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	1846503	1846503	1846503	1846503
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	16	31	82	35
# misassembled contigs	6	14	8	13
Misassembled contigs length	1394085	1644649	1616855	1813490
# local misassemblies	31	63	39	64
# unaligned contigs	736 + 2 part	742 + 5 part	89 + 16 part	135 + 16 part
Unaligned length	582483	679647	173374	196315
Genome fraction (%)	93.629	90.130	61.877	89.606
Duplication ratio	1.054	1.117	1.535	1.149
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	1467.14	2427.33	3564.26	2444.20
# indels per 100 kbp	46.45	60.93	84.46	67.87
Largest alignment	336208	133389	82226	172795
NA50	73975	28953	8470	45225
NGA50	102421	45451	9098	54354
NA75	-	-	-	9250
NGA75	41080	26499	-	27757
LA50	9	21	47	14
LGA50	6	11	43	11
LA75	-	-	-	33
LGA75	13	25	-	23

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).
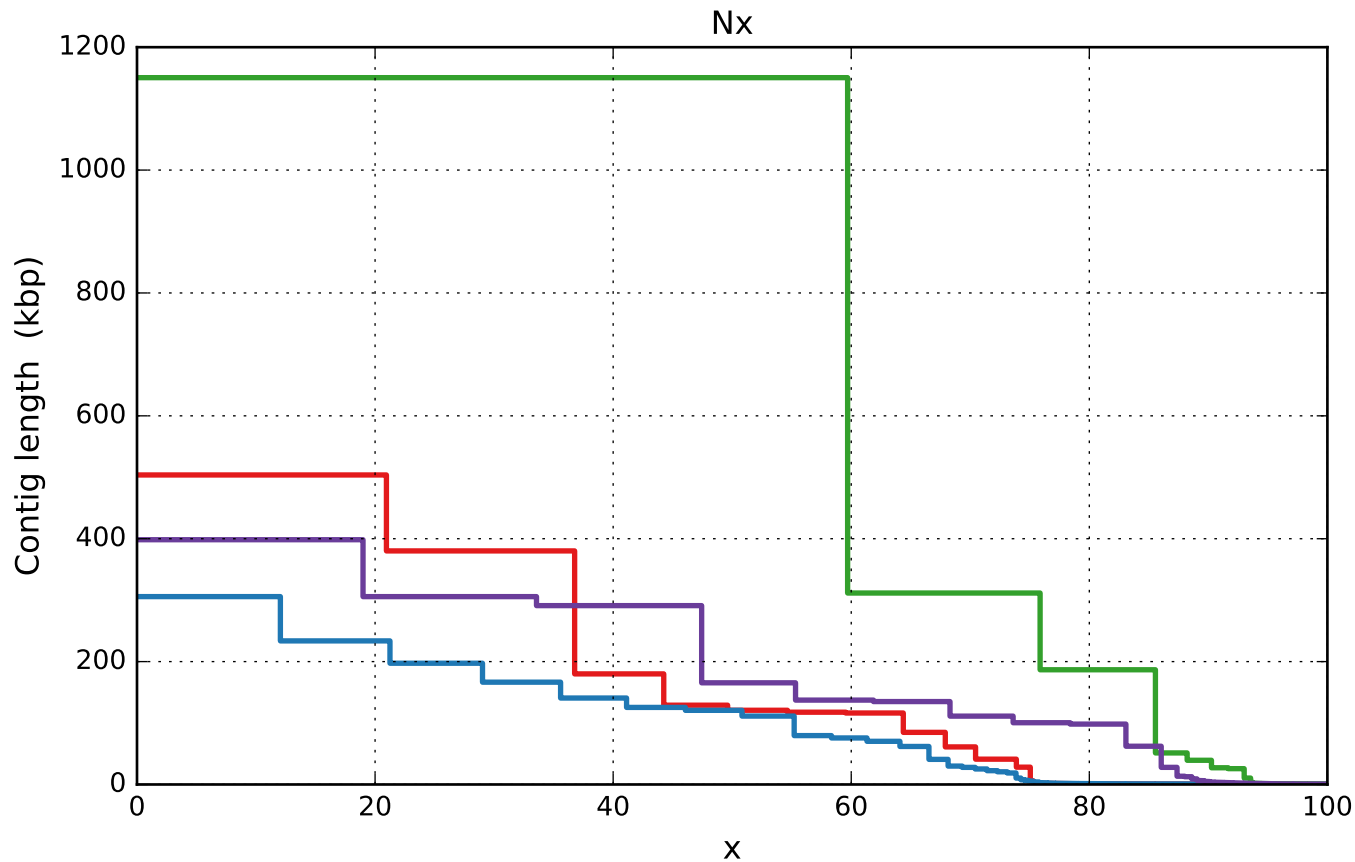
Misassemblies report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	16	31	82	35
# relocations	16	31	80	35
# translocations	0	0	0	0
# inversions	0	0	2	0
# misassembled contigs	6	14	8	13
Misassembled contigs length	1394085	1644649	1616855	1813490
# local misassemblies	31	63	39	64
# mismatches	25365	40397	40724	40441
# indels	803	1014	965	1123
# short indels	712	895	881	995
# long indels	91	119	84	128
Indels length	2720	3473	2477	3471

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).
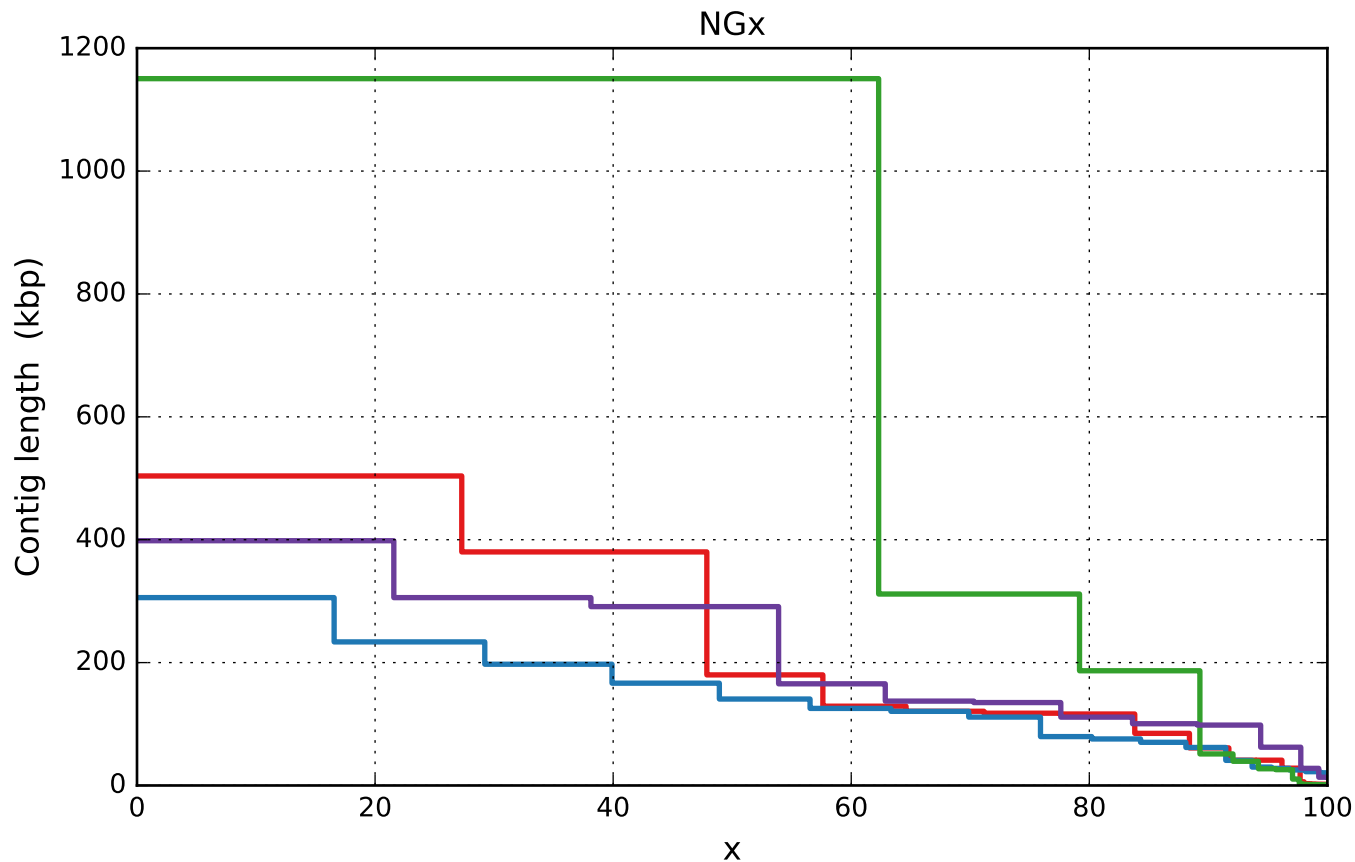
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	736	742	89	135
Fully unaligned length	580773	652214	72883	169923
# partially unaligned contigs	2	5	16	16
# with misassembly	0	1	2	1
# both parts are significant	1	1	1	3
Partially unaligned length	1710	27433	100491	26392
# 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

NGx

Contig length (kbp)

x

M05964_contigs   M10540_contigs   M16180_contigs
M07572_contigs

Cumulative length
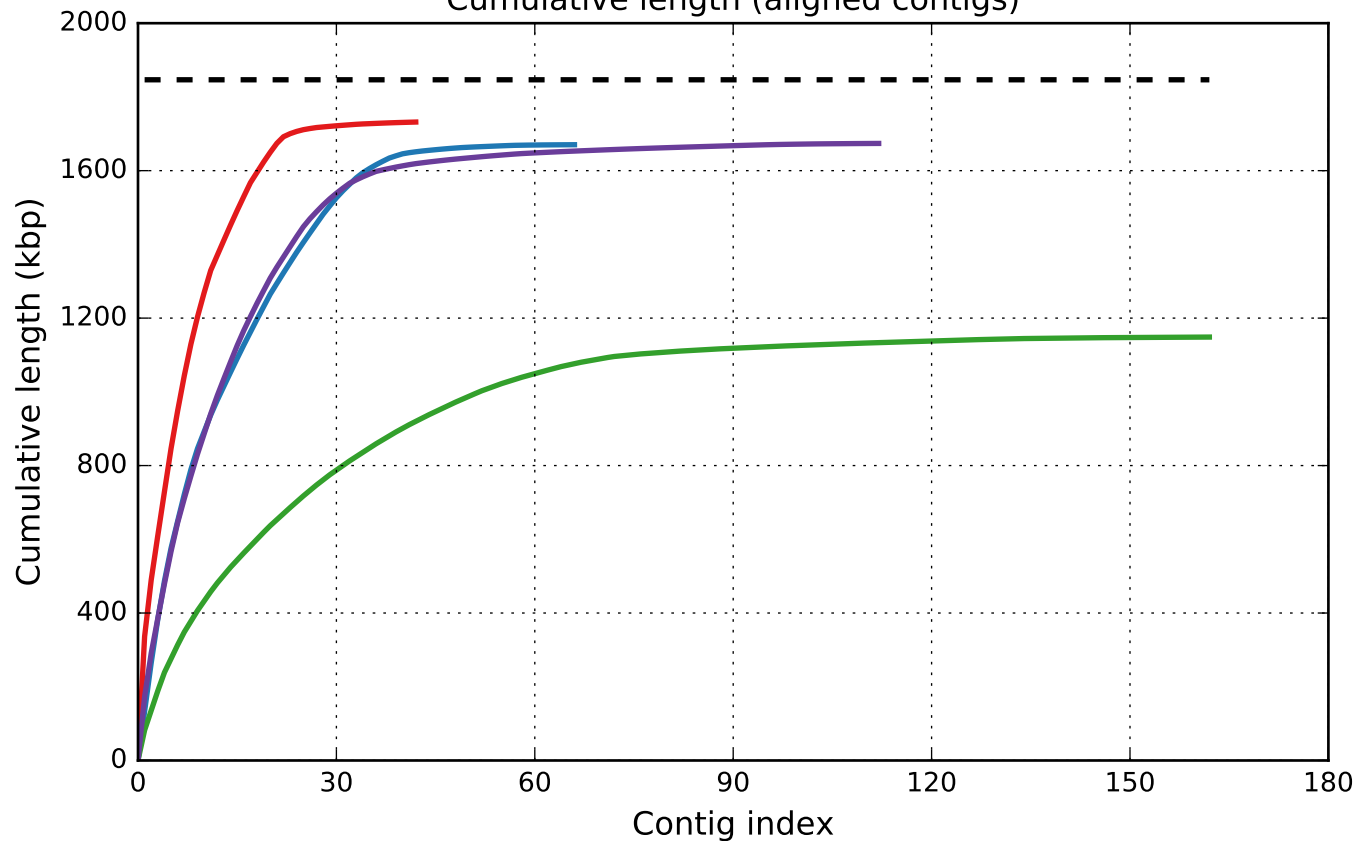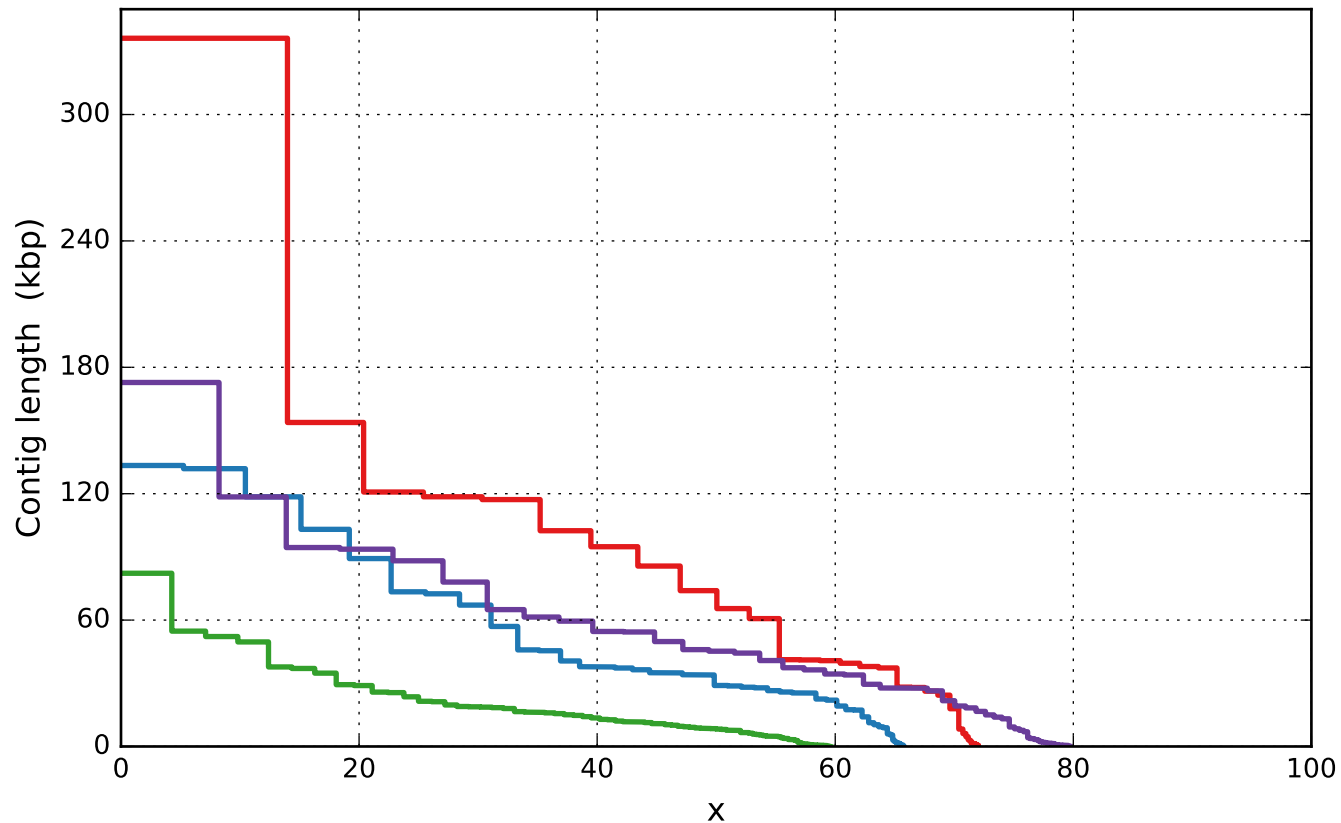
Legend:
- M05964_contigs (red)
- M07572_contigs (blue)
- M10540_contigs (green)
- M16180_contigs (purple)
- Reference (black dashed)

X-axis: Contig index
Y-axis: Cumulative length (kbp)

GC content

windows

GC (%)

M05964_contigs
M07572_contigs
M10540_contigs
M16180_contigs
Reference
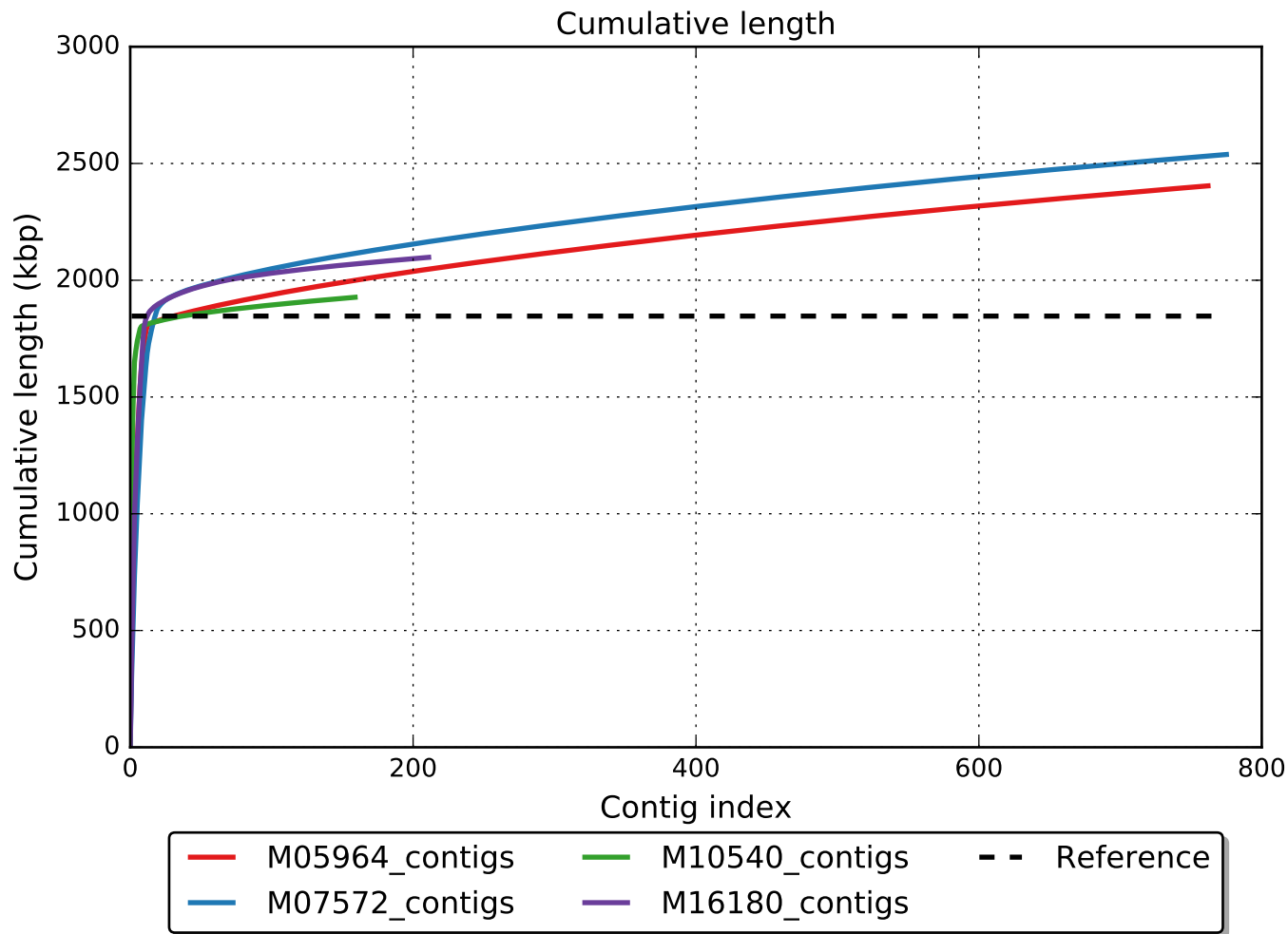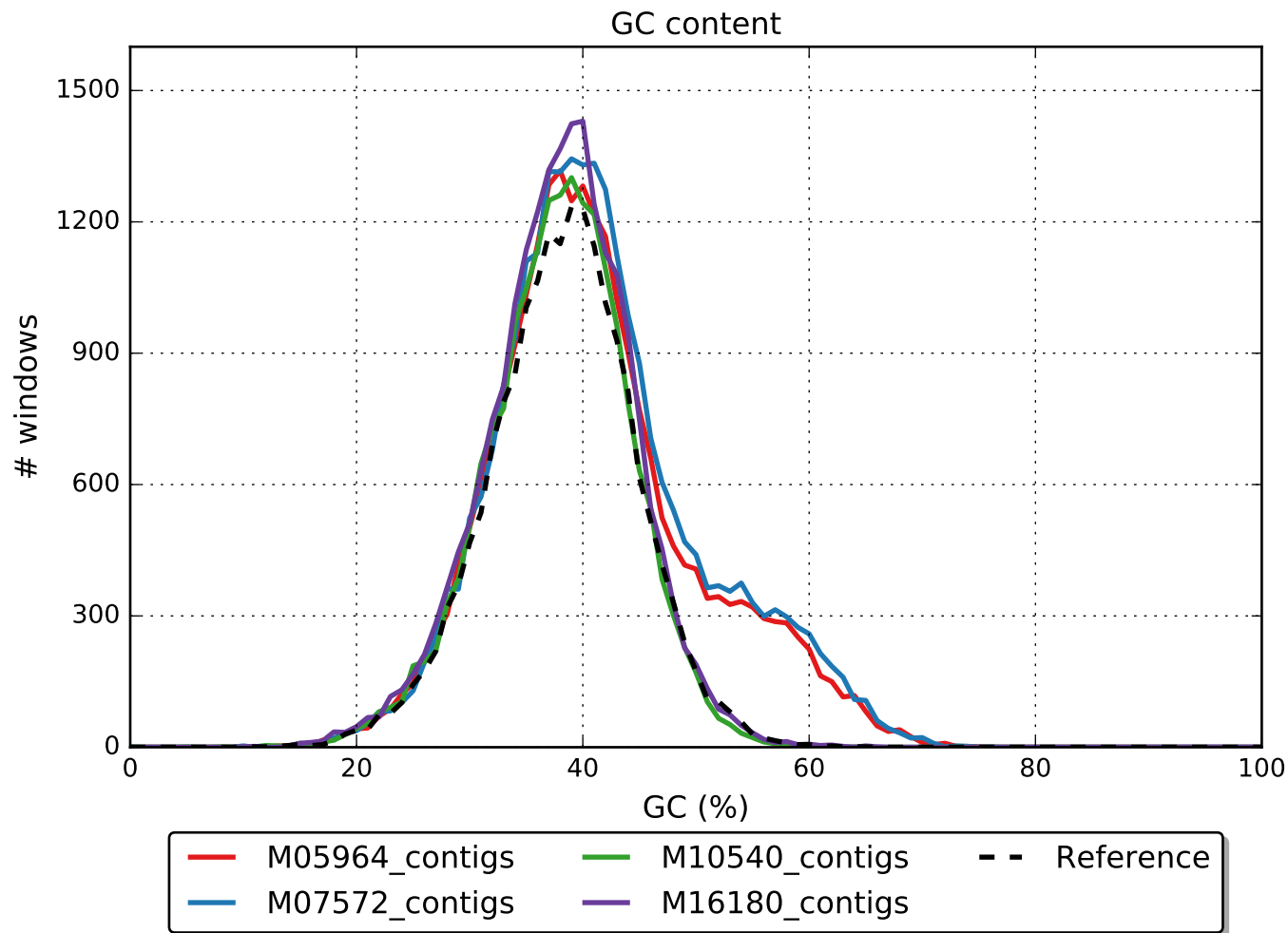
Misassemblies
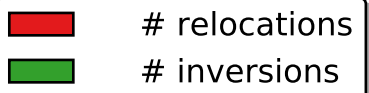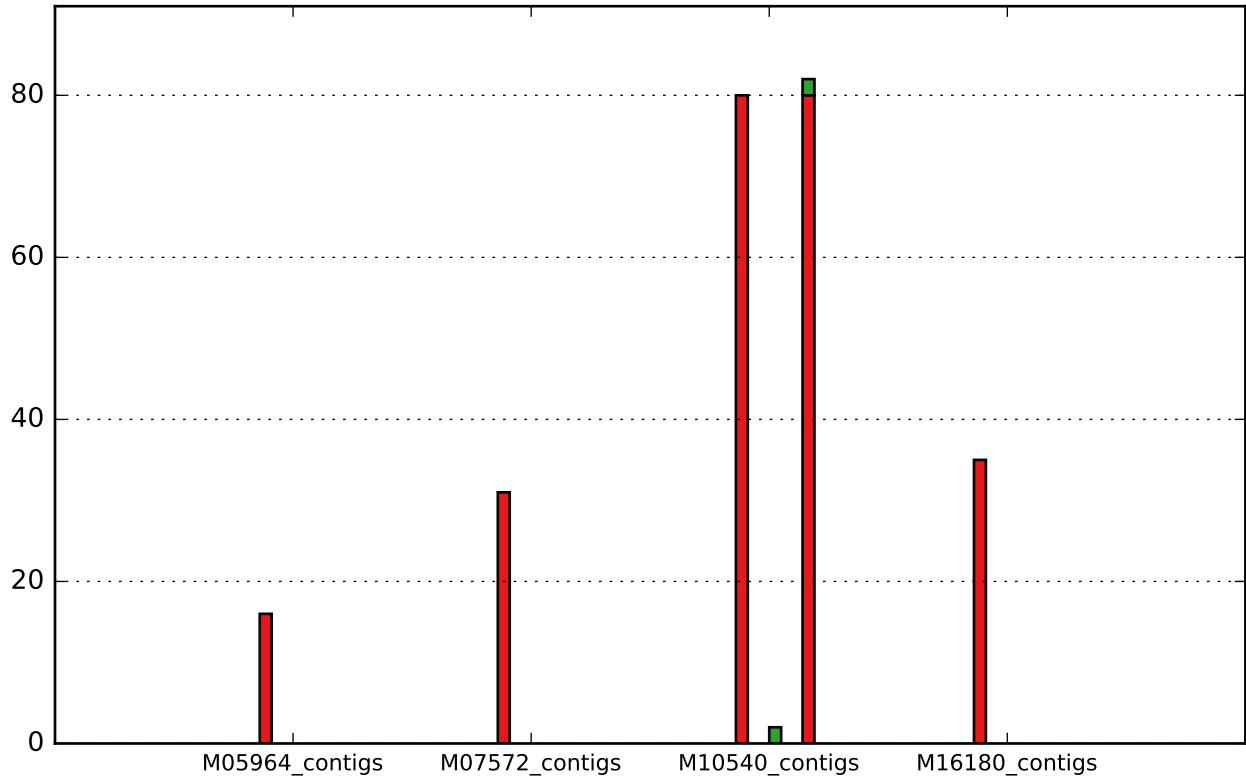
Cumulative length (aligned contigs)