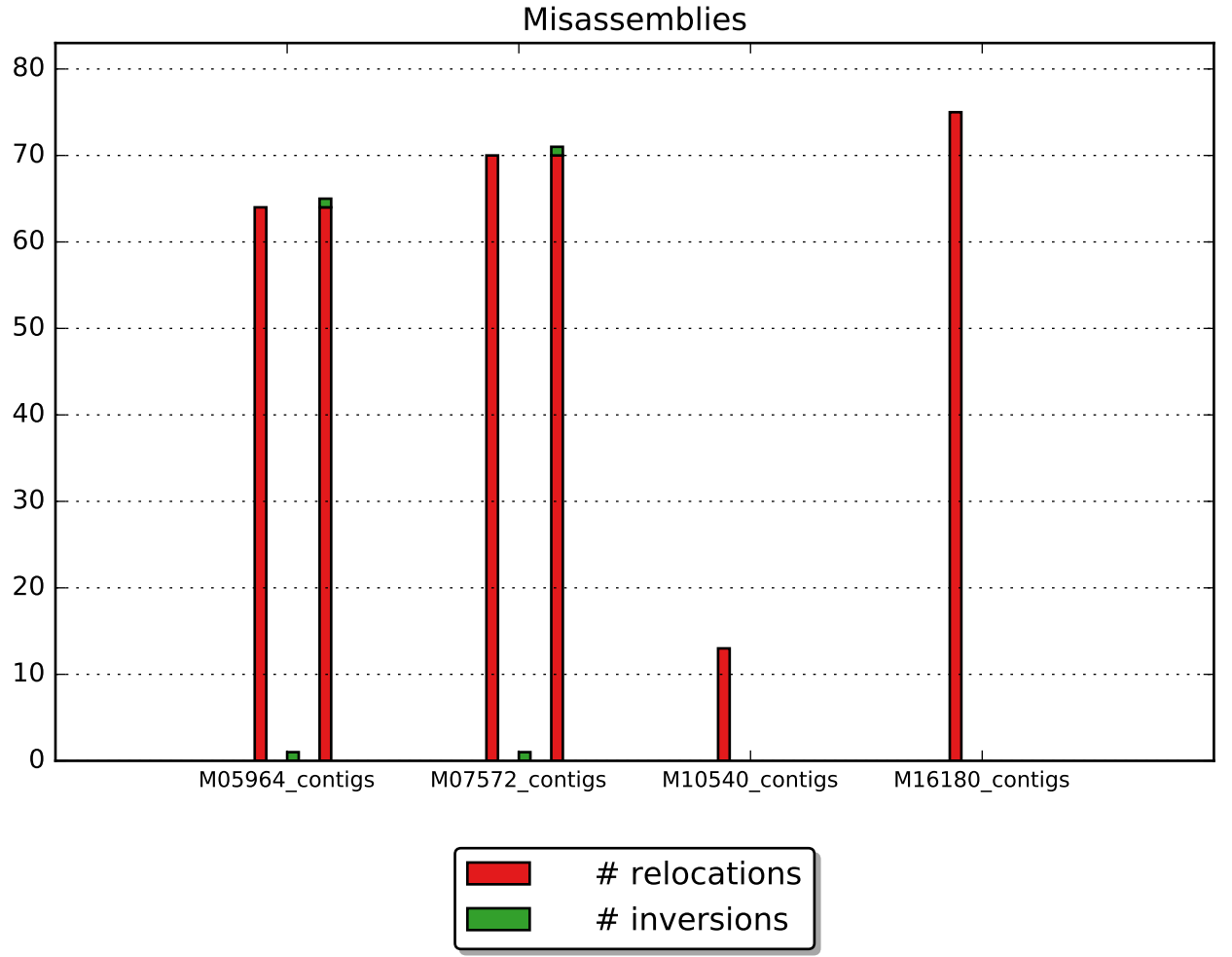
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

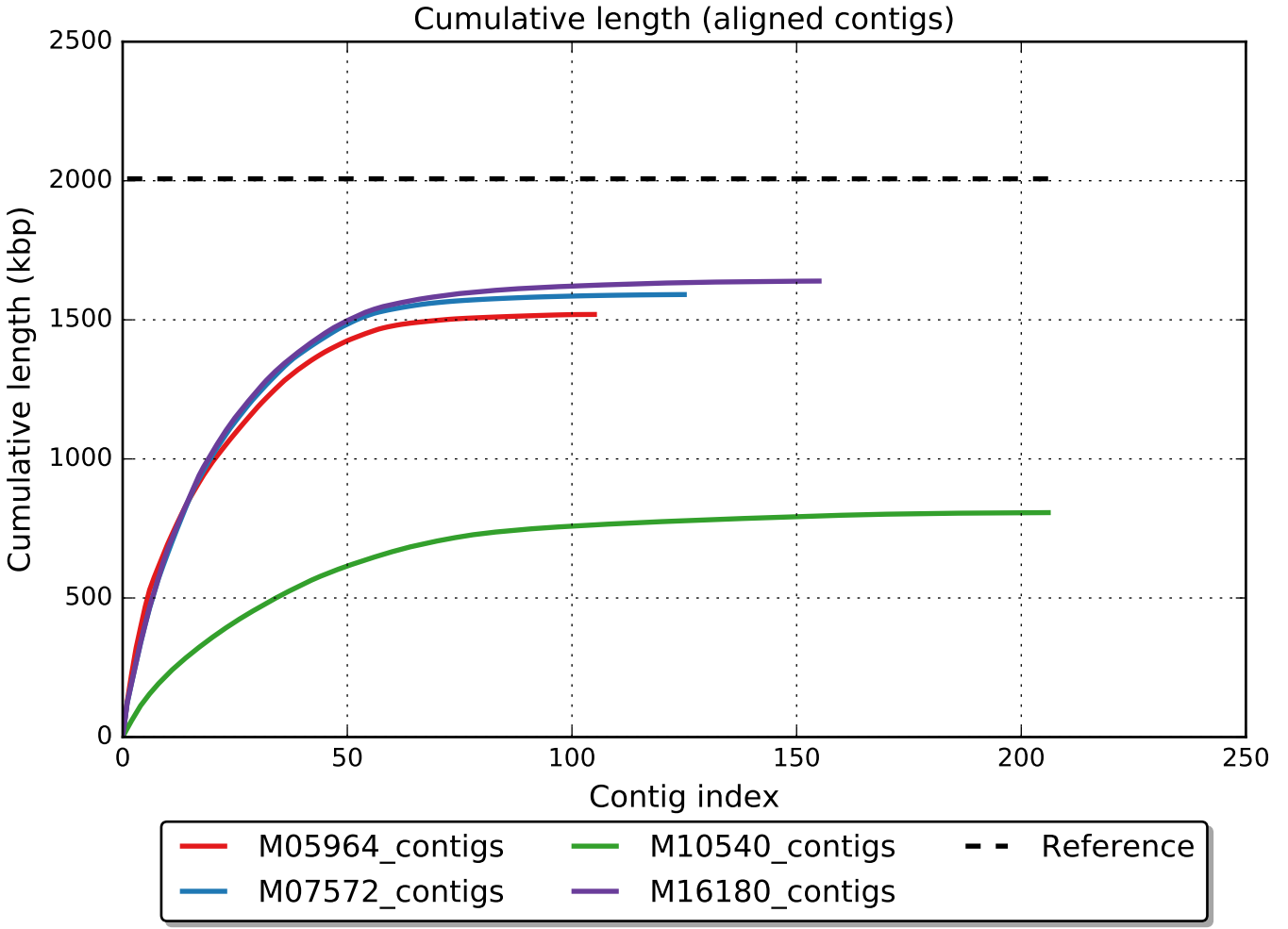

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

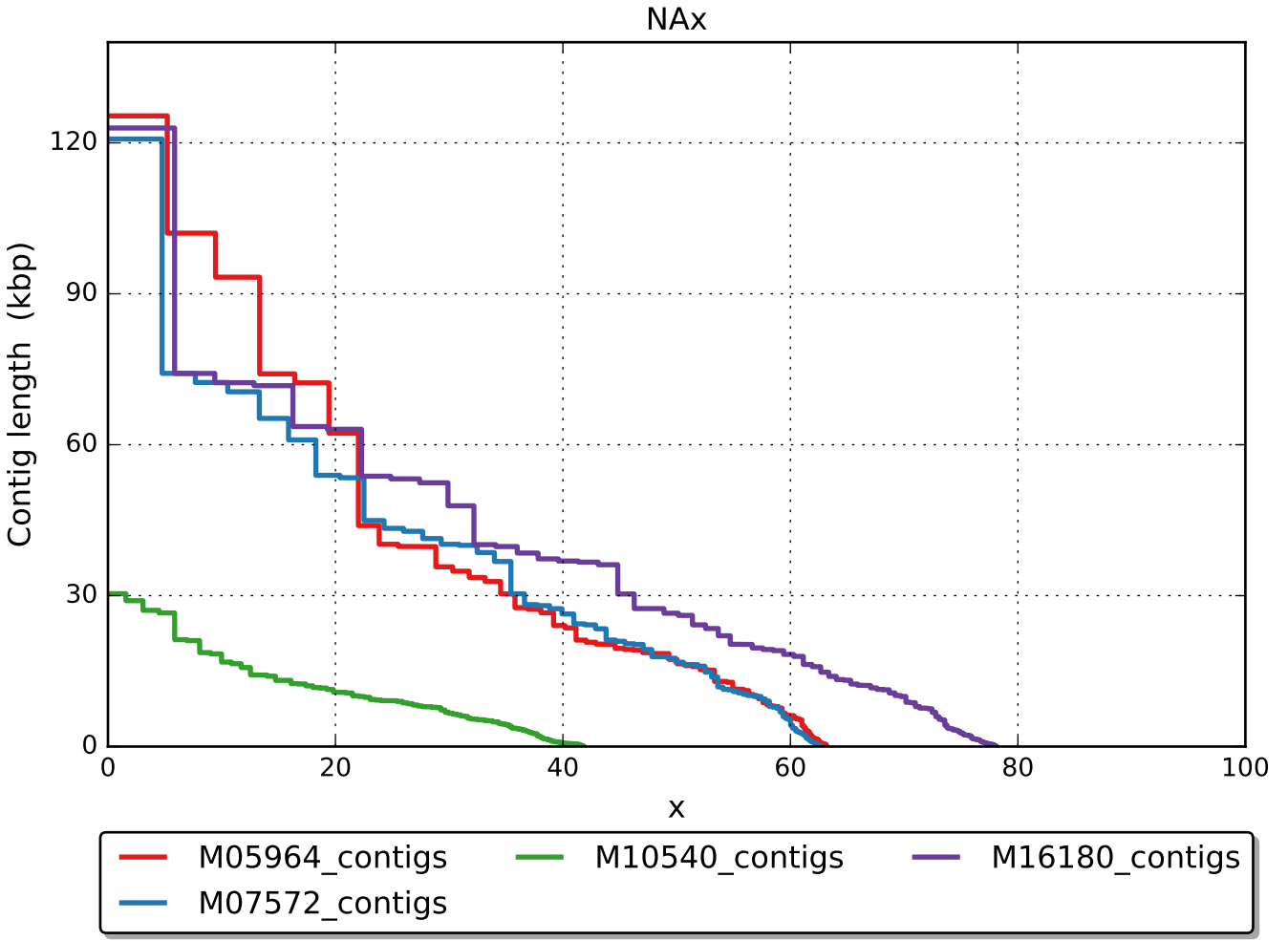

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

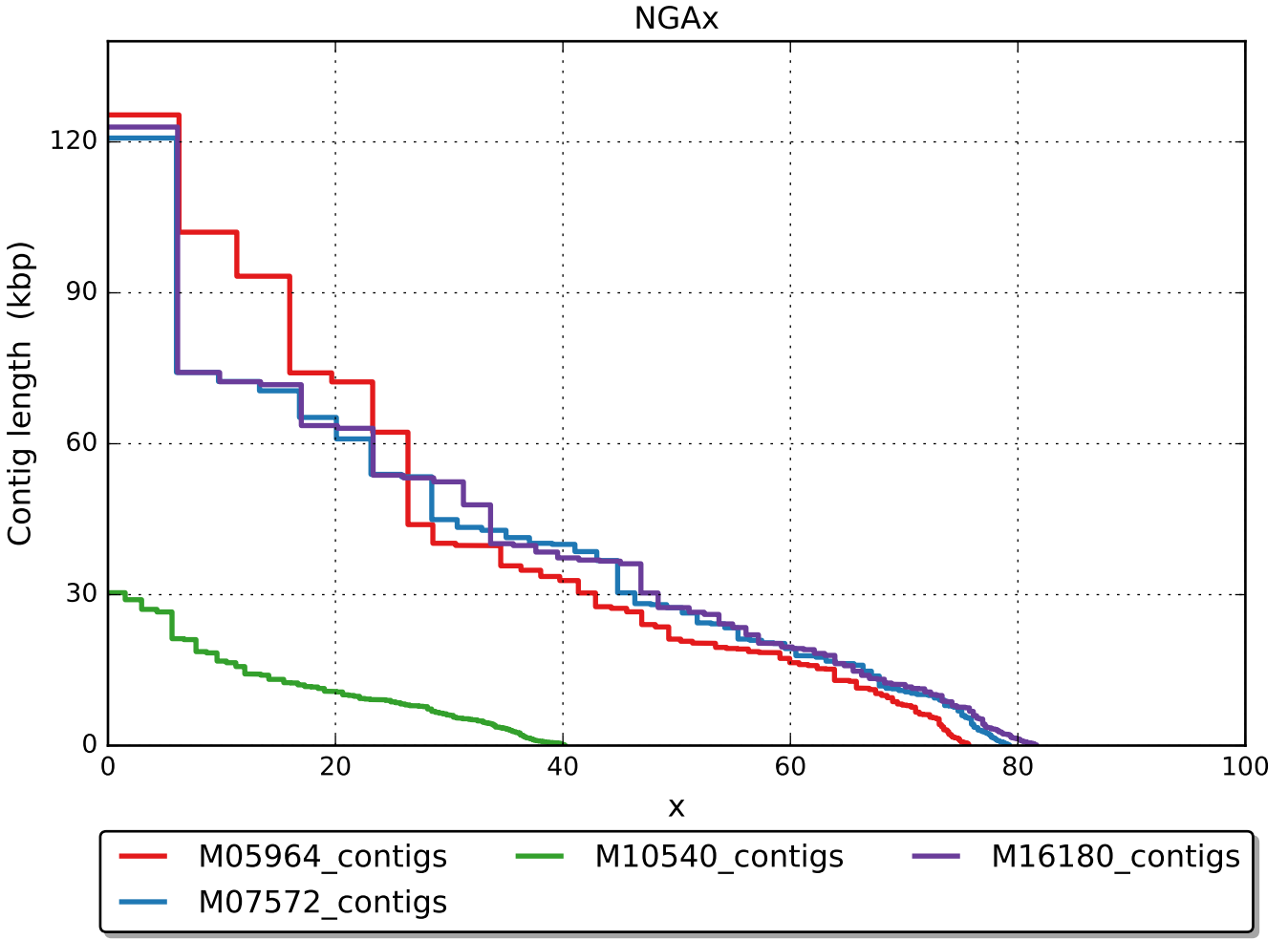

Cumulative length
Cumulative length (kbp)
Contig index
0
500
1000
1500
2000
2500
3000
0
200
400
600
800
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

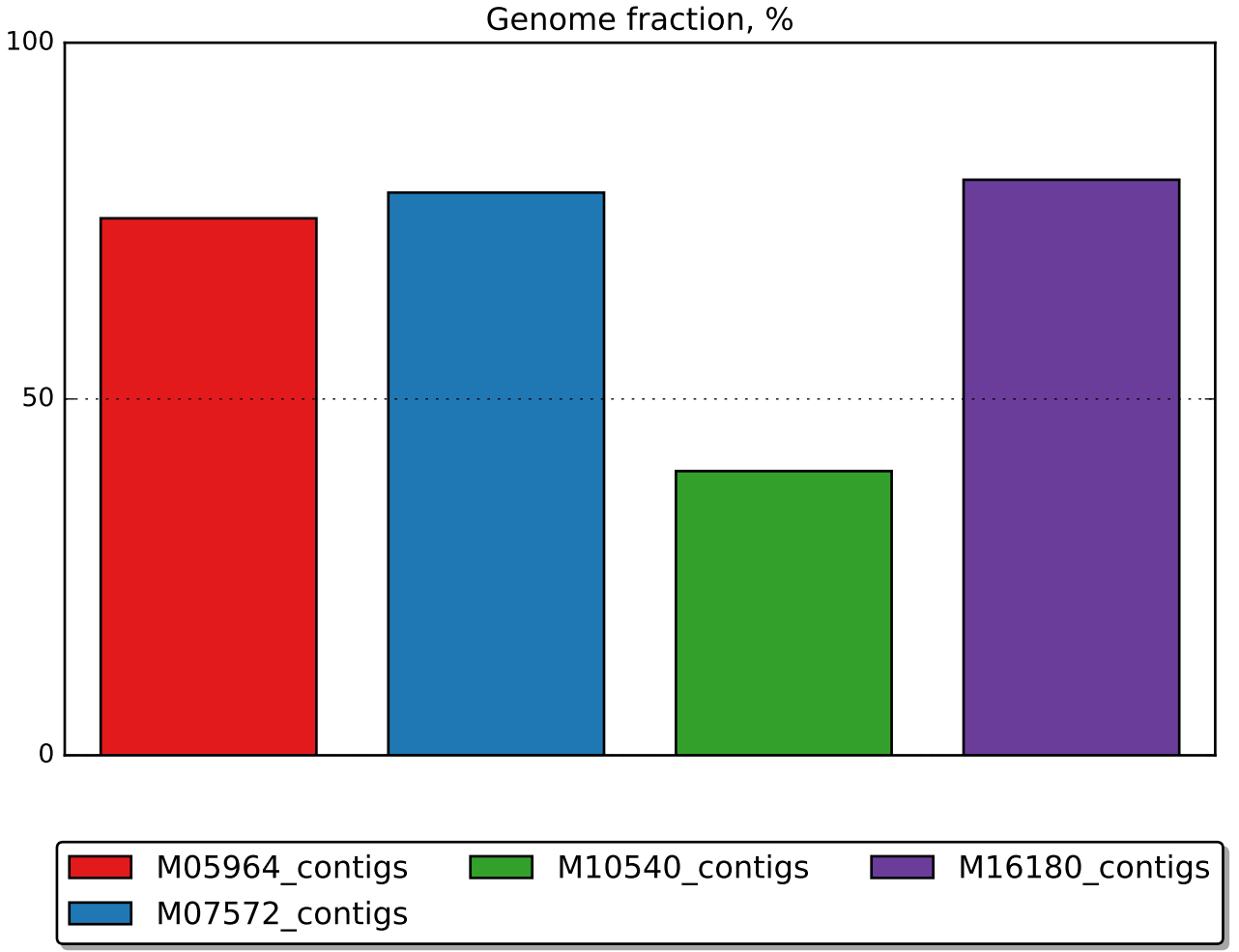

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


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)
Contig index
0
500
1000
1500
2000
2500
0
50
100
150
200
250
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
M10540_contigs
M16180_contigs
M07572_contigs


Genome fraction, %
100
50
0
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs