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	1846259	1846259	1846259	1846259
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	117636	111326	311604	134943
L50	5	7	1	4
LG50	3	5	1	3
L75	12	23	2	8
LG75	6	8	2	6
# misassemblies	42	14	74	16
# misassembled contigs	11	10	7	6
Misassembled contigs length	1716227	1107861	1606417	1359486
# local misassemblies	63	44	40	35
# unaligned contigs	728 + 3 part	738 + 10 part	88 + 15 part	155 + 20 part
Unaligned length	577435	688500	188899	233283
Genome fraction (%)	86.341	92.891	59.230	94.557
Duplication ratio	1.146	1.079	1.590	1.068
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2529.87	1775.61	3448.53	1479.98
# indels per 100 kbp	67.56	52.83	88.61	41.41
Largest alignment	110479	221979	69003	233944
NA50	37591	60596	8236	111243
NGA50	51245	115329	9573	133279
NA75	-	-	-	33418
NGA75	21339	44112	-	60827
LA50	18	10	46	7
LGA50	12	6	41	6
LA75	-	-	-	15
LGA75	25	13	-	12

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

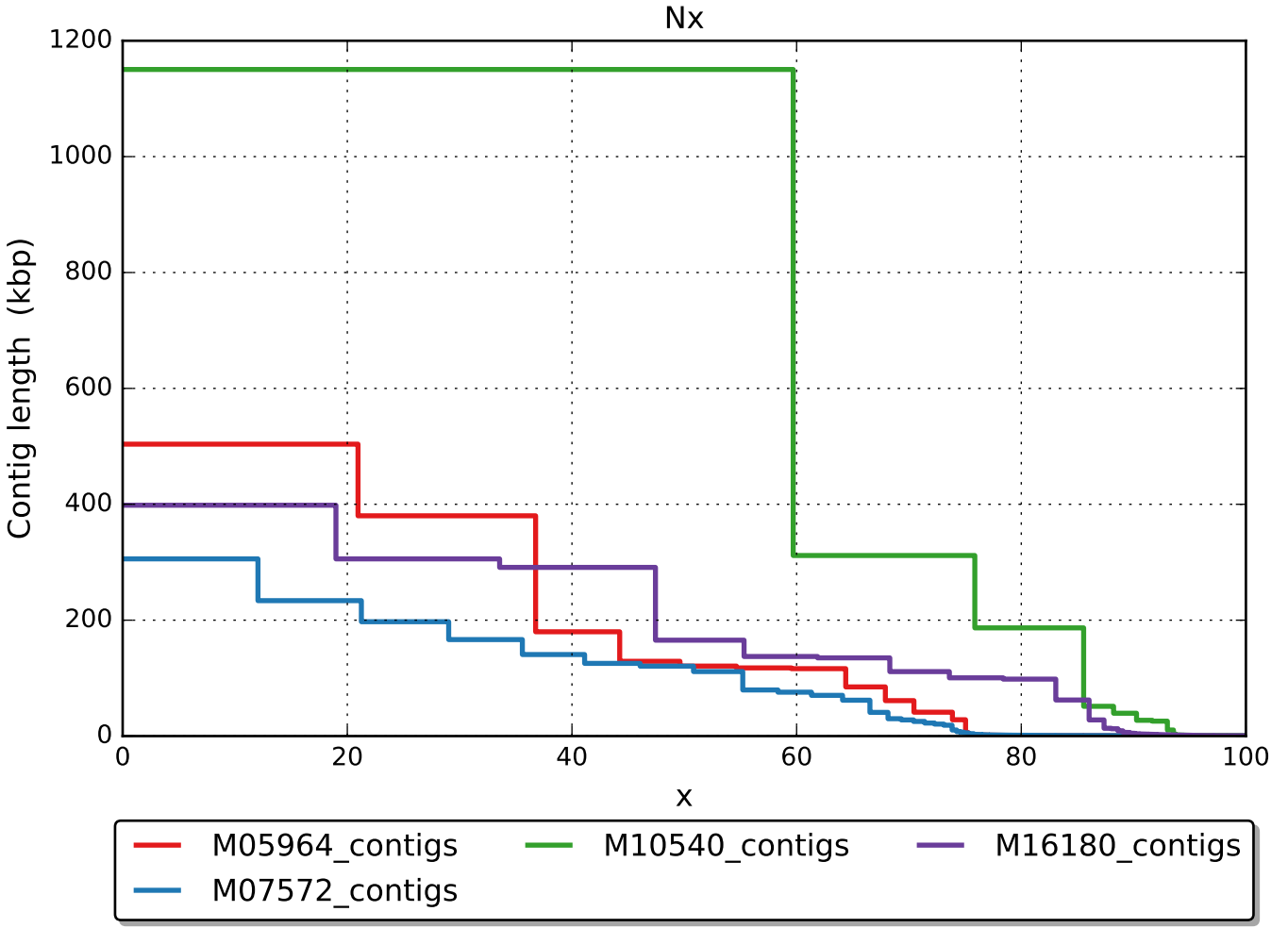
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	42	14	74	16
# relocations	42	14	72	16
# translocations	0	0	0	0
# inversions	0	0	2	0
# misassembled contigs	11	10	7	6
Misassembled contigs length	1716227	1107861	1606417	1359486
# local misassemblies	63	44	40	35
# mismatches	40328	30452	37711	25837
# indels	1077	906	969	723
# short indels	952	802	865	642
# long indels	125	104	104	81
Indels length	3382	2953	2598	2178

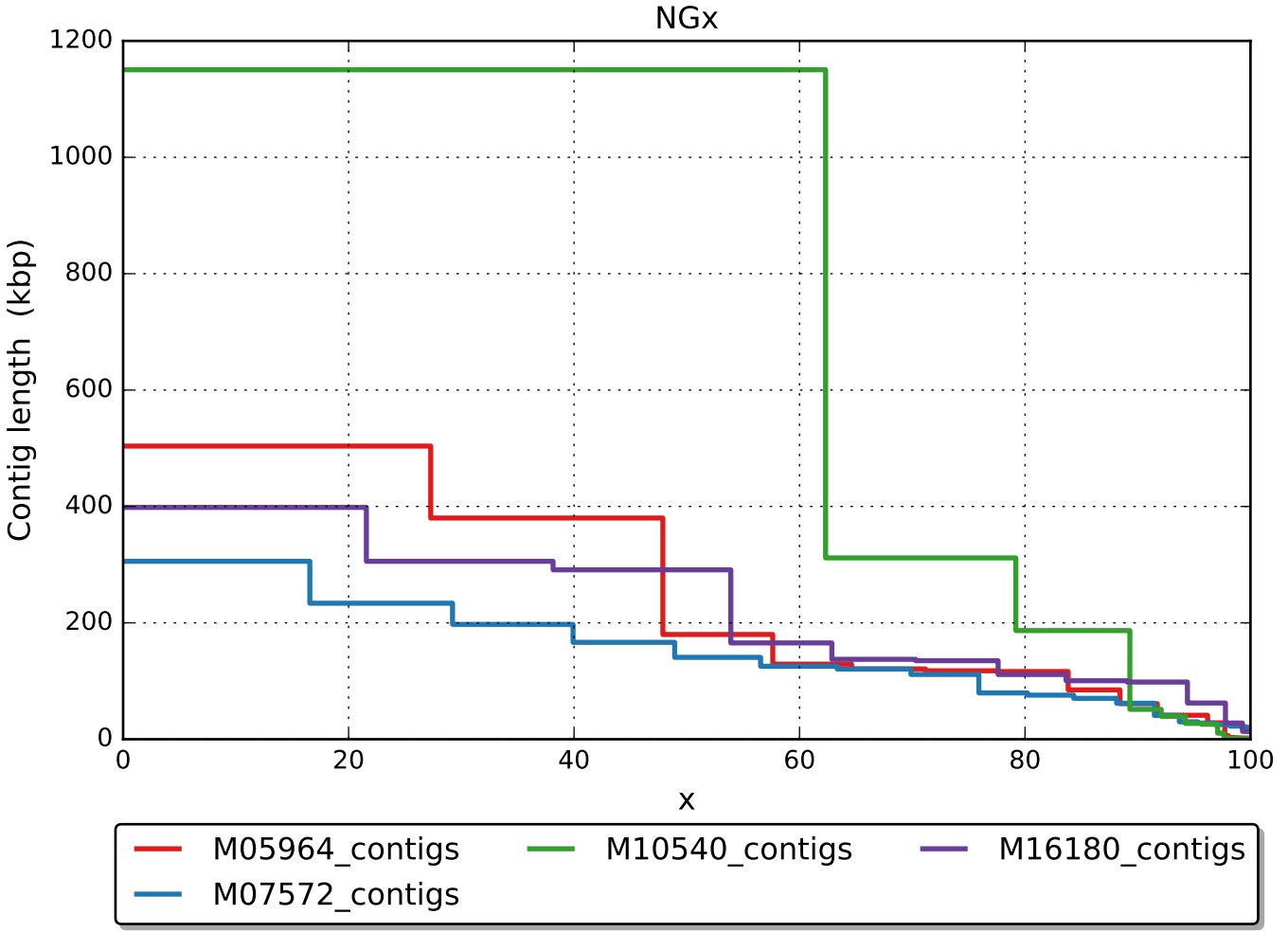
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

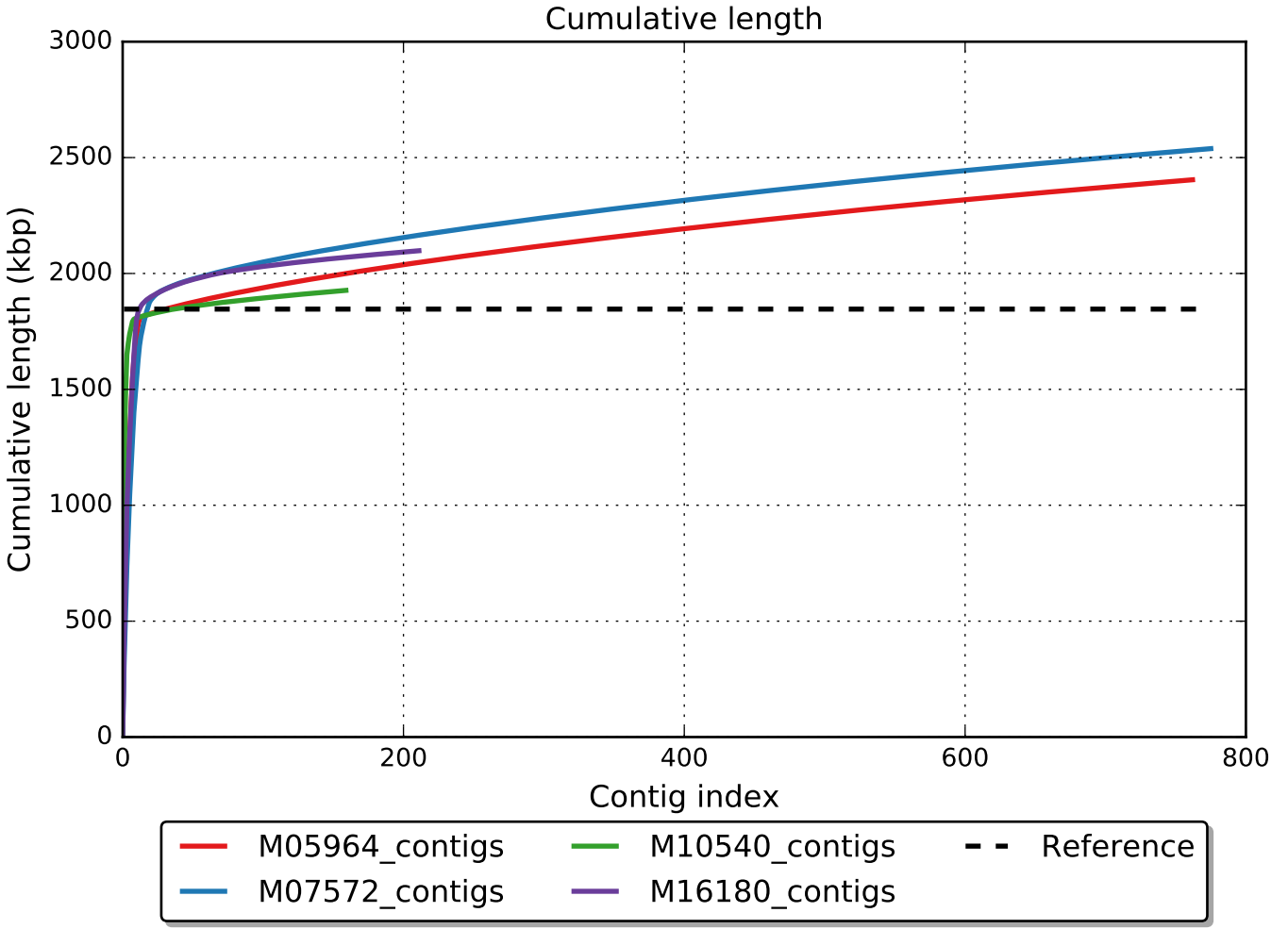
Unaligned report

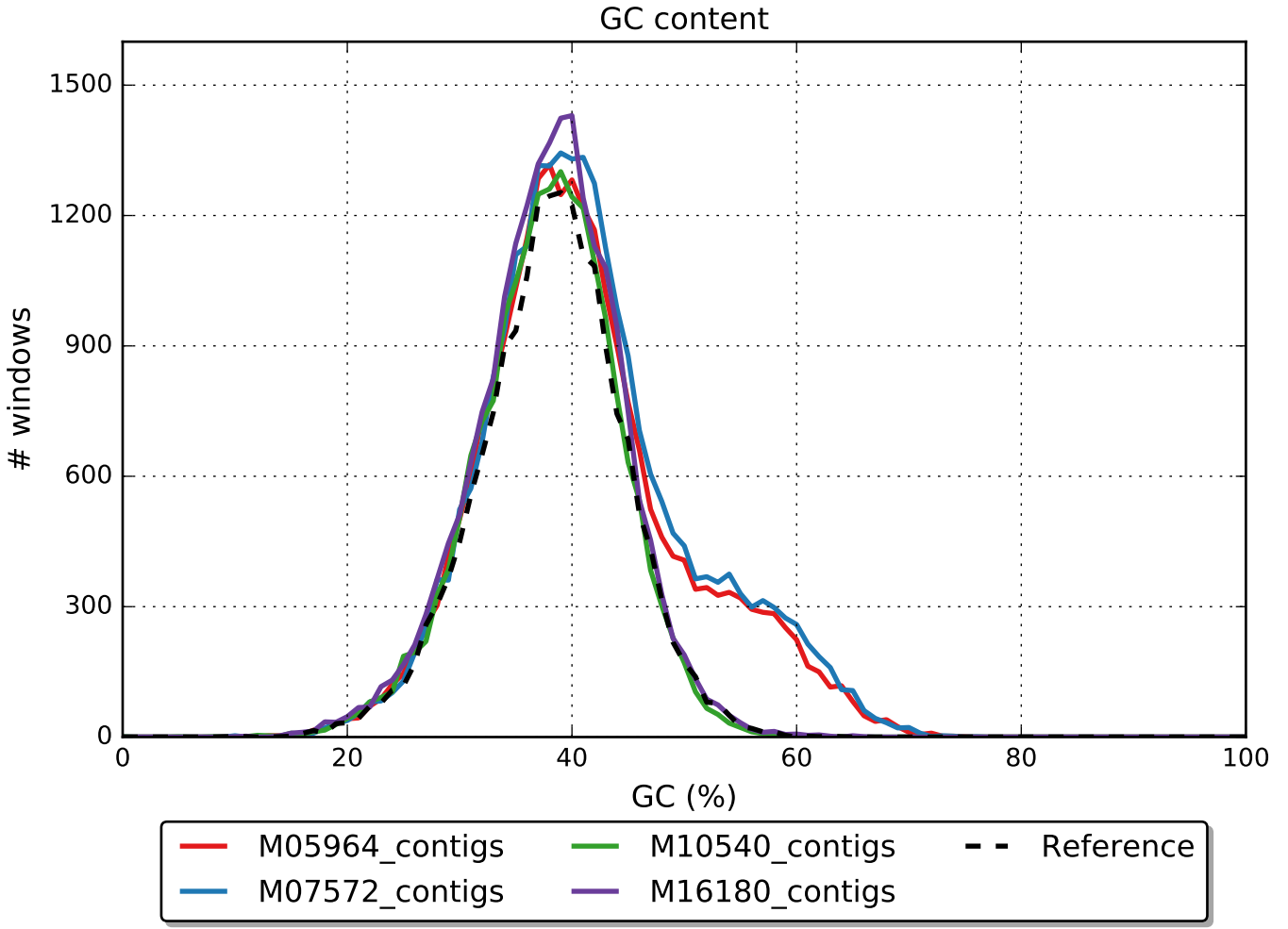
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	728	738	88	155
Fully unaligned length	575988	650139	71795	194552
# partially unaligned contigs	3	10	15	20
# with misassembly	0	1	4	1
# both parts are significant	1	5	2	1
Partially unaligned length	1447	38361	117104	38731
# N's	0	0	0	0

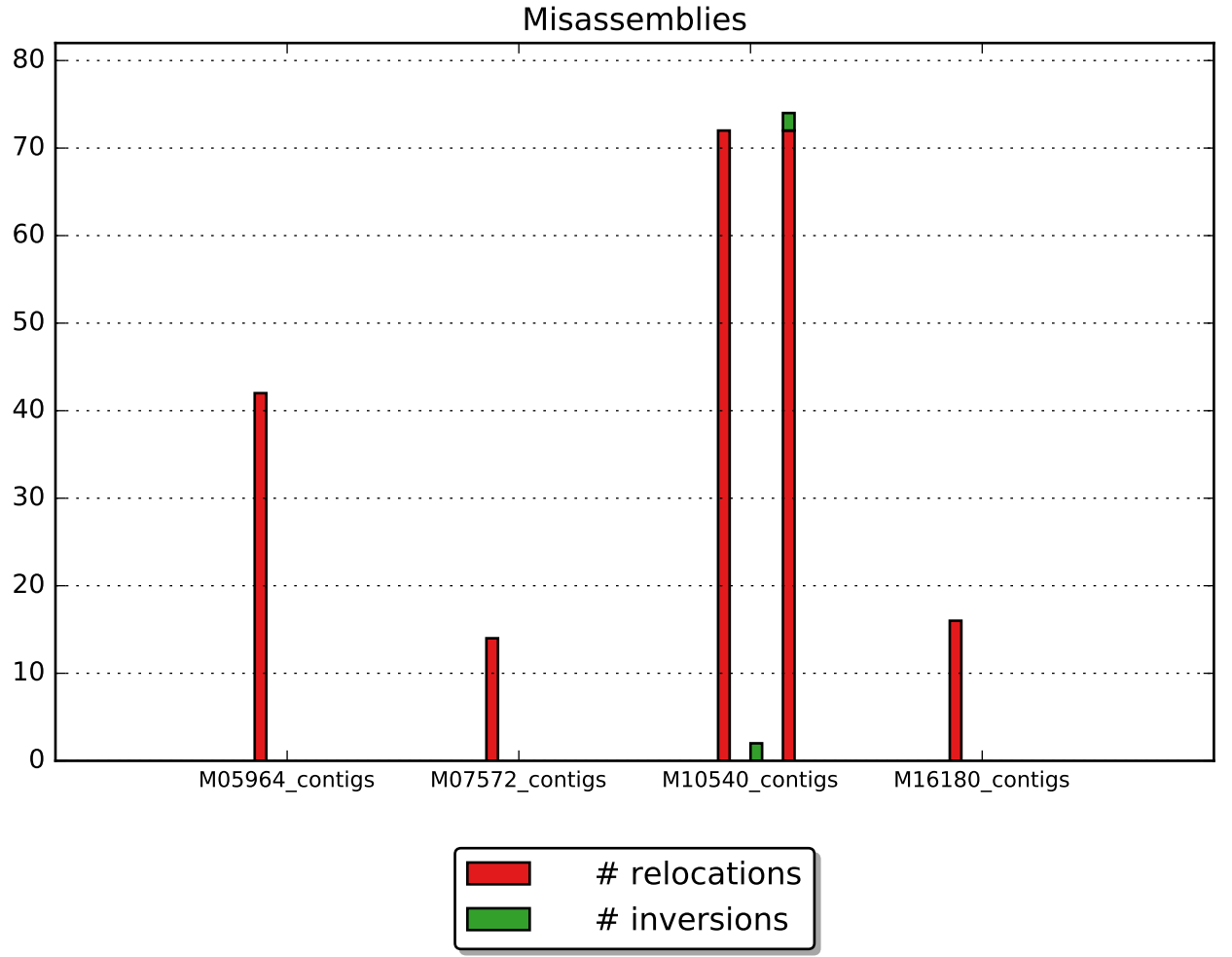
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

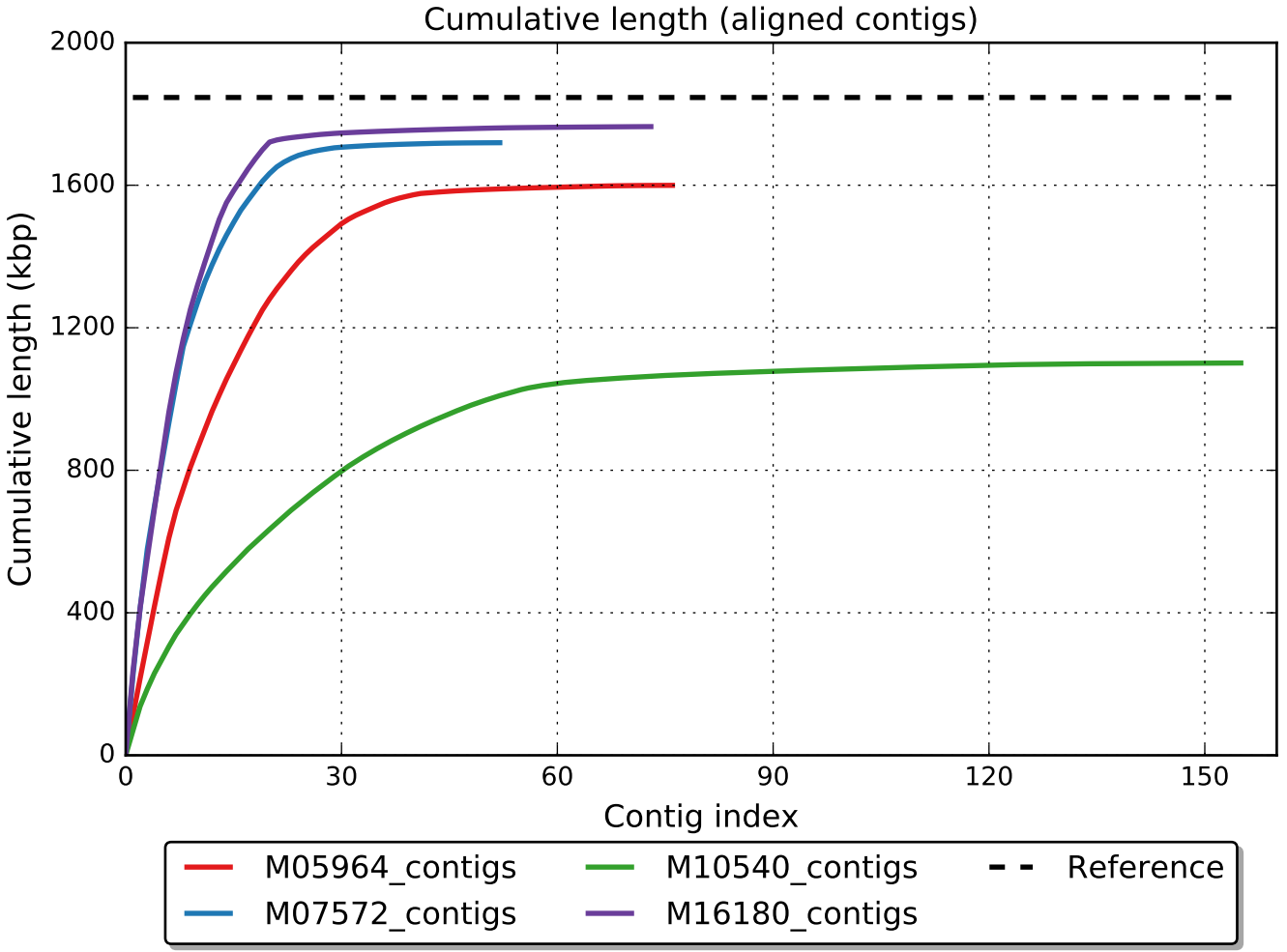

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

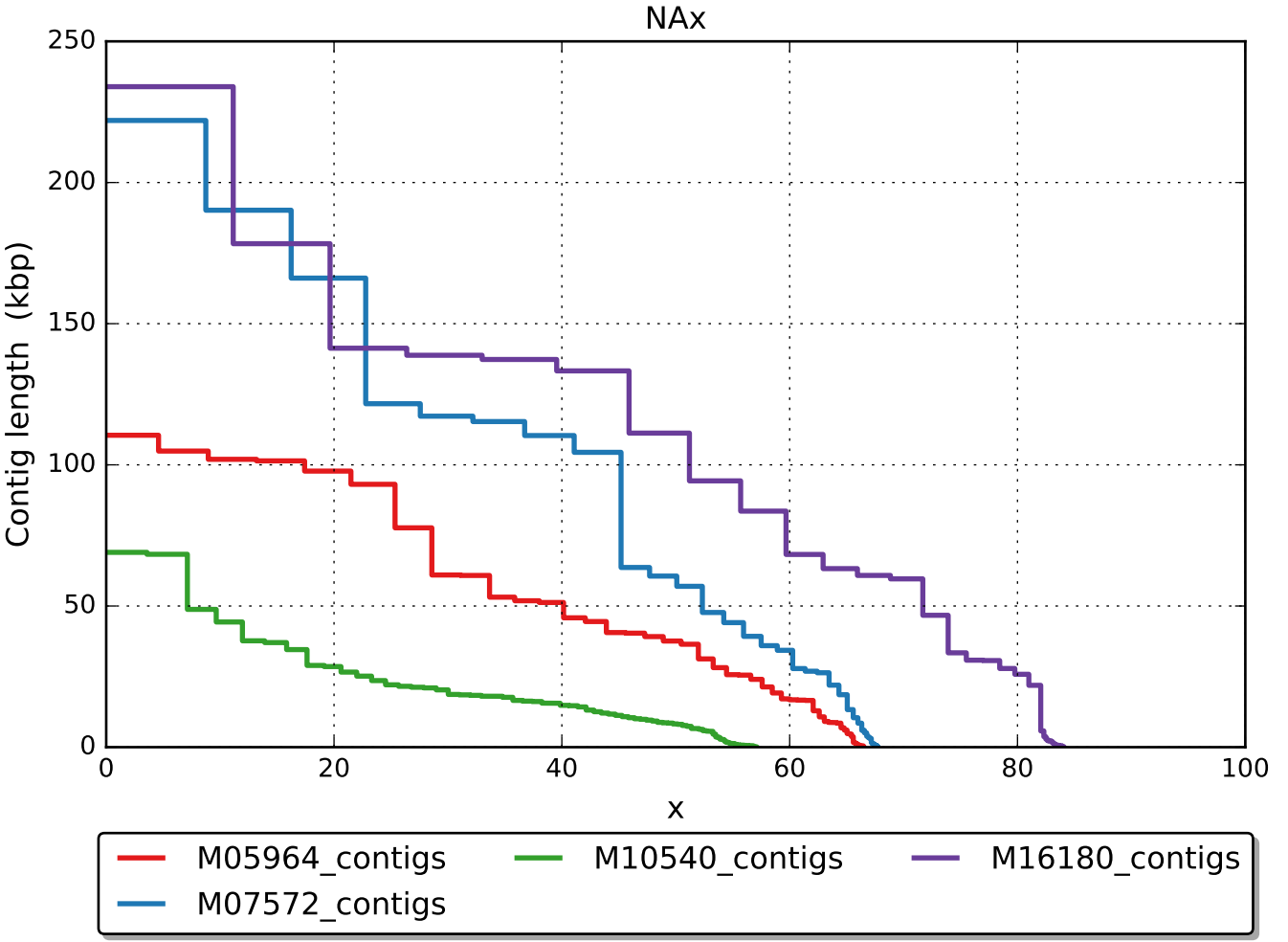

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

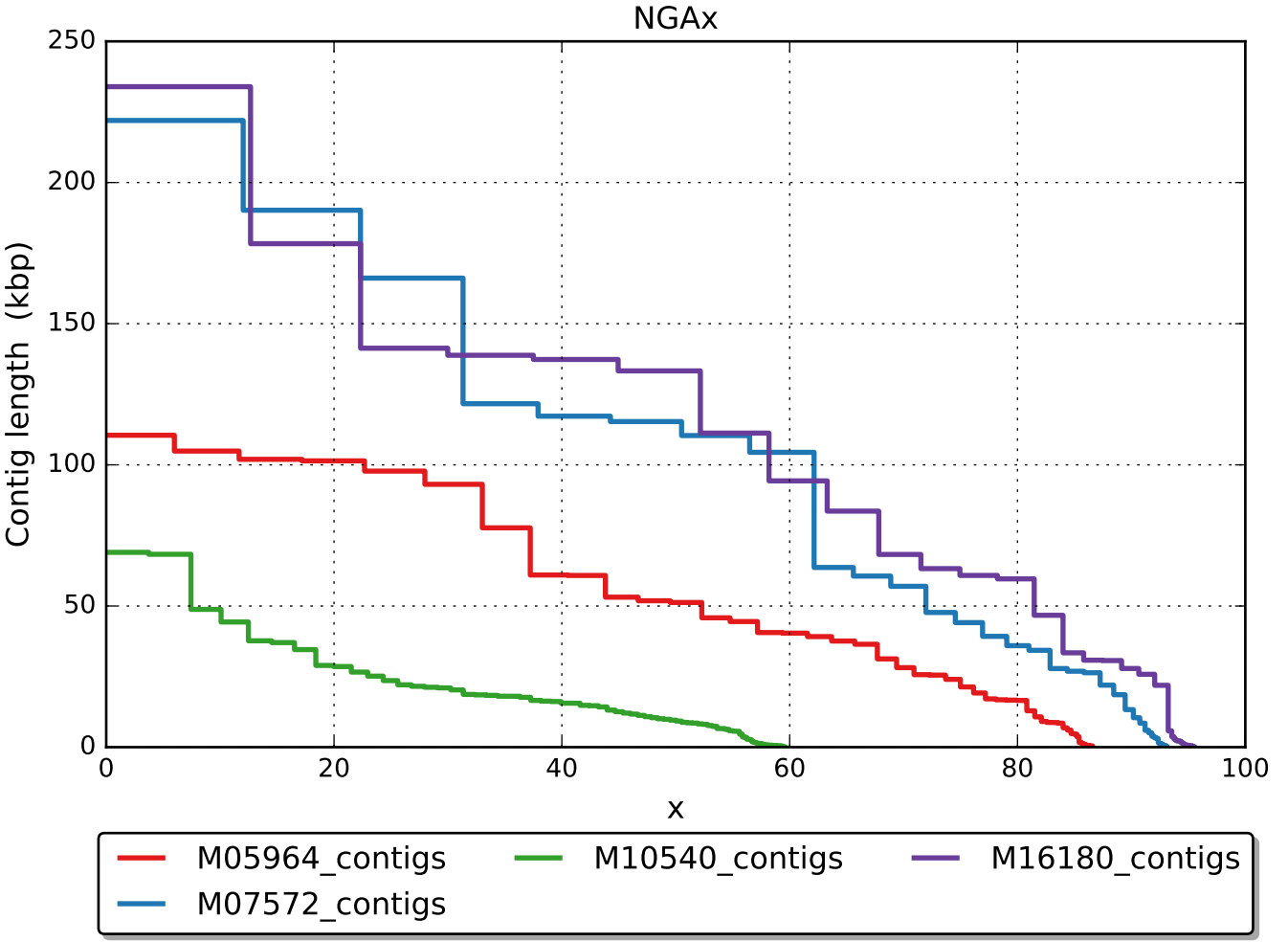

Cumulative length
Cumulative length (kbp)
3000
2500
2000
1500
1000
500
0
0
200
400
600
800
Contig index
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

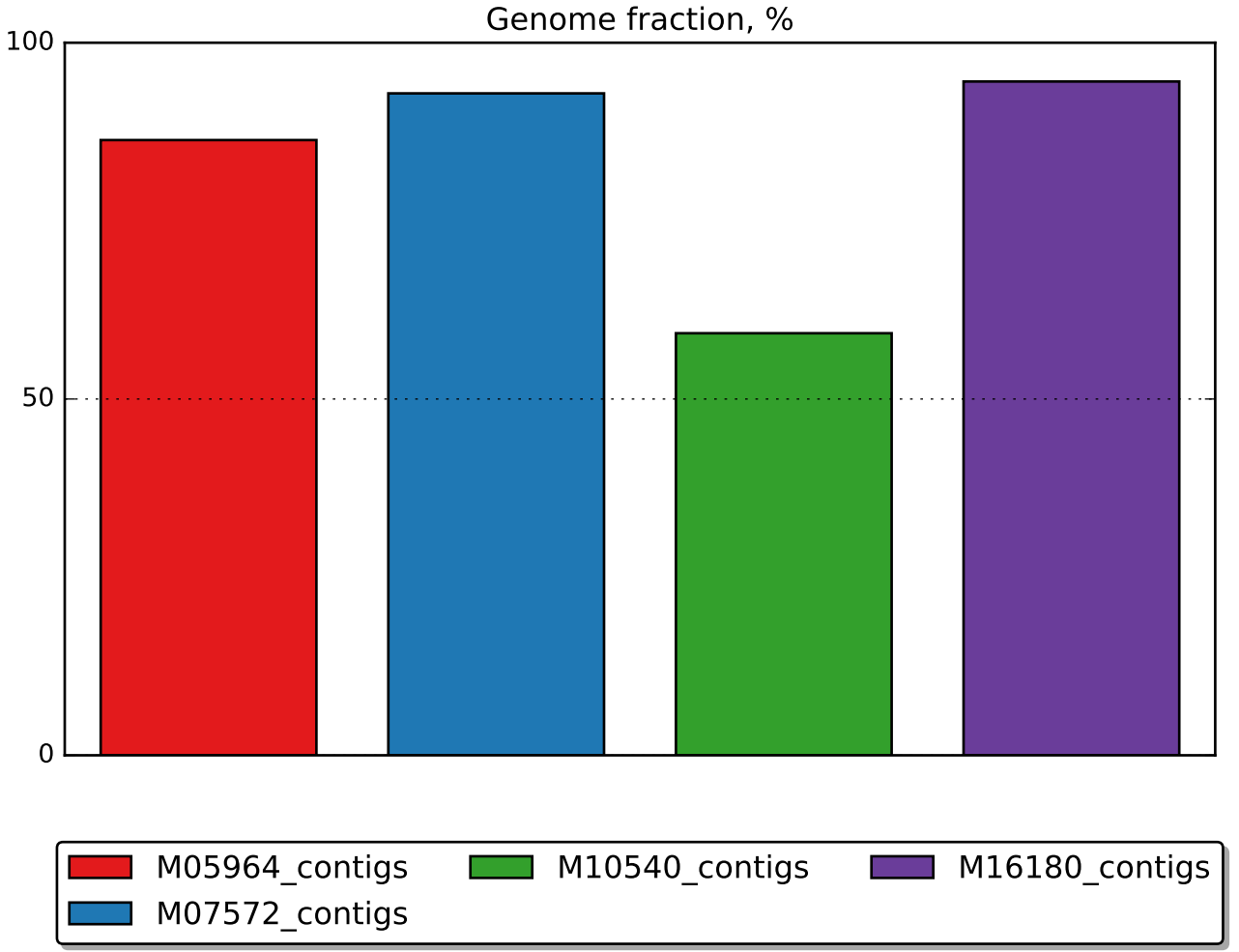

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


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
Contig index
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


NAx
Contig length (kbp)
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)
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