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	1890645	1890645	1890645	1890645
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.23	38.23	38.23	38.23
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	48	9	86	23
# misassembled contigs	12	8	7	7
Misassembled contigs length	1777375	1154195	1741781	1494429
# local misassemblies	65	16	44	34
# unaligned contigs	716 + 2 part	732 + 5 part	87 + 19 part	146 + 20 part
Unaligned length	568902	635360	121826	218951
Genome fraction (%)	85.769	95.736	59.544	90.220
Duplication ratio	1.132	1.051	1.604	1.102
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2401.71	695.07	3501.89	1676.58
# indels per 100 kbp	60.68	22.15	77.90	44.73
Largest alignment	150891	244412	47680	228567
NA50	26490	61872	8526	62086
NGA50	38866	101545	8646	89728
NA75	-	-	-	21958
NGA75	17107	47097	-	34356
LA50	22	10	47	9
LGA50	14	6	45	8
LA75	-	-	-	22
LGA75	31	13	-	16

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

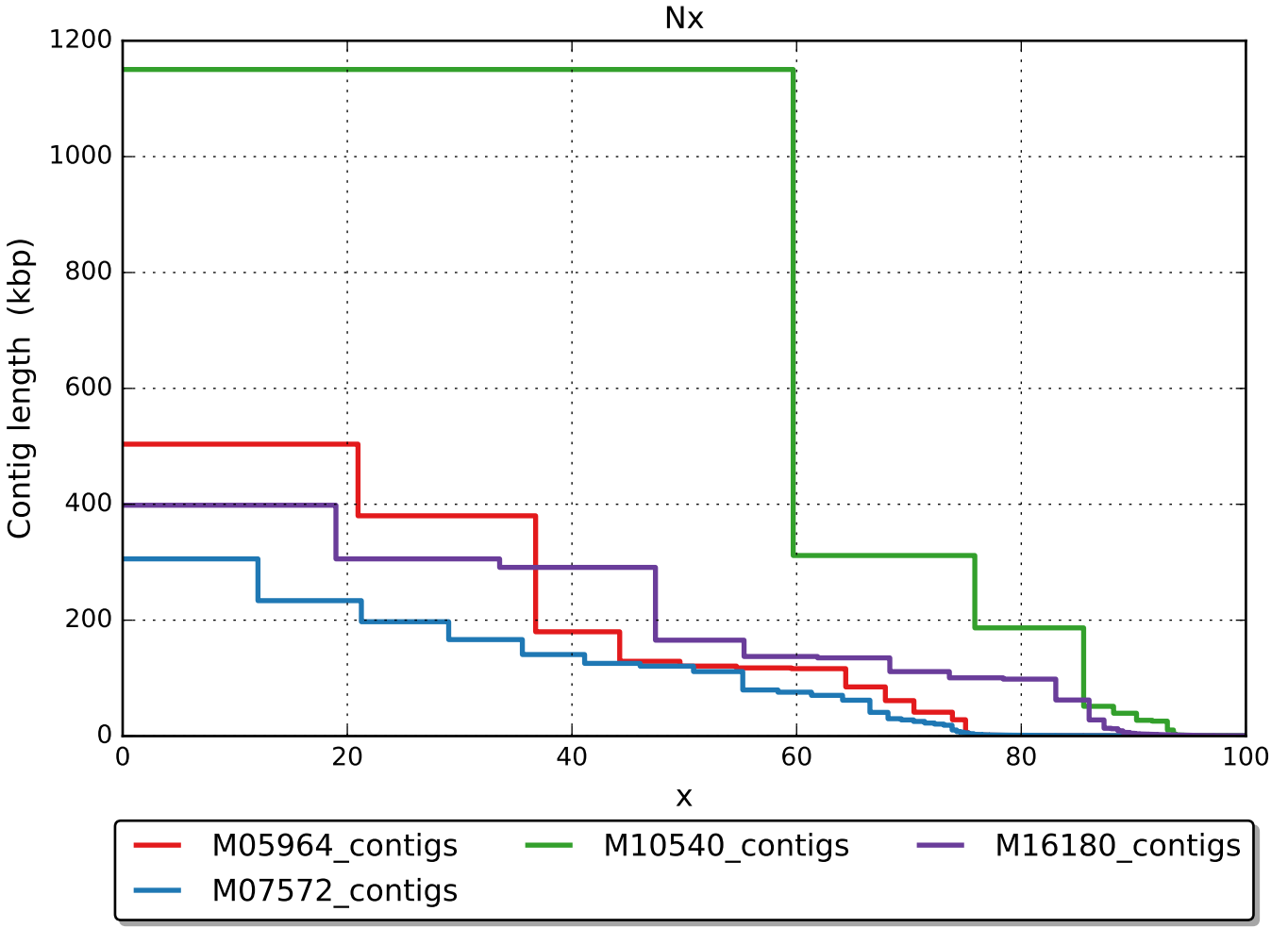
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	48	9	86	23
# relocations	47	9	86	23
# translocations	0	0	0	0
# inversions	1	0	0	0
# misassembled contigs	12	8	7	7
Misassembled contigs length	1777375	1154195	1741781	1494429
# local misassemblies	65	16	44	34
# mismatches	38946	12581	39423	28598
# indels	984	401	877	763
# short indels	868	339	788	662
# long indels	116	62	89	101
Indels length	3165	2003	2191	2805

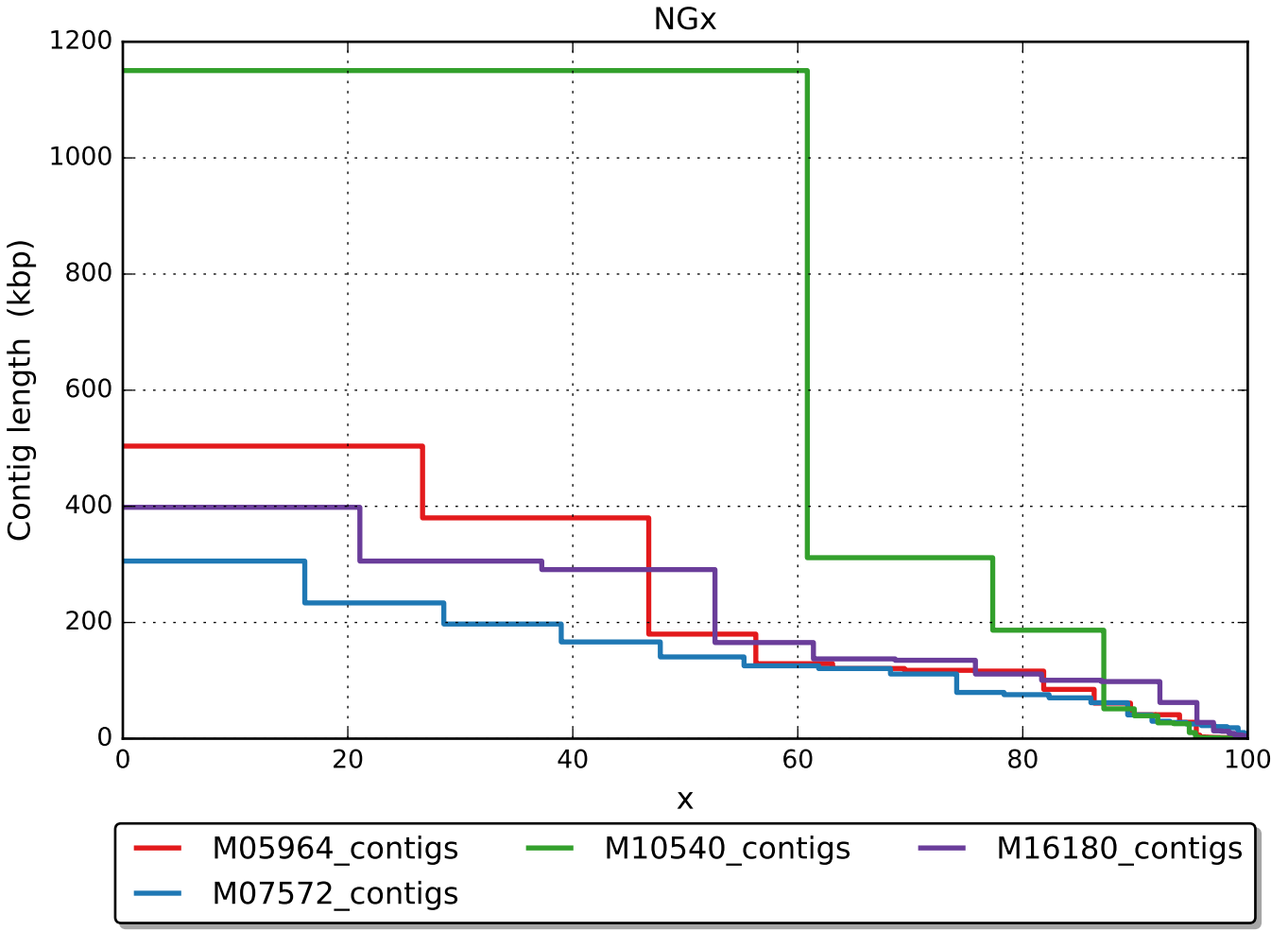
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

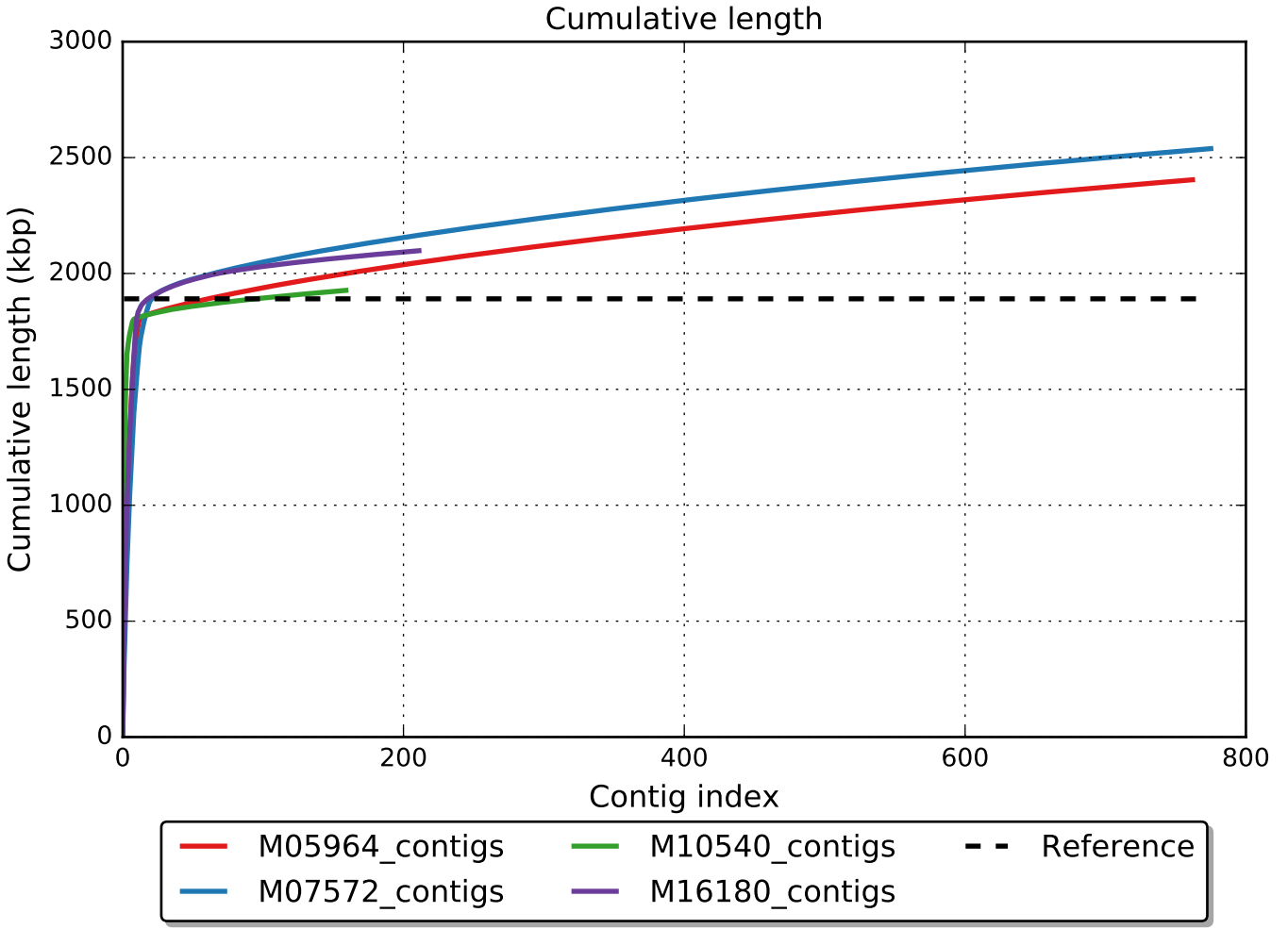
Unaligned report

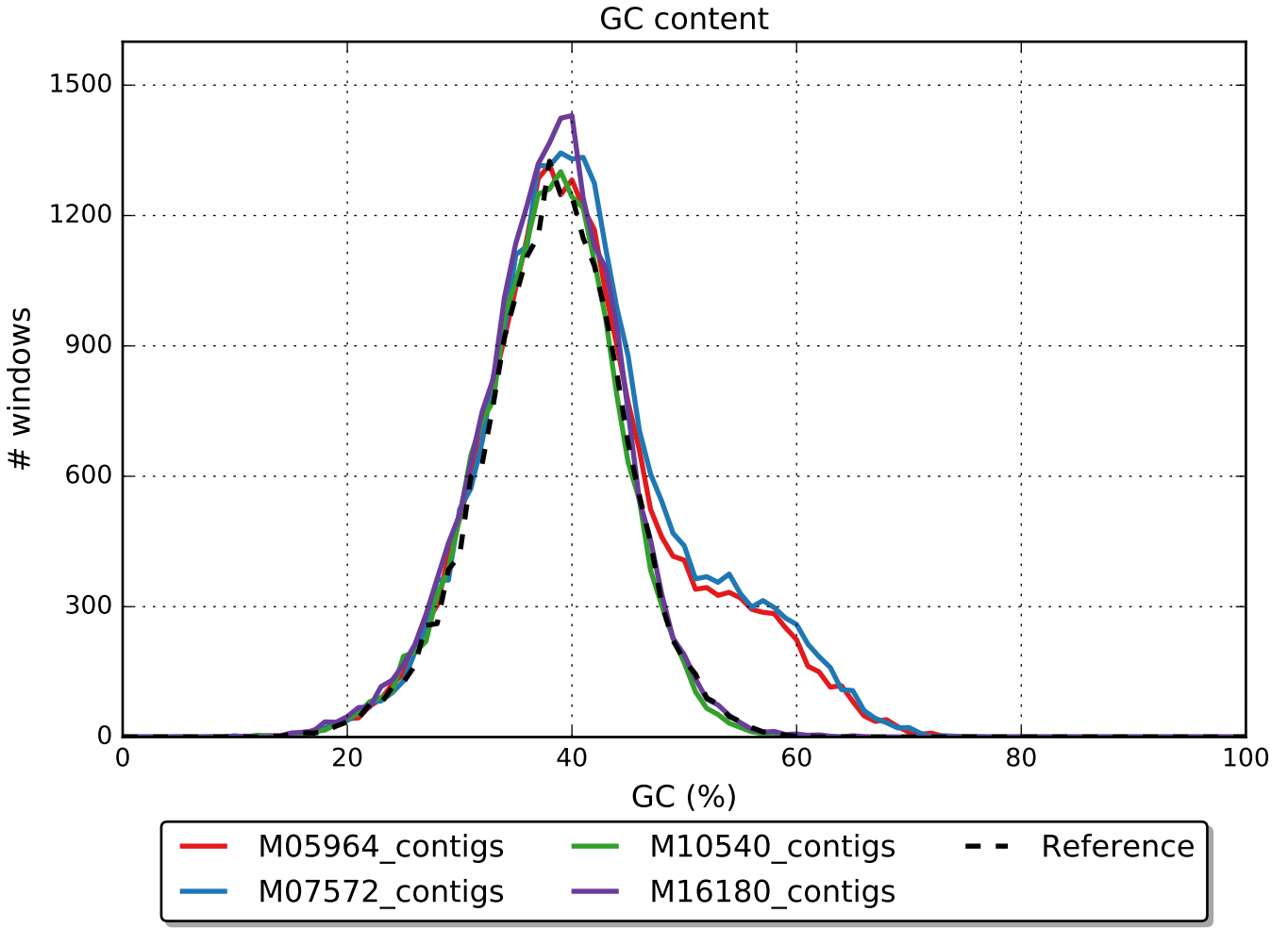
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	716	732	87	146
Fully unaligned length	565749	596582	69724	184339
# partially unaligned contigs	2	5	19	20
# with misassembly	0	3	5	2
# both parts are significant	2	3	1	2
Partially unaligned length	3153	38778	52102	34612
# N's	0	0	0	0

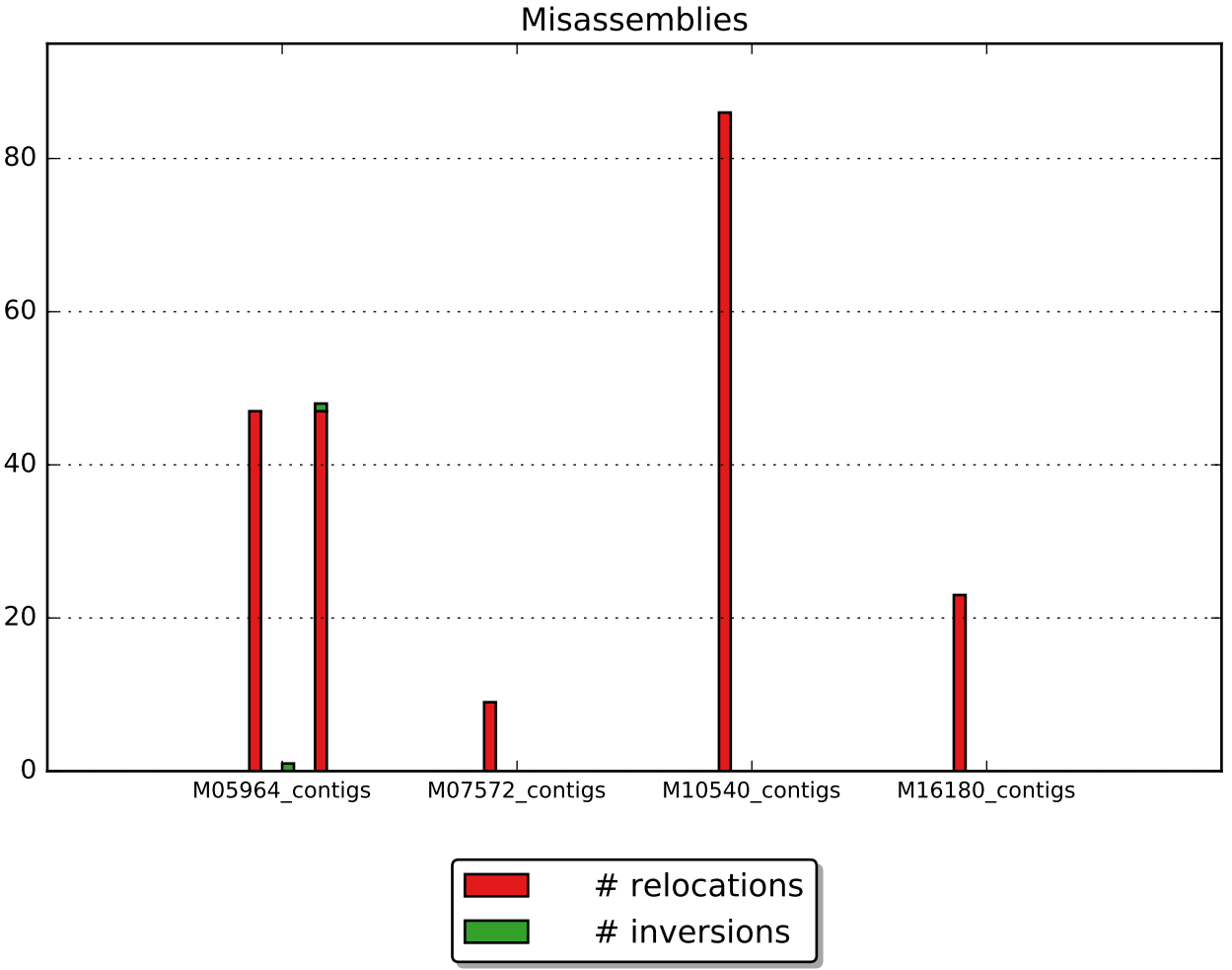
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

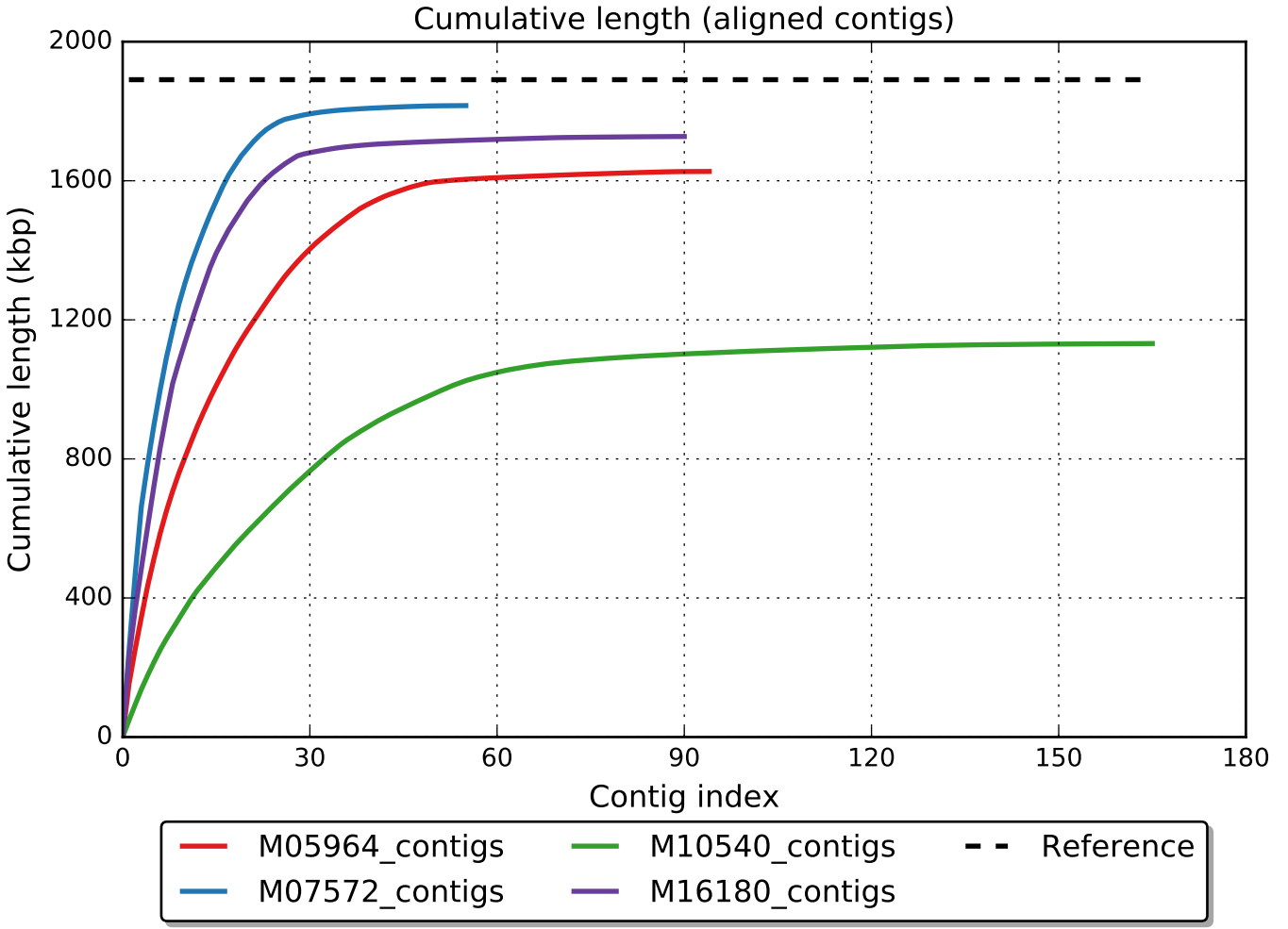

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

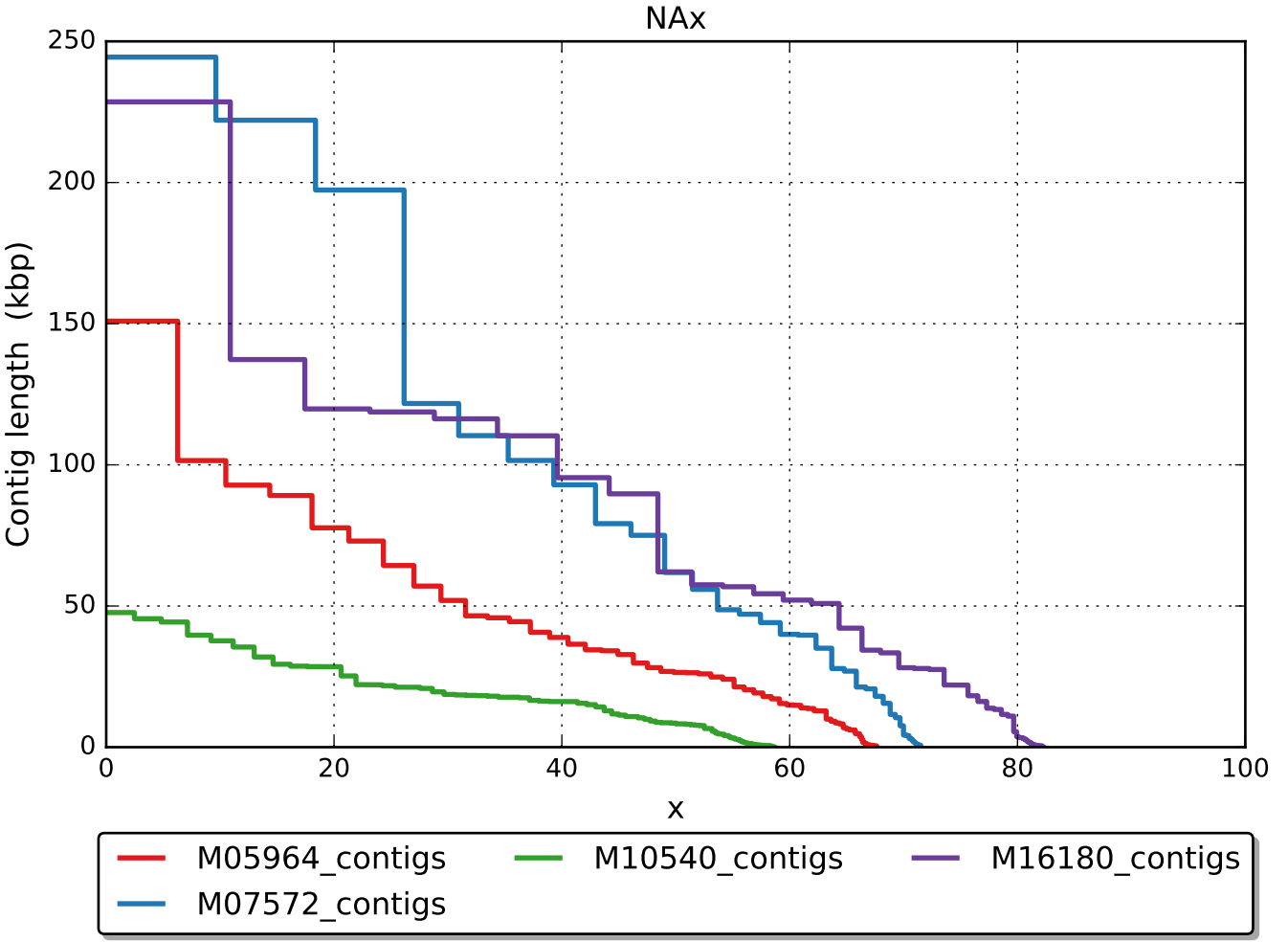

NGx
Contig length (kbp)
1200
1000
800
600
400
200
0
0
20
40
60
80
100
x
M05964_contigs
M10540_contigs
M16180_contigs
M07572_contigs

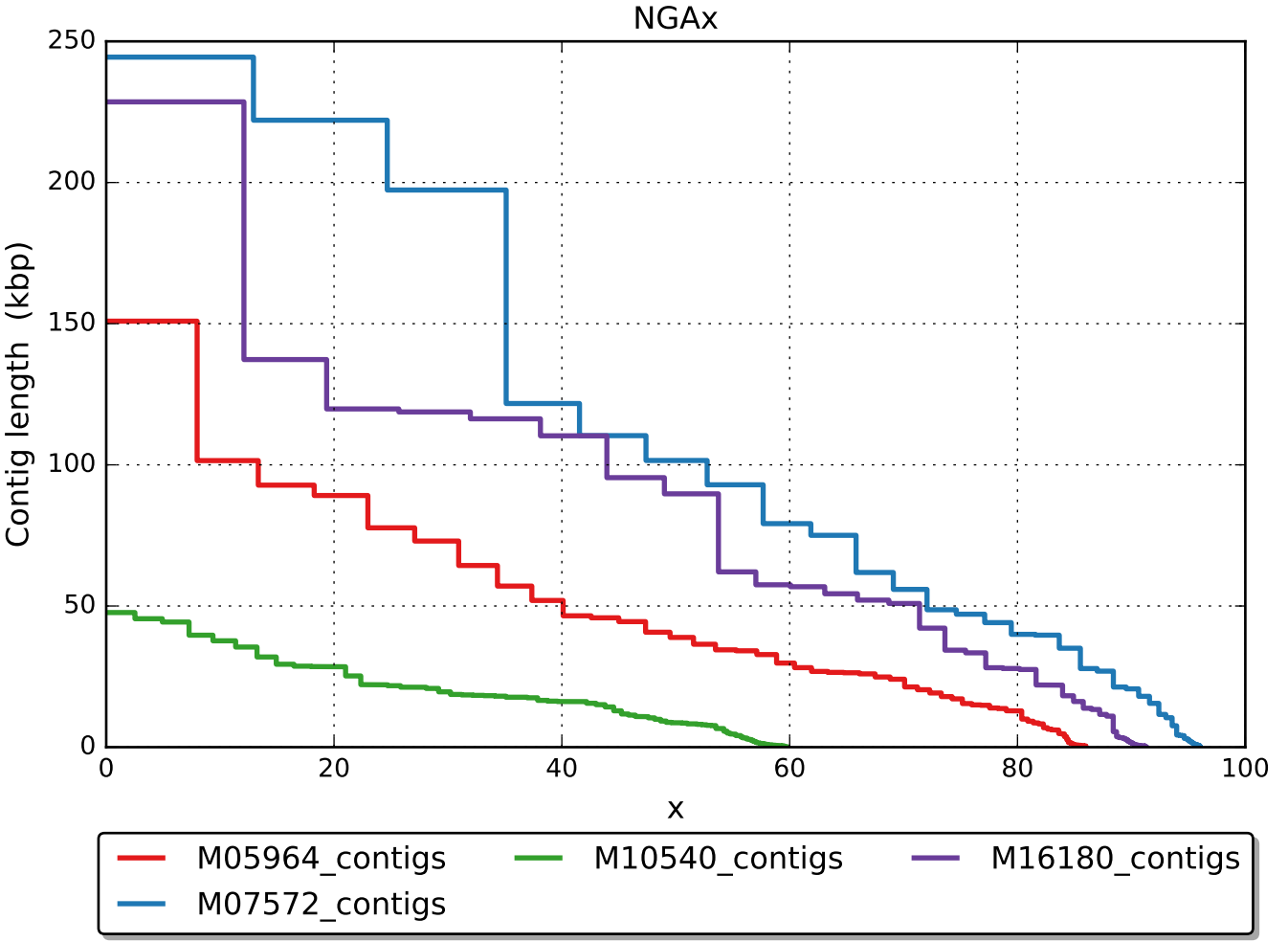

Cumulative length
Cumulative length (kbp)
3000
2500
2000
1500
1000
500
0
0
200
400
600
800
Contig index
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference

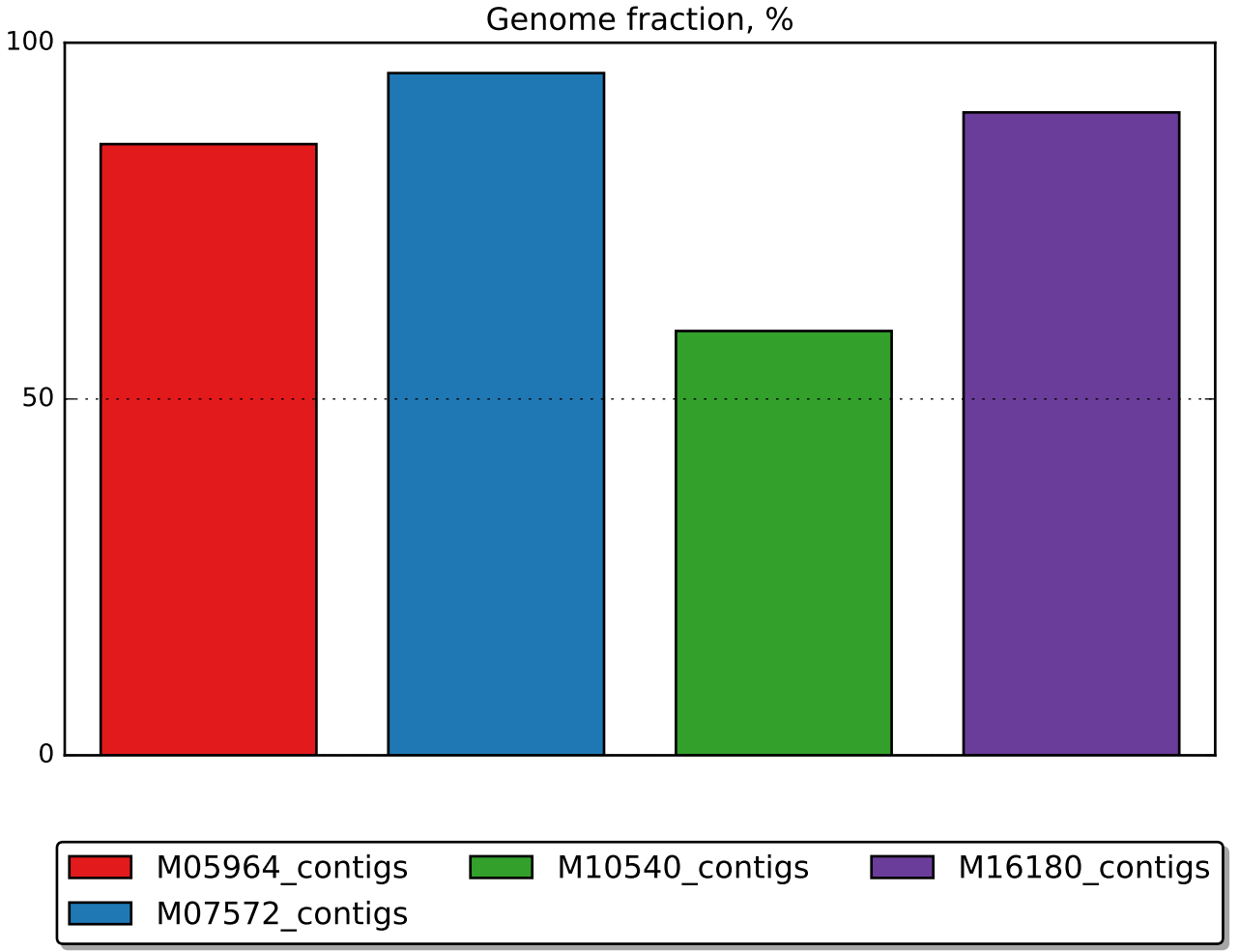

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference


Misassemblies
80
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)
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