Report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# contigs (>= 0 bp)	42	56	18	7028
# contigs (>= 1000 bp)	14	36	11	621
# contigs (>= 5000 bp)	11	22	8	3
# contigs (>= 10000 bp)	10	18	8	0
# contigs (>= 25000 bp)	10	14	7	0
# contigs (>= 50000 bp)	8	12	4	0
Total length (>= 0 bp)	1831657	1965102	1811331	3320808
Total length (>= 1000 bp)	1821194	1955209	1808761	1071265
Total length (>= 5000 bp)	1816377	1924256	1802504	16099
Total length (>= 10000 bp)	1810330	1897645	1802504	0
Total length (>= 25000 bp)	1810330	1840422	1792310	0
Total length (>= 50000 bp)	1739635	1787121	1700270	0
# contigs	19	45	12	1590
Largest contig	545971	305868	1150911	5936
Total length	1824603	1961709	1809438	1738815
Reference length	1887620	1887620	1887620	1887620
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.23	38.23	38.23	38.23
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1129
N75	179754	79547	311459	786
NG75	179754	112073	311459	691
L50	2	4	1	437
LG50	2	4	1	501
L75	4	8	2	884
LG75	4	7	2	1037
# misassemblies	42	19	78	10
# misassembled contigs	9	9	6	10
Misassembled contigs length	1782615	1101673	1741348	8914
# local misassemblies	66	39	45	6
# unaligned contigs	1 + 1 part	3 + 4 part	0 + 3 part	307 + 90 part
Unaligned length	3758	47024	34738	372174
Genome fraction (%)	83.591	94.009	59.192	66.994
Duplication ratio	1.154	1.079	1.588	1.081
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2349.91	1190.96	3563.99	1541.77
# indels per 100 kbp	62.87	31.67	81.53	32.03
Largest alignment	202939	283509	60928	5923
NA50	44383	103465	10803	956
NGA50	44383	109642	8646	859
NA75	20262	44348	-	528
NGA75	16714	51778	-	-
LA50	11	7	36	530
LGA50	11	6	40	613
LA75	25	14	-	1150
LGA75	28	13	-	-

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).
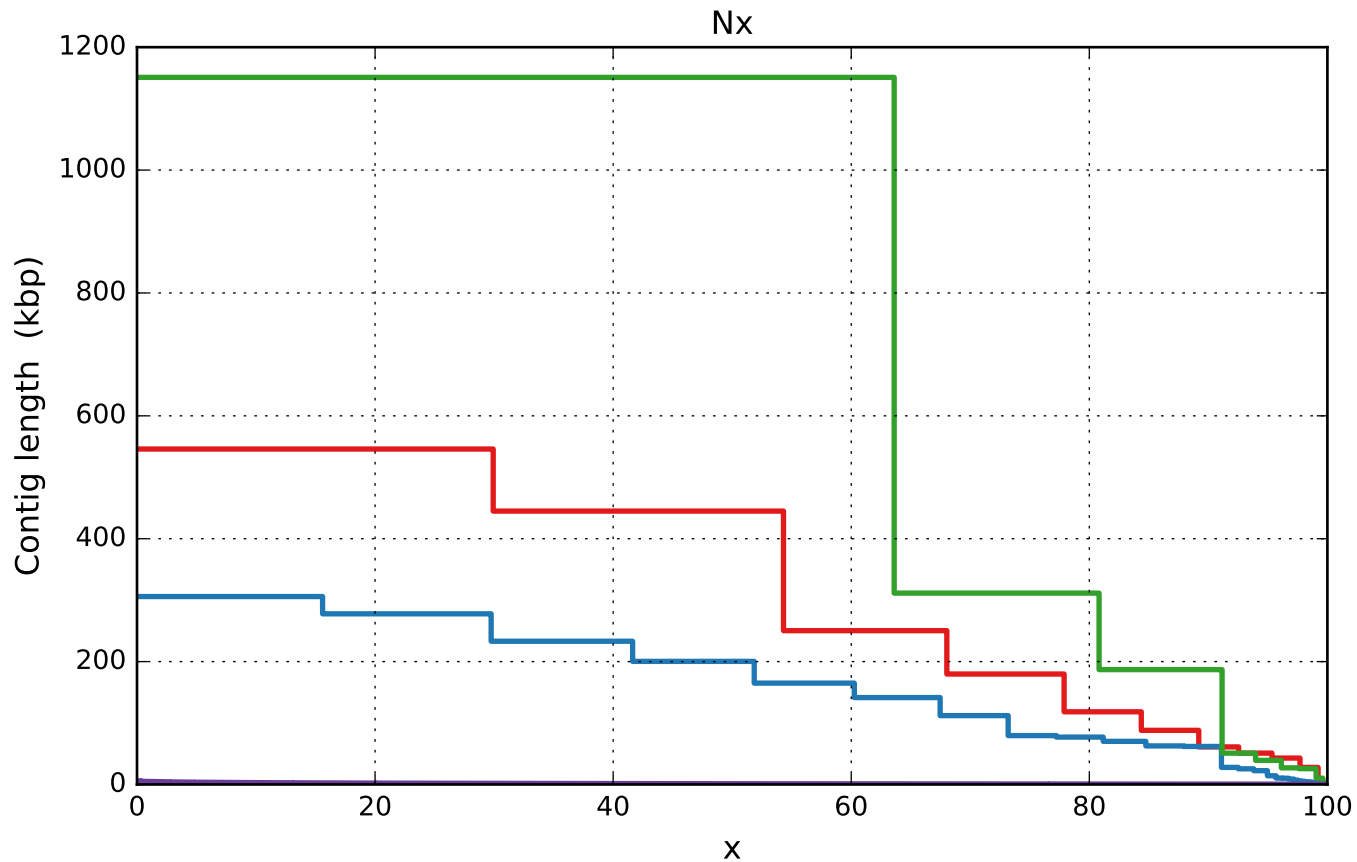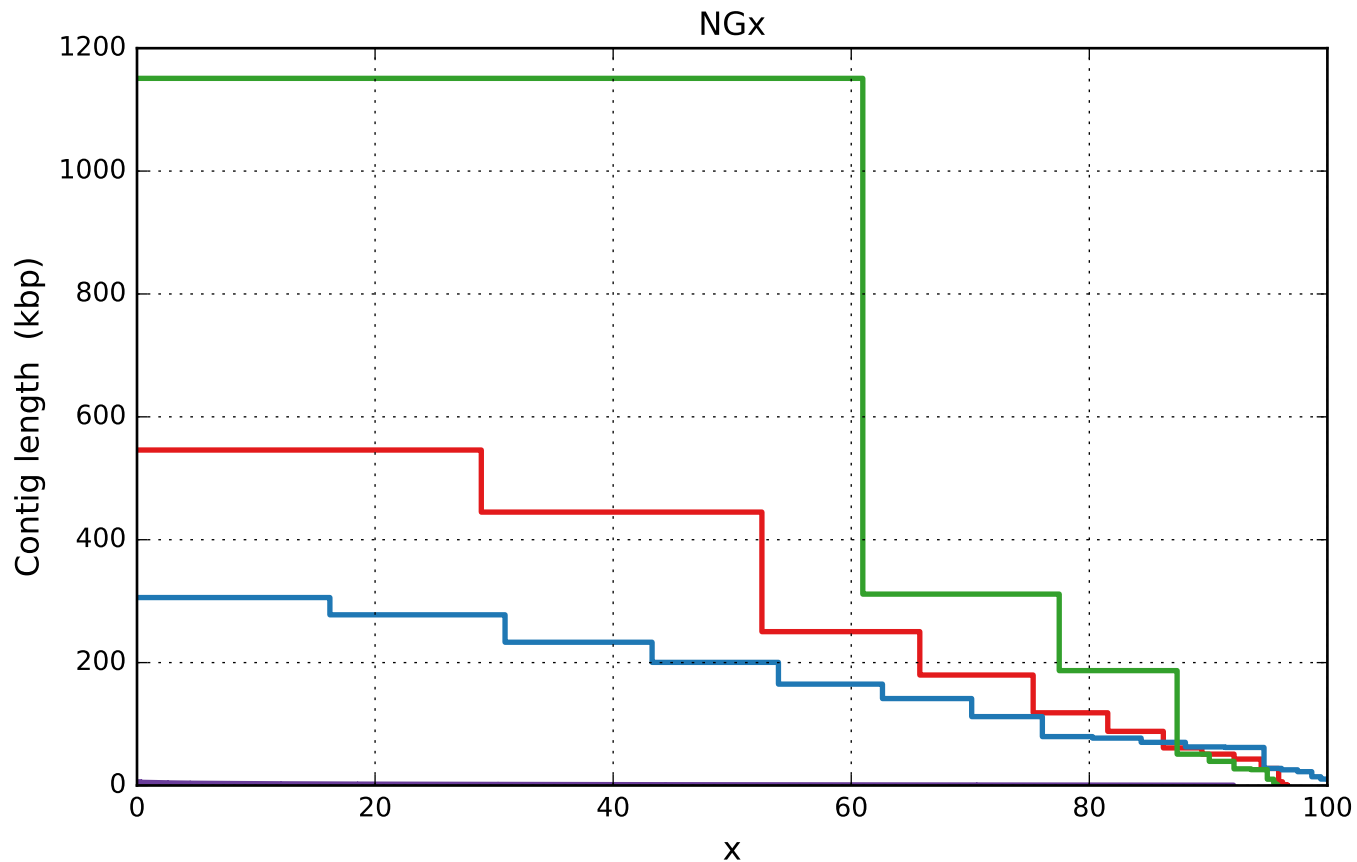
Misassemblies report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	42	19	78	10
# relocations	41	19	77	10
# translocations	0	0	0	0
# inversions	1	0	1	0
# misassembled contigs	9	9	6	10
Misassembled contigs length	1782615	1101673	1741348	8914
# local misassemblies	66	39	45	6
# mismatches	37079	21134	39821	19497
# indels	992	562	911	405
# short indels	883	482	817	366
# long indels	109	80	94	39
Indels length	3139	2022	2357	1172

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	1	3	0	307
Fully unaligned length	2293	11157	0	319986
# partially unaligned contigs	1	4	3	90
# with misassembly	0	2	2	3
# both parts are significant	1	2	1	16
Partially unaligned length	1465	35867	34738	52188
# N's	1086	1127	693	1471

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

M05964_contigs   M10540_contigs   M16180_contigs
M07572_contigs

Cumulative length

GC content
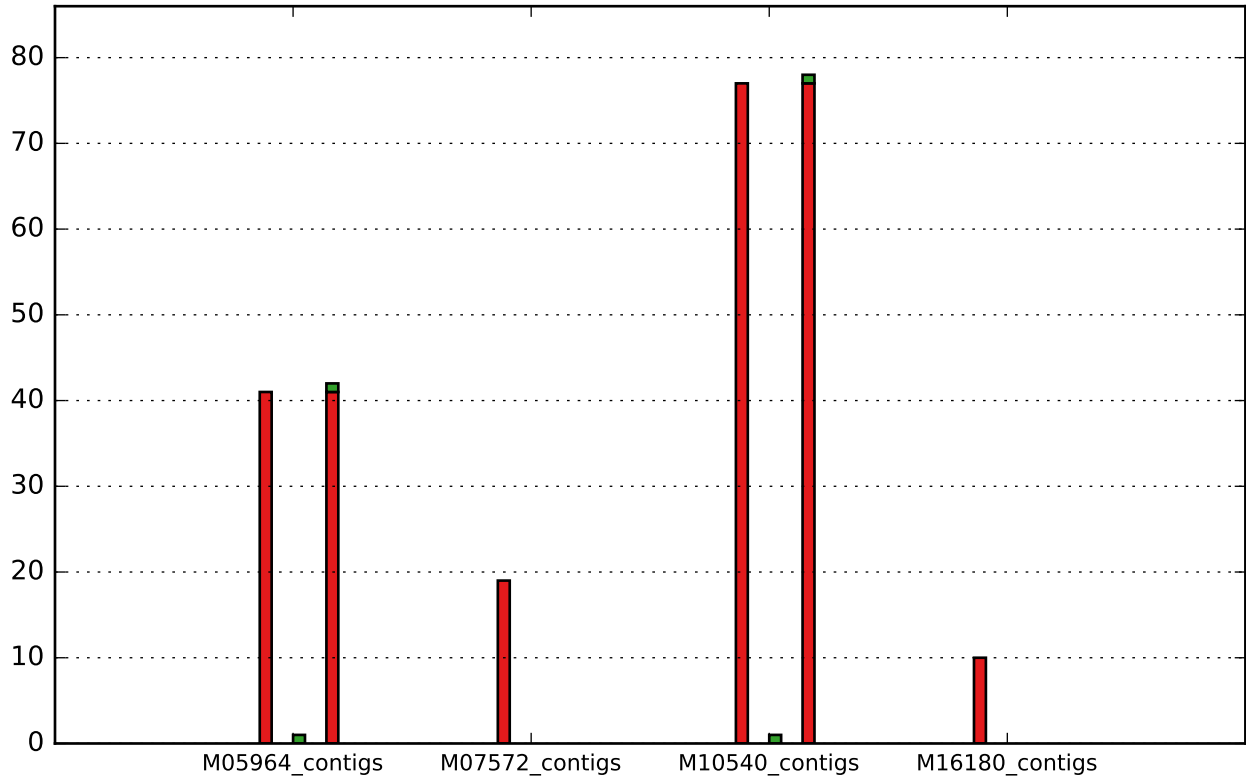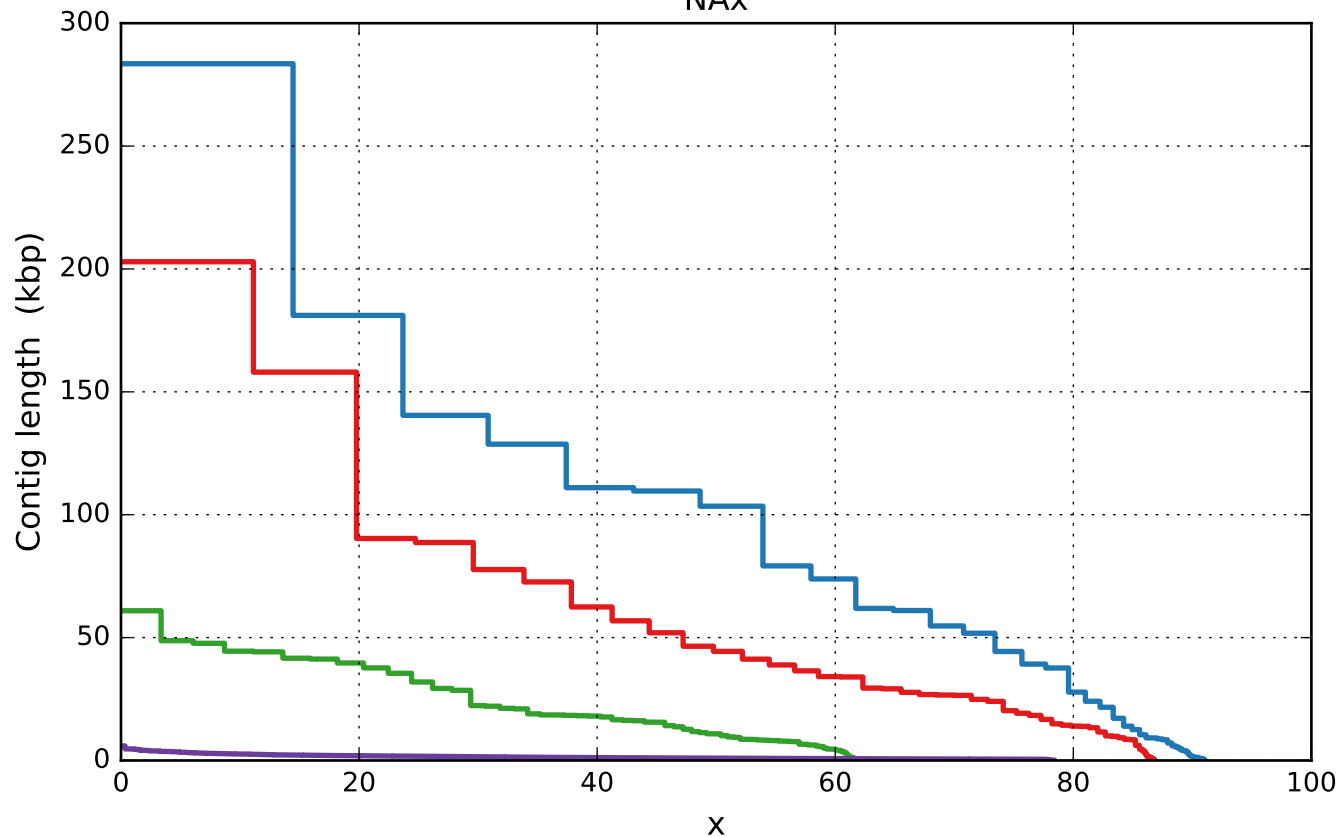
windows

GC (%)

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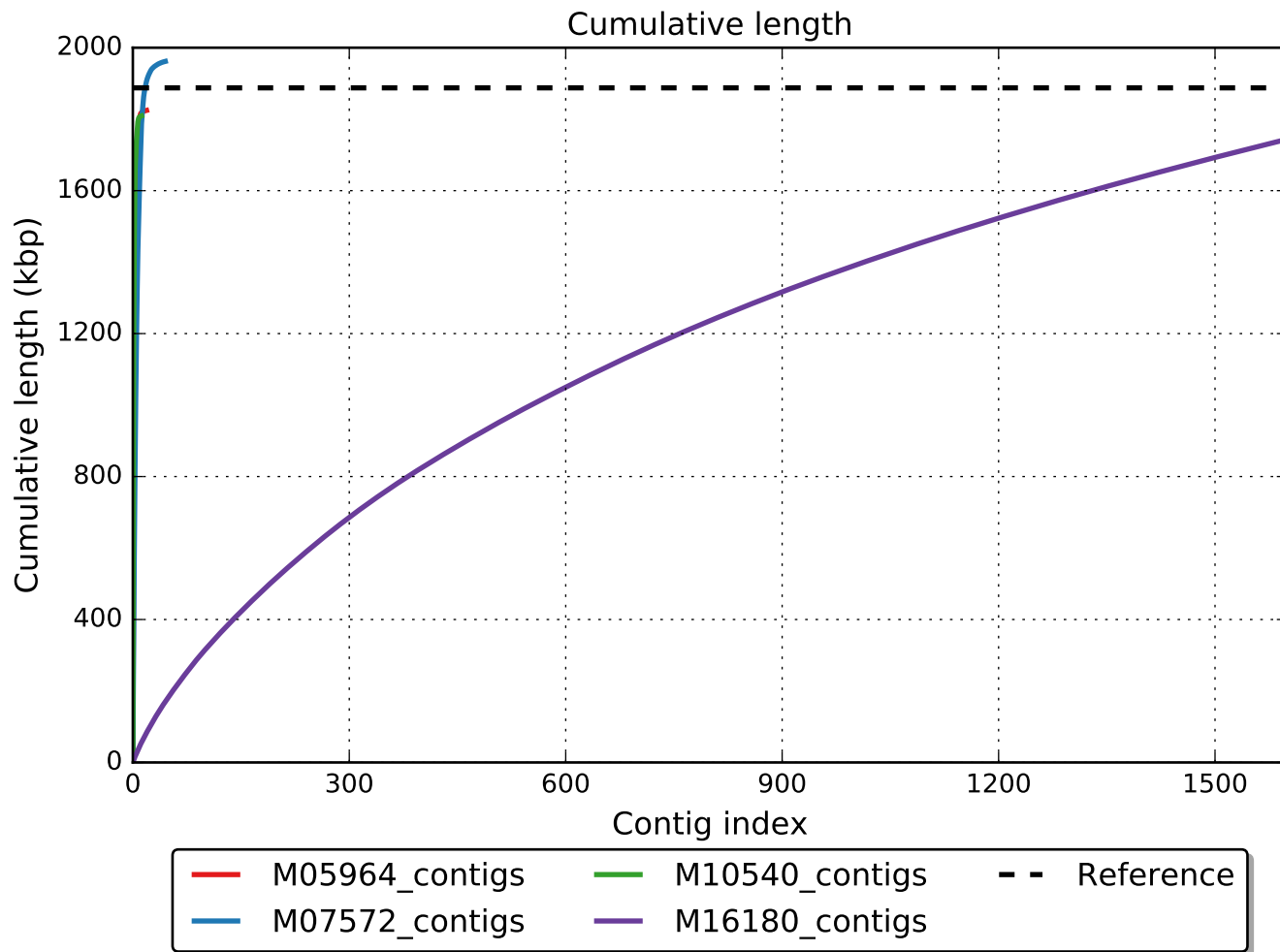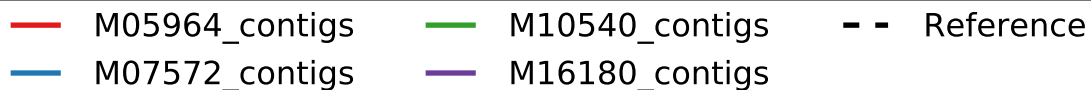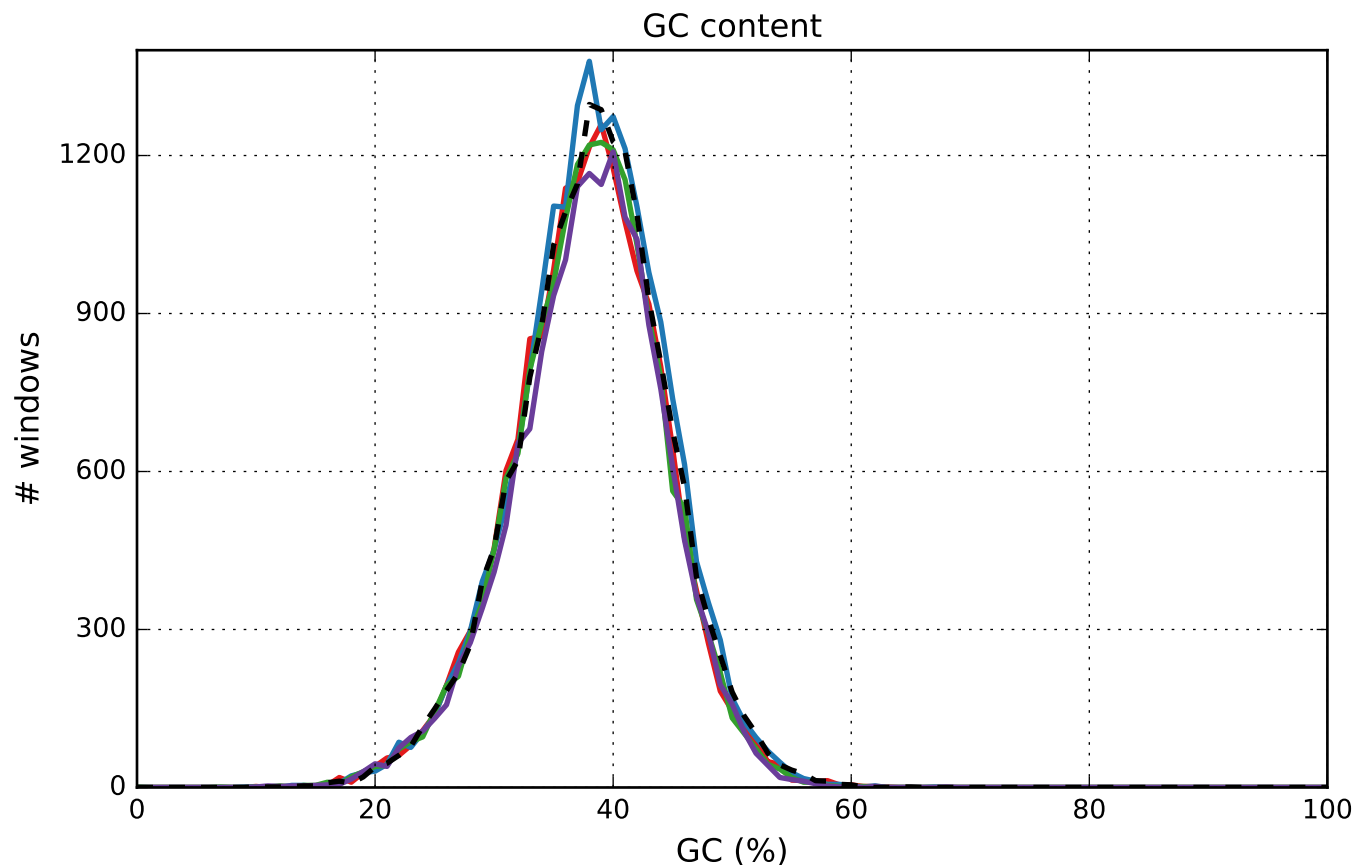
Misassemblies
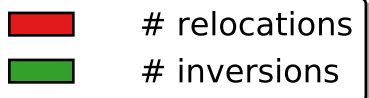
Cumulative length (aligned contigs)

Genome fraction, %