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	1887192	1887192	1887192	1887192
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.01	38.01	38.01	38.01
N50	120793	120675	1150417	165472
NG50	179983	140698	1150417	291100
N75	28168	5904	311604	100510
NG75	117636	79549	311604	134943
L50	5	7	1	4
LG50	3	5	1	3
L75	12	23	2	8
LG75	6	9	2	6
# misassemblies	55	41	92	39
# misassembled contigs	11	15	10	10
Misassembled contigs length	1736208	1717344	1807016	1805243
# local misassemblies	71	60	40	70
# unaligned contigs	730 + 3 part	740 + 9 part	73 + 18 part	136 + 23 part
Unaligned length	584292	697067	67419	203155
Genome fraction (%)	84.688	88.954	56.968	88.358
Duplication ratio	1.139	1.097	1.730	1.136
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2515.11	2410.68	3599.52	2384.62
# indels per 100 kbp	89.66	91.74	113.57	85.52
Largest alignment	178056	138984	66377	135526
NA50	24222	28137	4983	48579
NGA50	37958	55692	6605	55839
NA75	-	-	-	10647
NGA75	13879	26355	-	18831
LA50	23	20	54	14
LGA50	14	12	50	12
LA75	-	-	-	36
LGA75	34	26	-	25

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

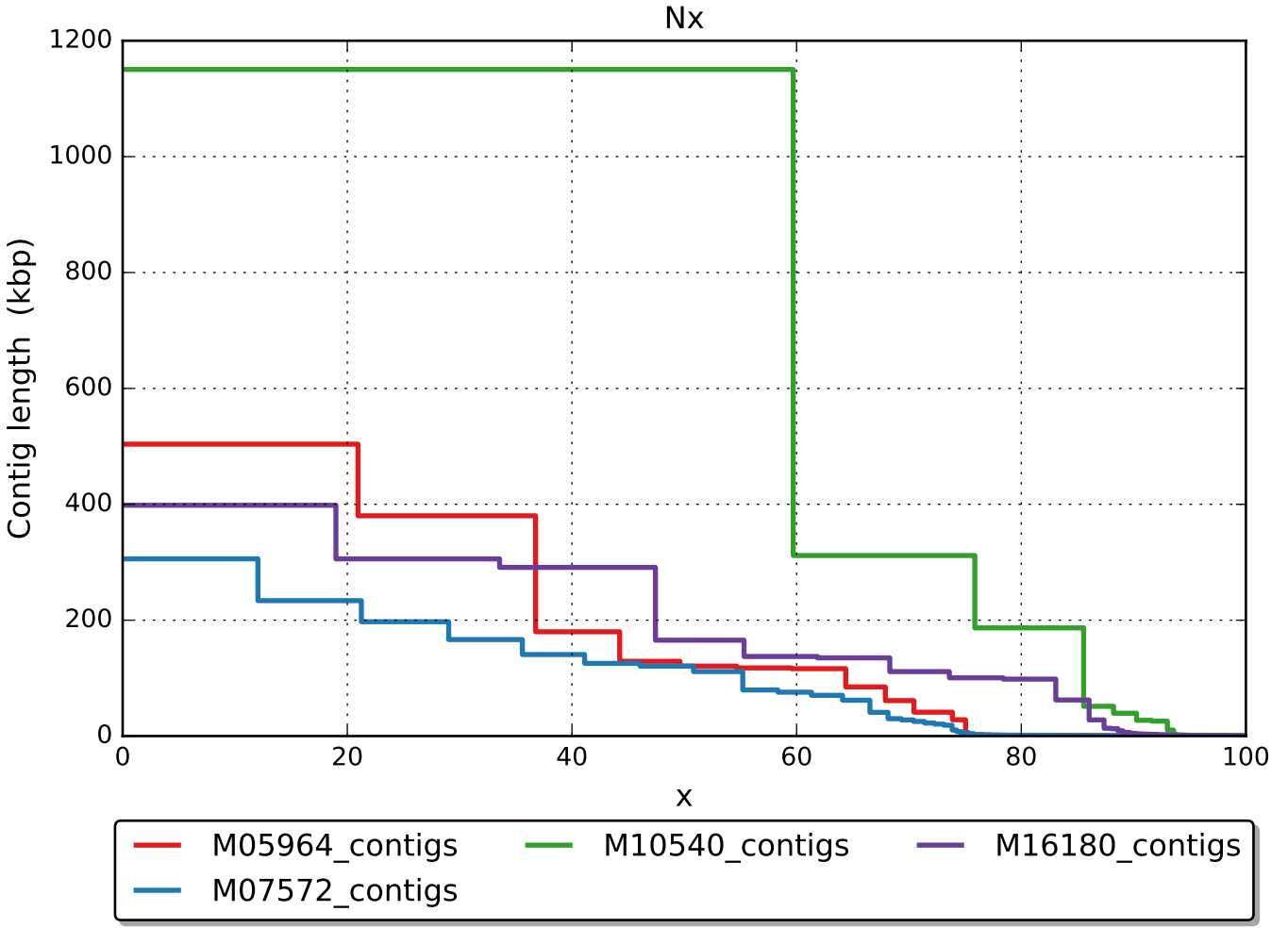
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	55	41	92	39
# relocations	55	41	90	38
# translocations	0	0	0	0
# inversions	0	0	2	1
# misassembled contigs	11	15	10	10
Misassembled contigs length	1736208	1717344	1807016	1805243
# local misassemblies	71	60	40	70
# mismatches	40197	40469	38698	39763
# indels	1433	1540	1221	1426
# short indels	1315	1410	1130	1303
# long indels	118	130	91	123
Indels length	3715	4323	2701	3598

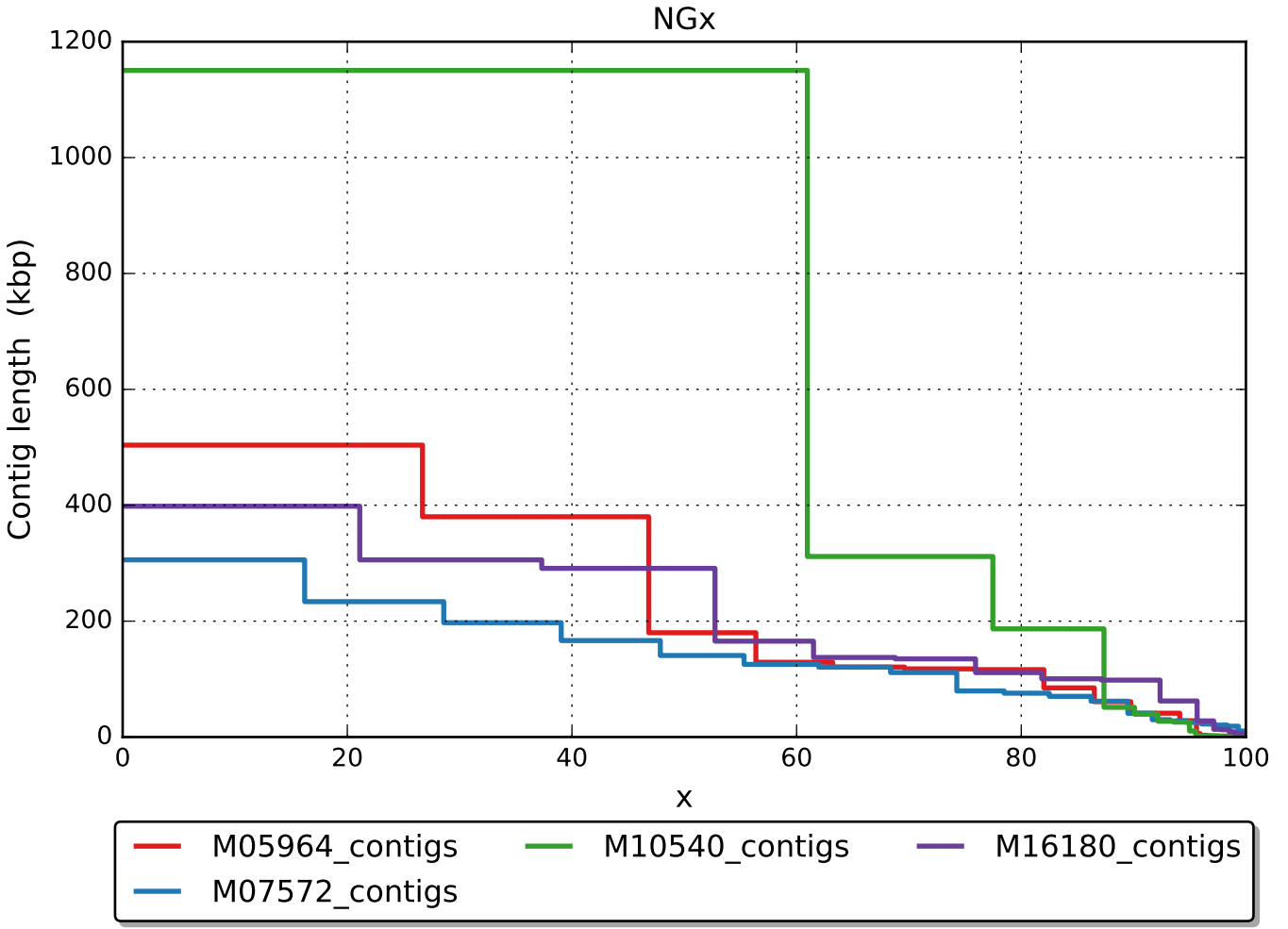
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

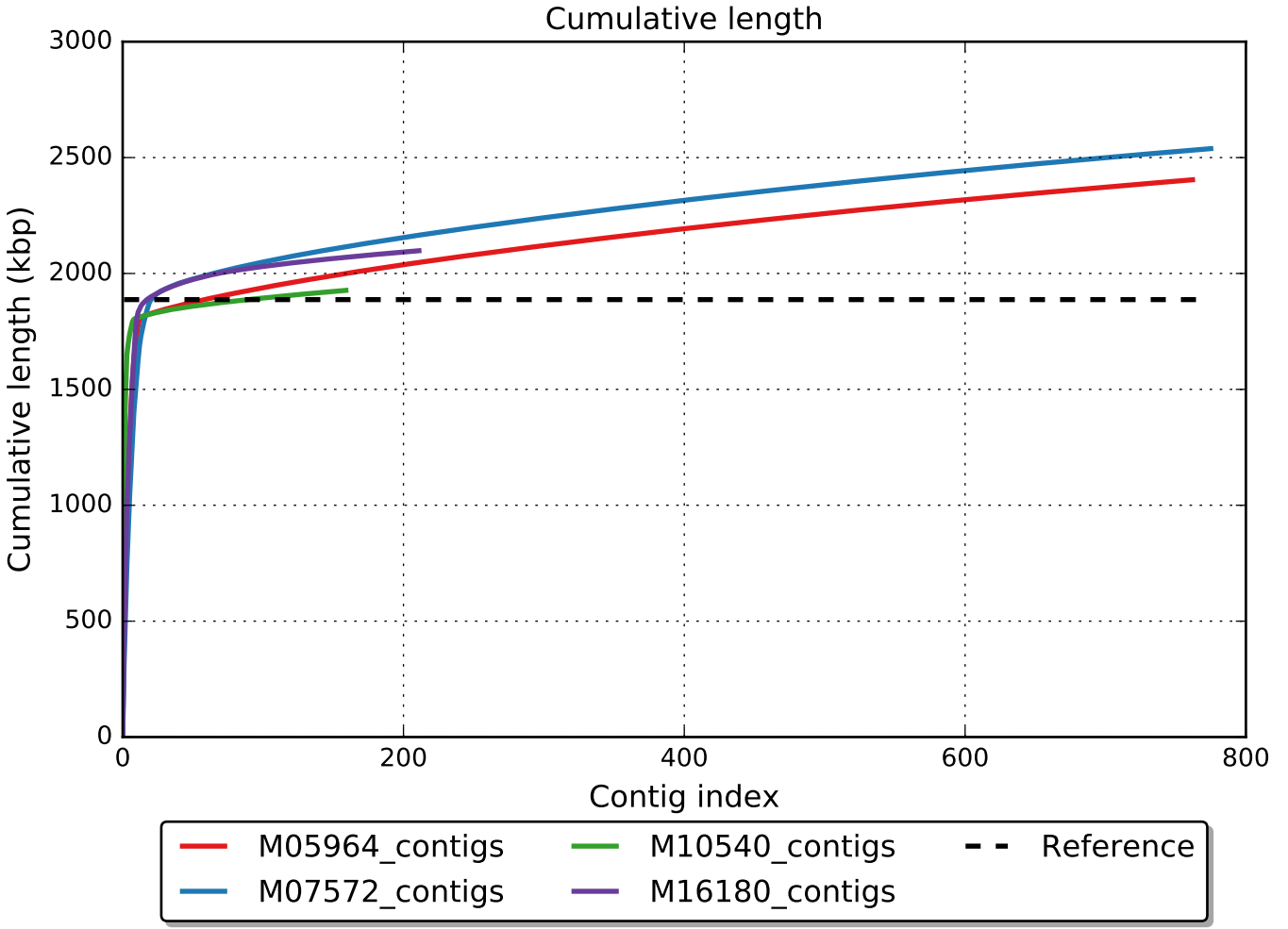
Unaligned report

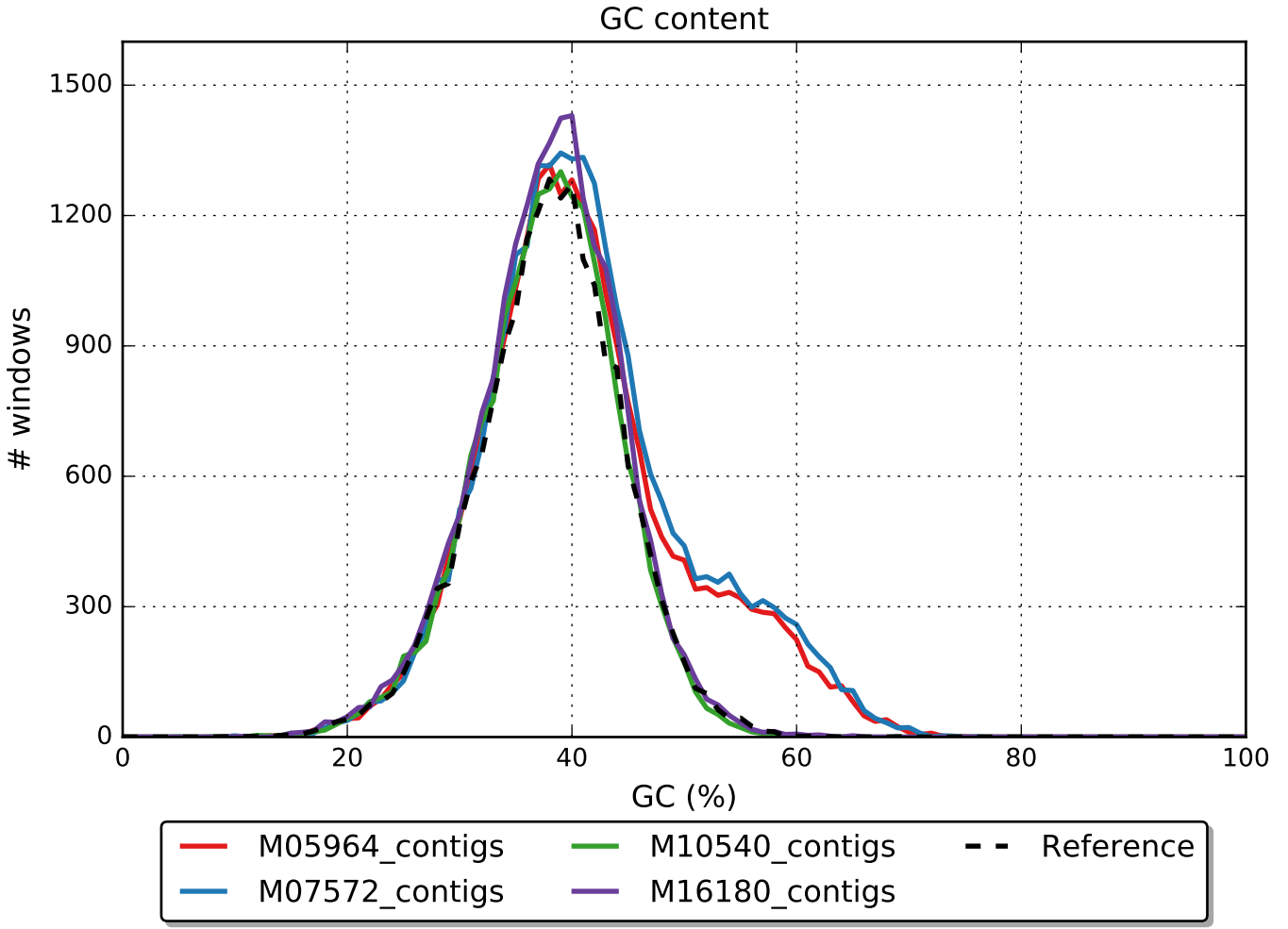
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	730	740	73	136
Fully unaligned length	582527	638469	59767	158518
# partially unaligned contigs	3	9	18	23
# with misassembly	0	2	2	4
# both parts are significant	0	3	0	5
Partially unaligned length	1765	58598	7652	44637
# N's	0	0	0	0

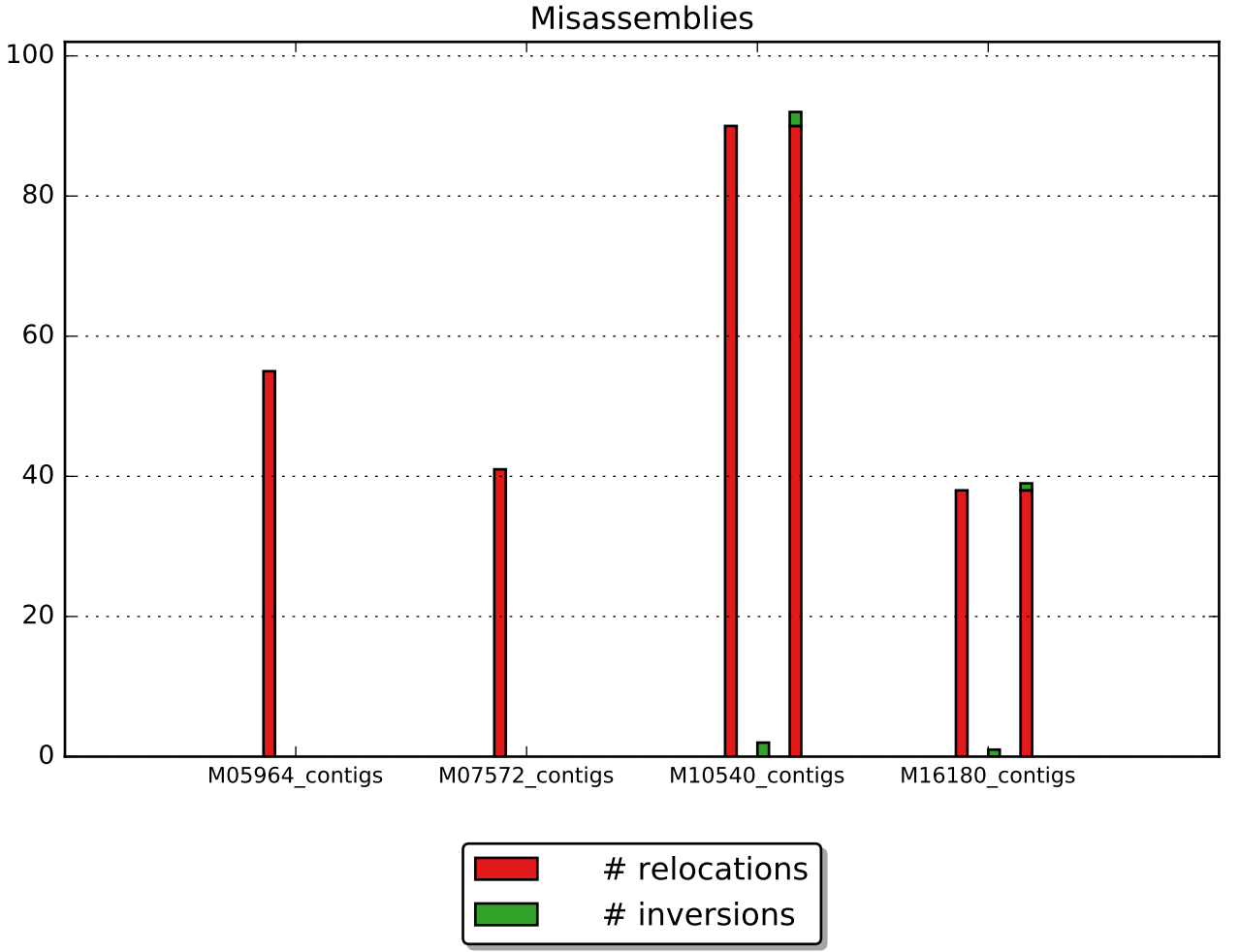
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

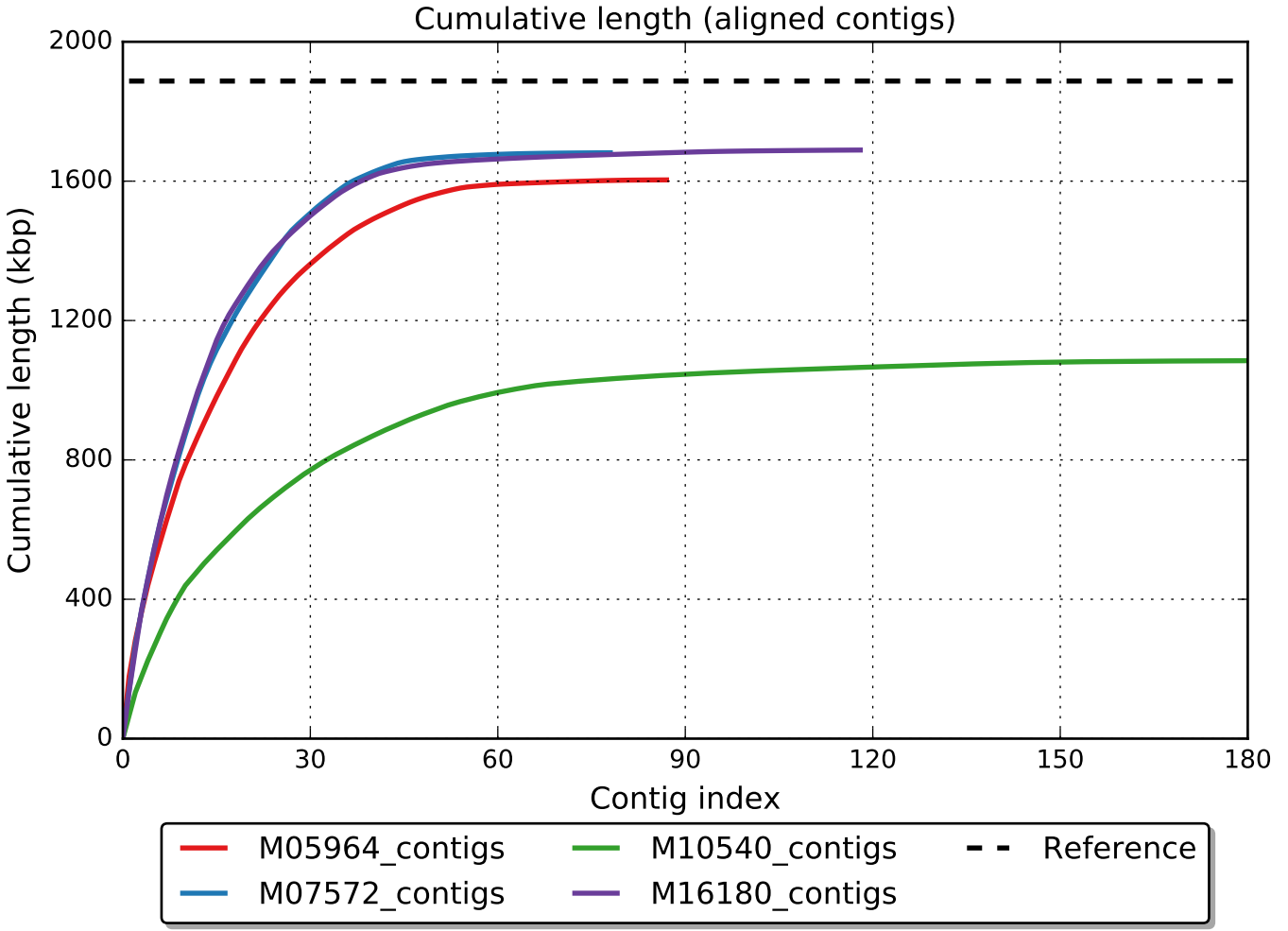

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

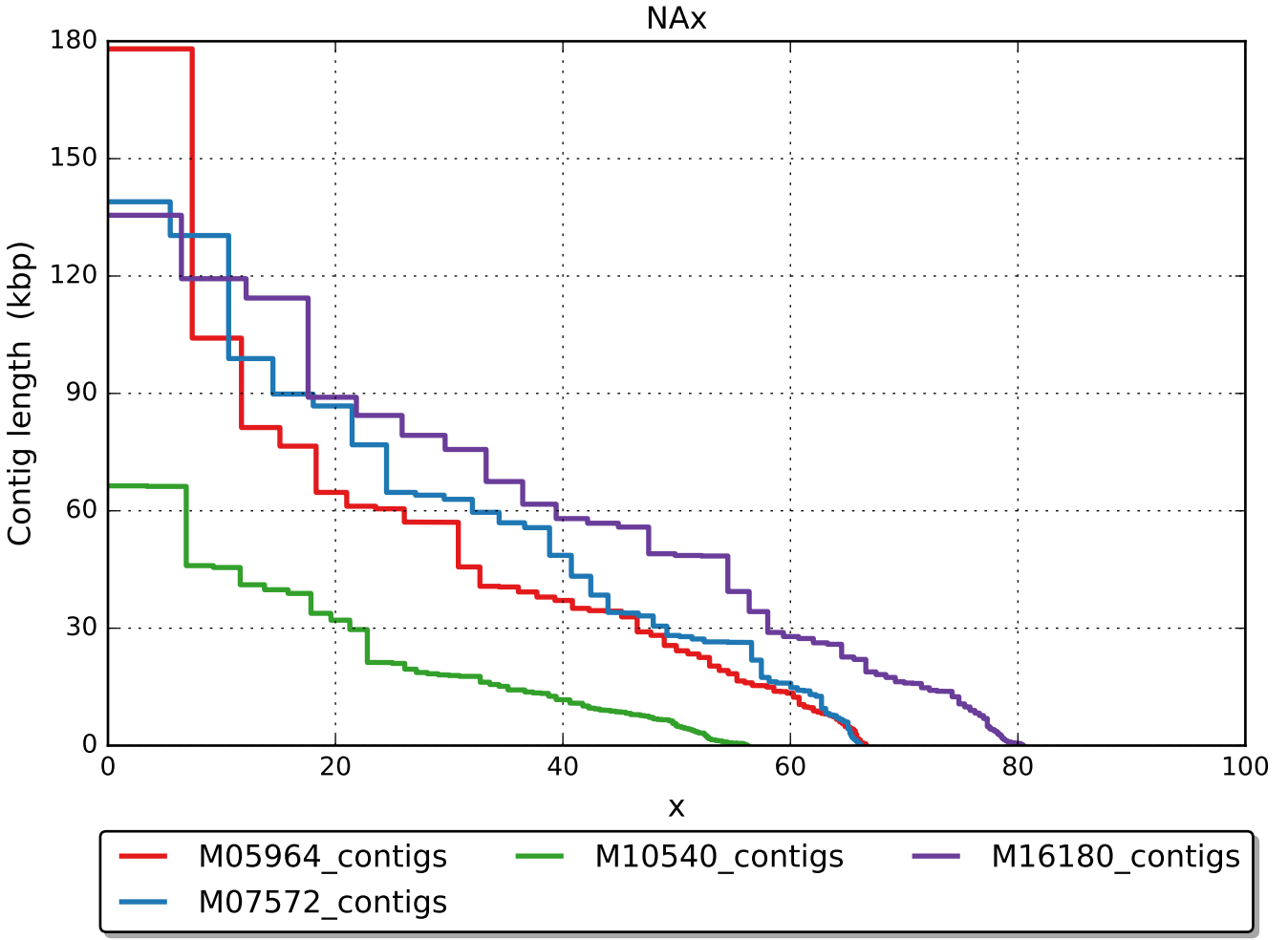

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

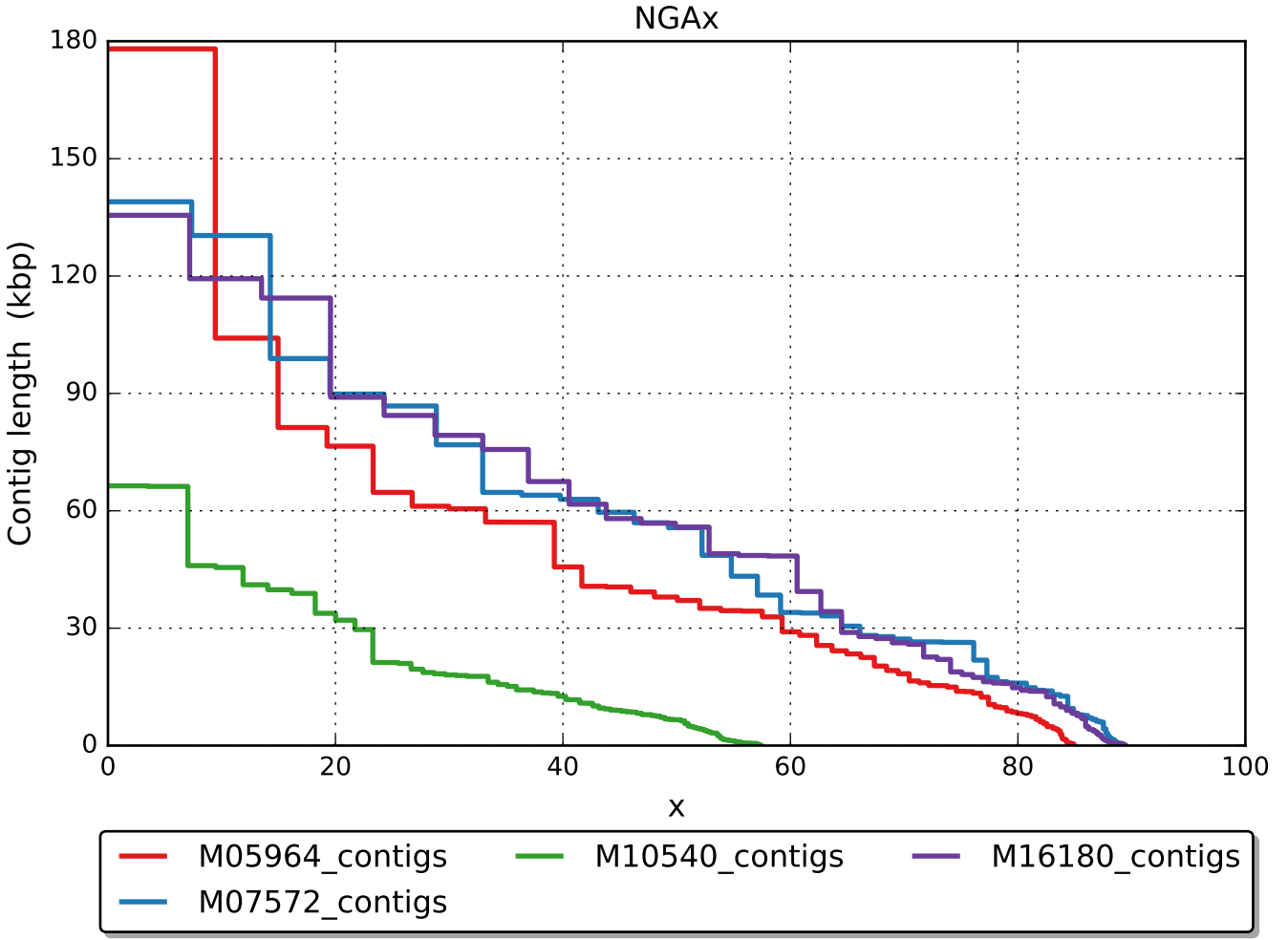

Cumulative length
Cumulative length (kbp)
Contig index
0
500
1000
1500
2000
2500
3000
0
200
400
600
800
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

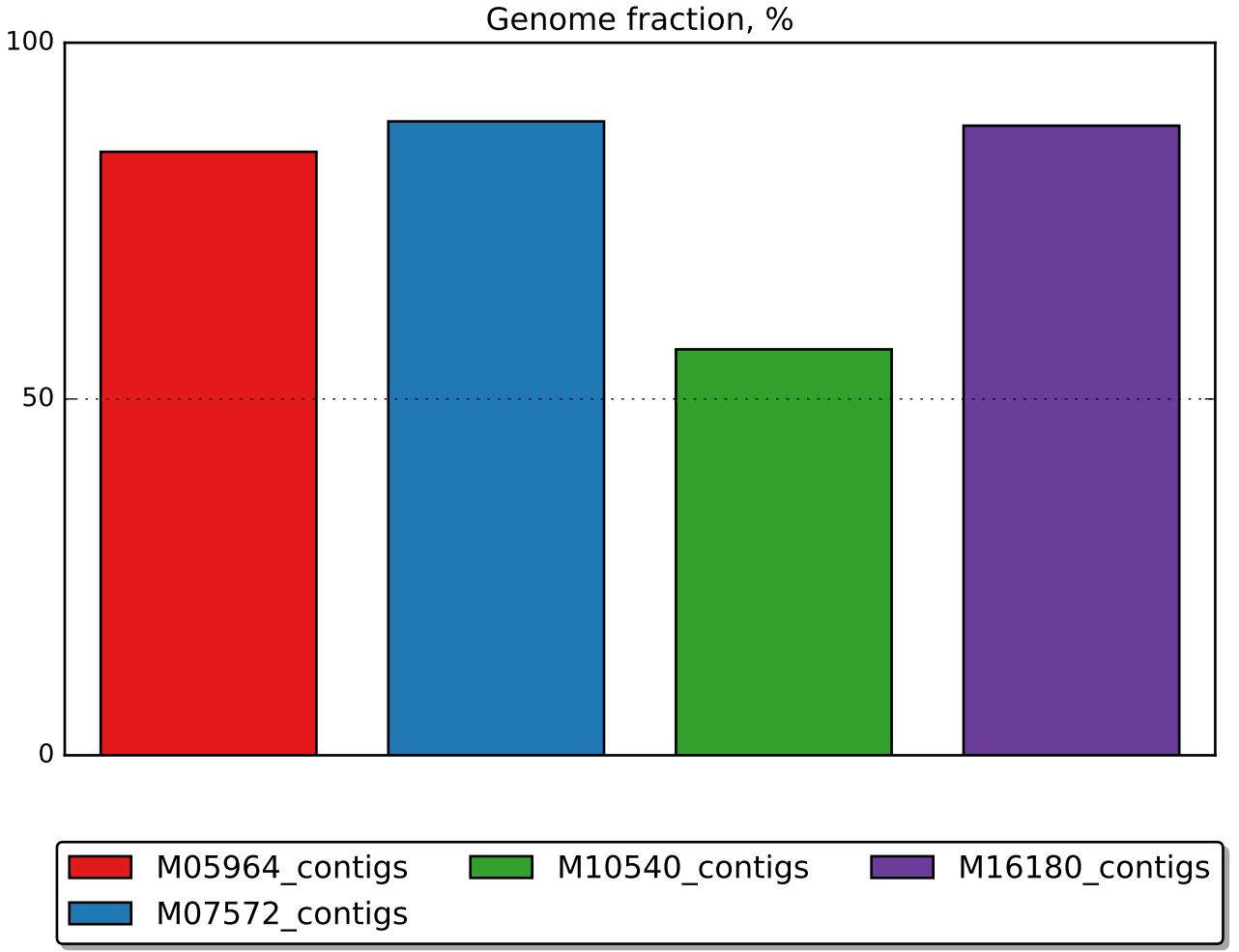

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


Misassemblies
100
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)
180
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)
180
150
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