

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	1846503	1846503	1846503	1846503
GC (%)	37.88	38.25	37.91	38.00
Reference GC (%)	38.16	38.16	38.16	38.16
N50	444952	200368	1150911	1206
NG50	444952	200368	1150911	1150
N75	179754	79547	311459	786
NG75	179754	112073	311459	712
L50	2	4	1	437
LG50	2	4	1	483
L75	4	8	2	884
LG75	4	7	2	993
# misassemblies	19	34	85	6
# misassembled contigs	6	13	7	6
Misassembled contigs length	1560190	1797552	1792310	9445
# local misassemblies	29	63	39	12
# unaligned contigs	1 + 1 part	17 + 4 part	0 + 3 part	376 + 100 part
Unaligned length	3692	98469	1282	476416
Genome fraction (%)	93.160	89.884	59.559	62.942
Duplication ratio	1.059	1.123	1.644	1.086
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	1460.93	2422.65	3608.88	2032.47
# indels per 100 kbp	45.52	61.64	83.20	46.55
Largest alignment	336151	133389	66894	4706
NA50	118538	37745	9348	835
NGA50	118538	46017	8646	777
NA75	40740	25362	-	-
NGA75	40740	26499	-	-
LA50	5	13	42	582
LGA50	5	11	44	649
LA75	11	28	-	-
LGA75	11	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

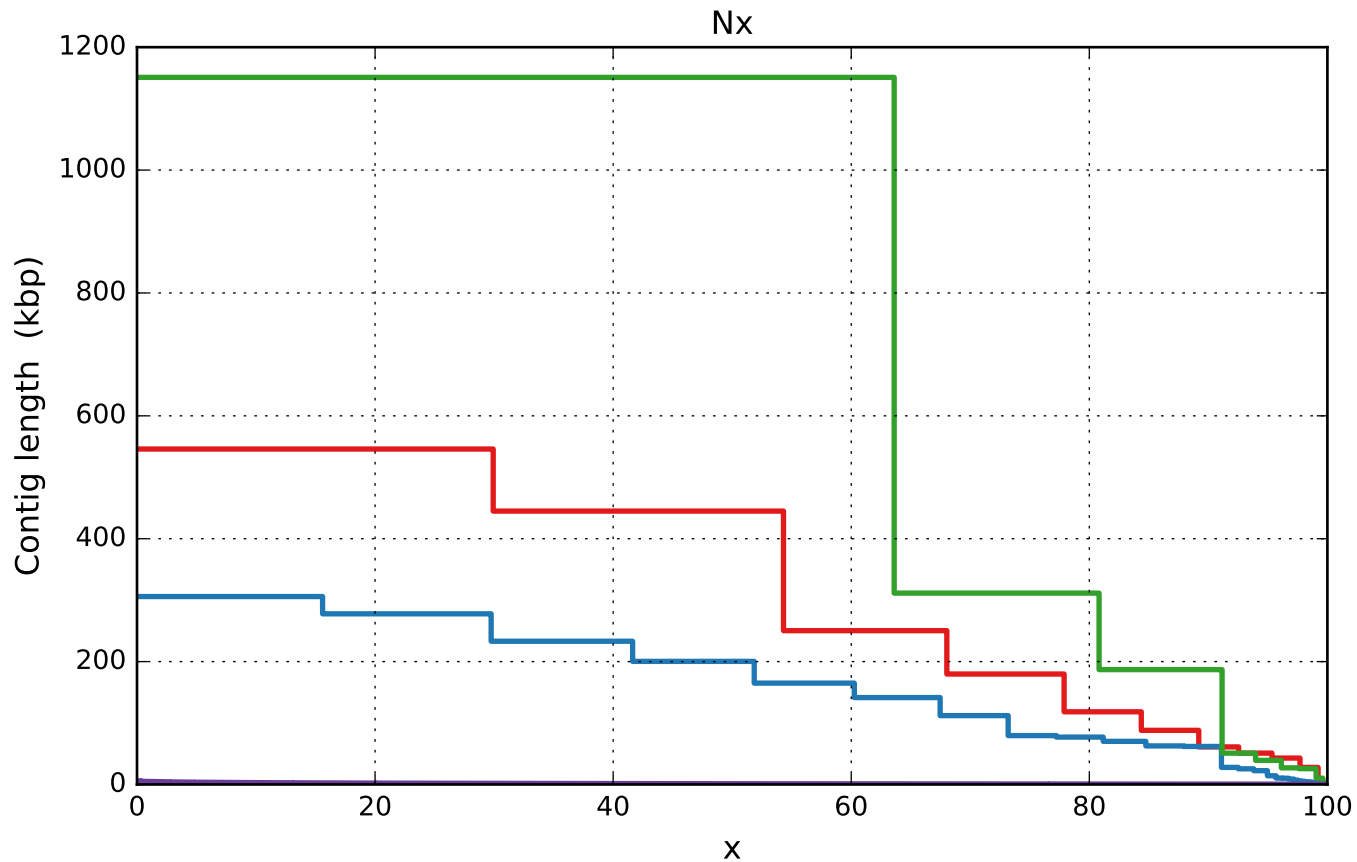
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	19	34	85	6
# relocations	19	33	83	6
# translocations	0	0	0	0
# inversions	0	1	2	0
# misassembled contigs	6	13	7	6
Misassembled contigs length	1560190	1797552	1792310	9445
# local misassemblies	29	63	39	12
# mismatches	25131	40209	39689	23622
# indels	783	1023	915	541
# short indels	687	903	836	490
# long indels	96	120	79	51
Indels length	2807	3578	2196	1395

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).

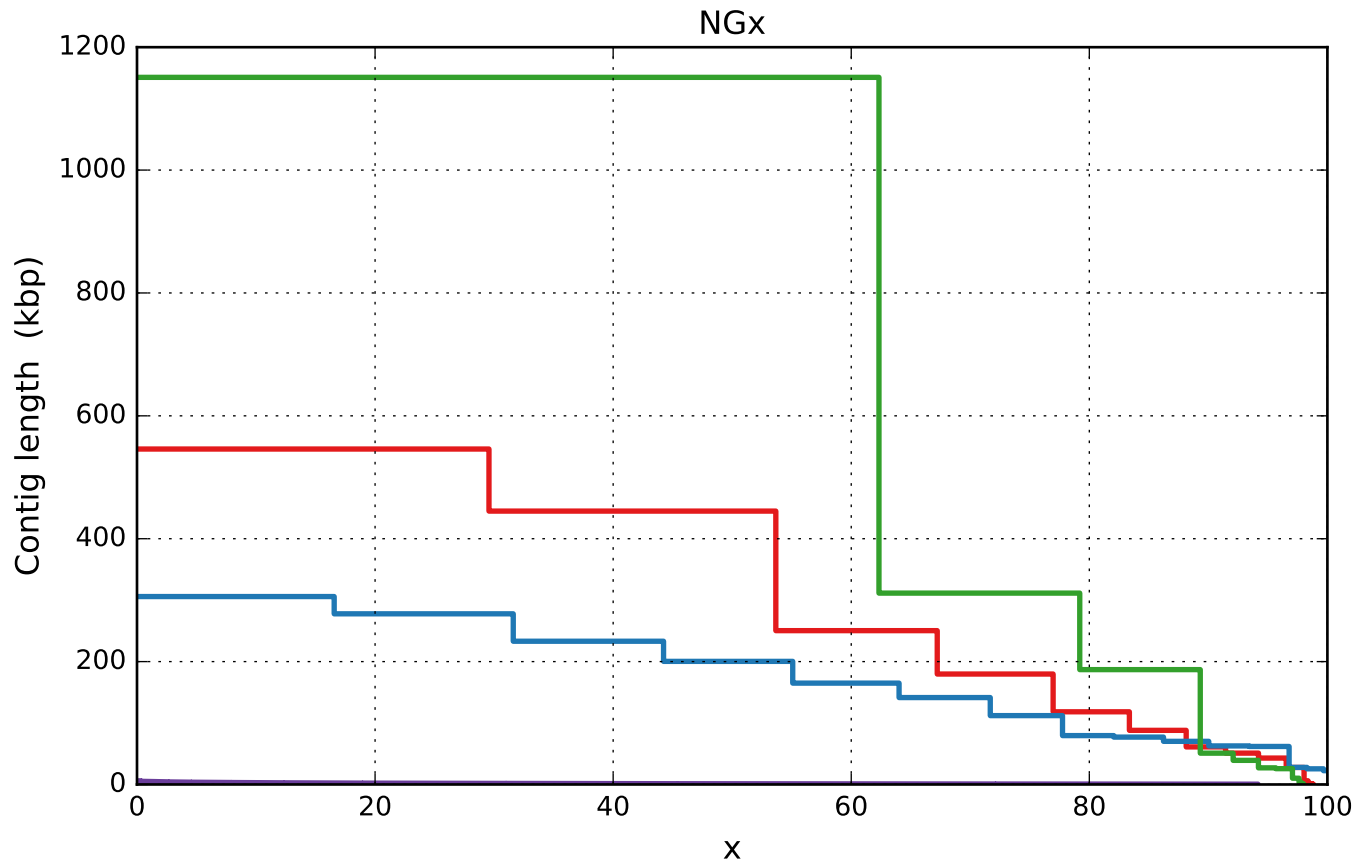
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	1	17	0	376
Fully unaligned length	2293	64371	0	413756
# partially unaligned contigs	1	4	3	100
# with misassembly	0	1	1	4
# both parts are significant	1	1	1	22
Partially unaligned length	1399	34098	1282	62660
# 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).



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

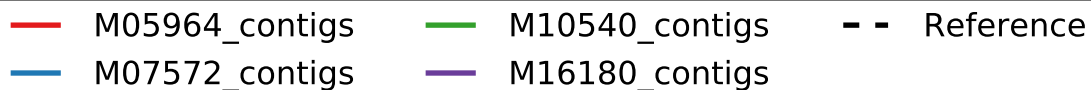
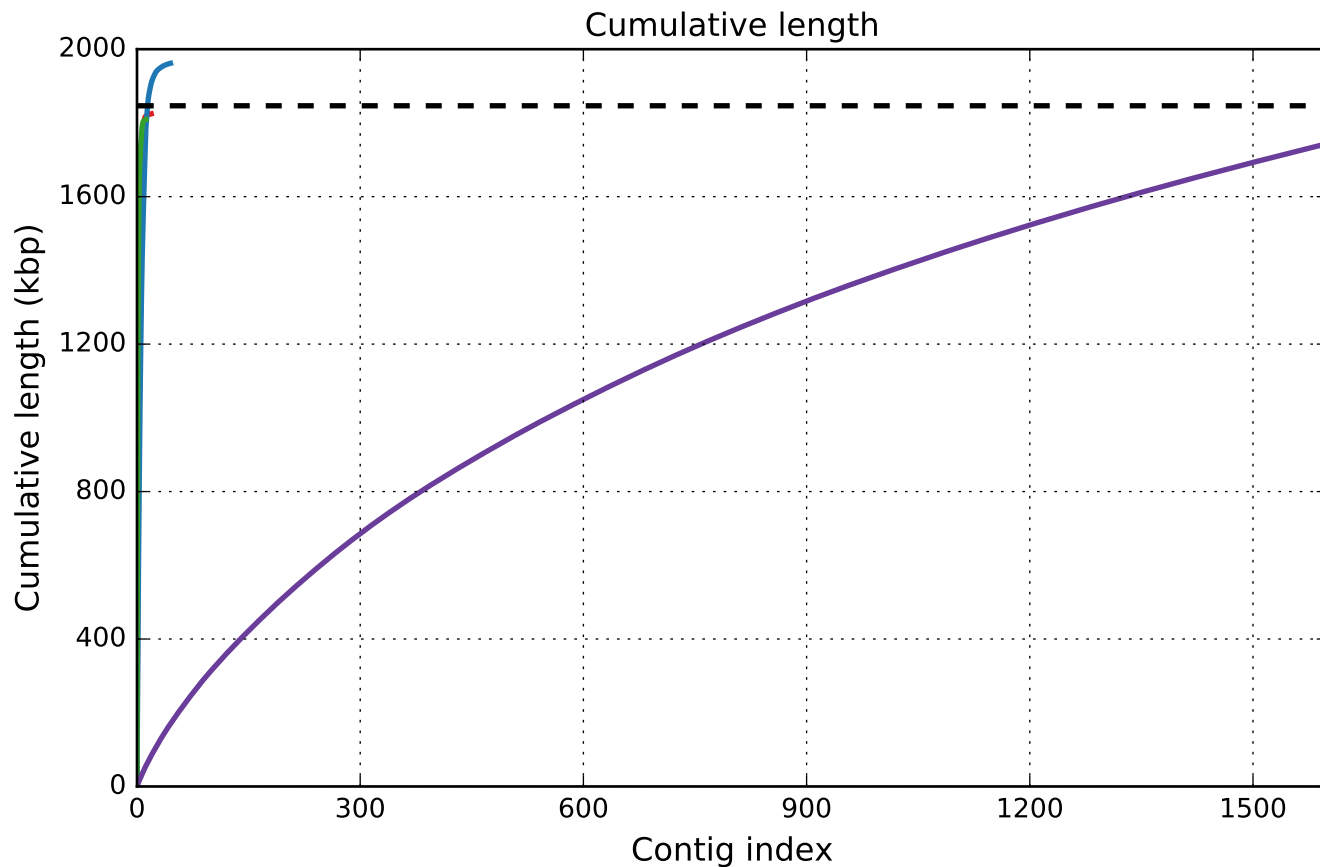


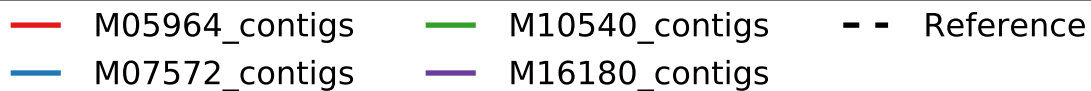
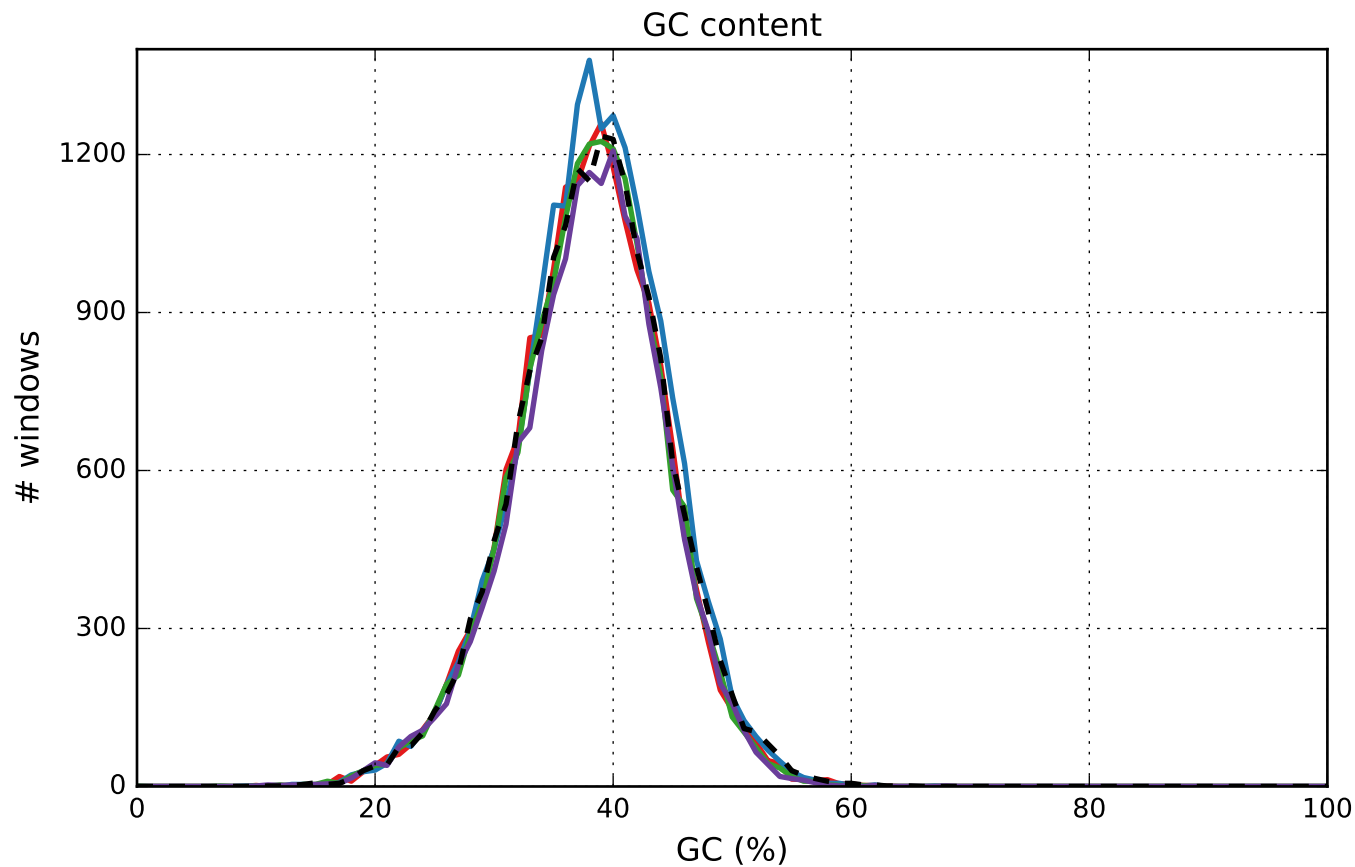
M05964_contigs

M10540_contigs

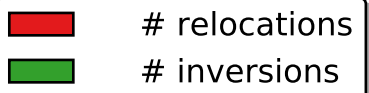
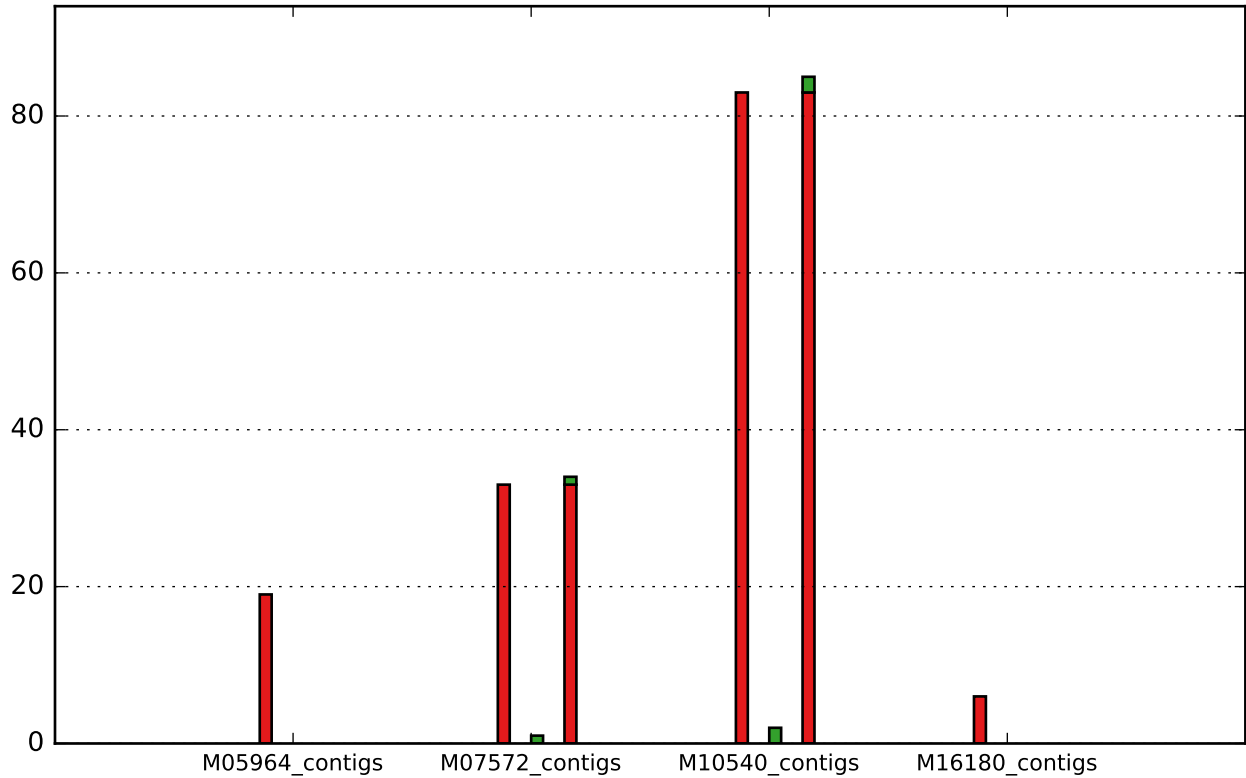
M16180_contigs

M07572_contigs

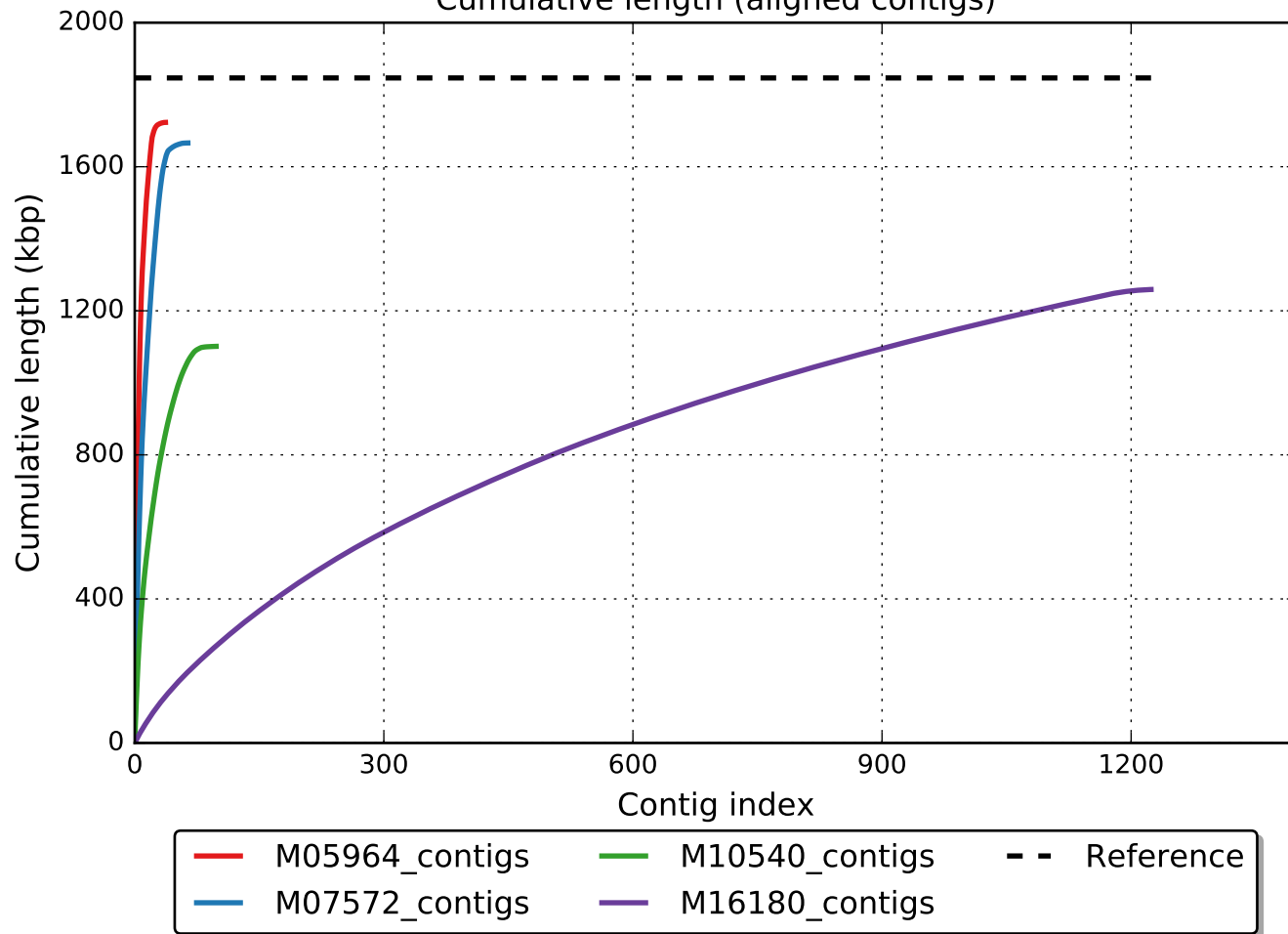




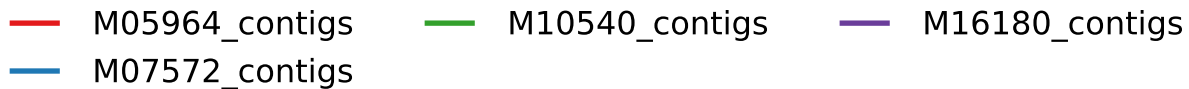
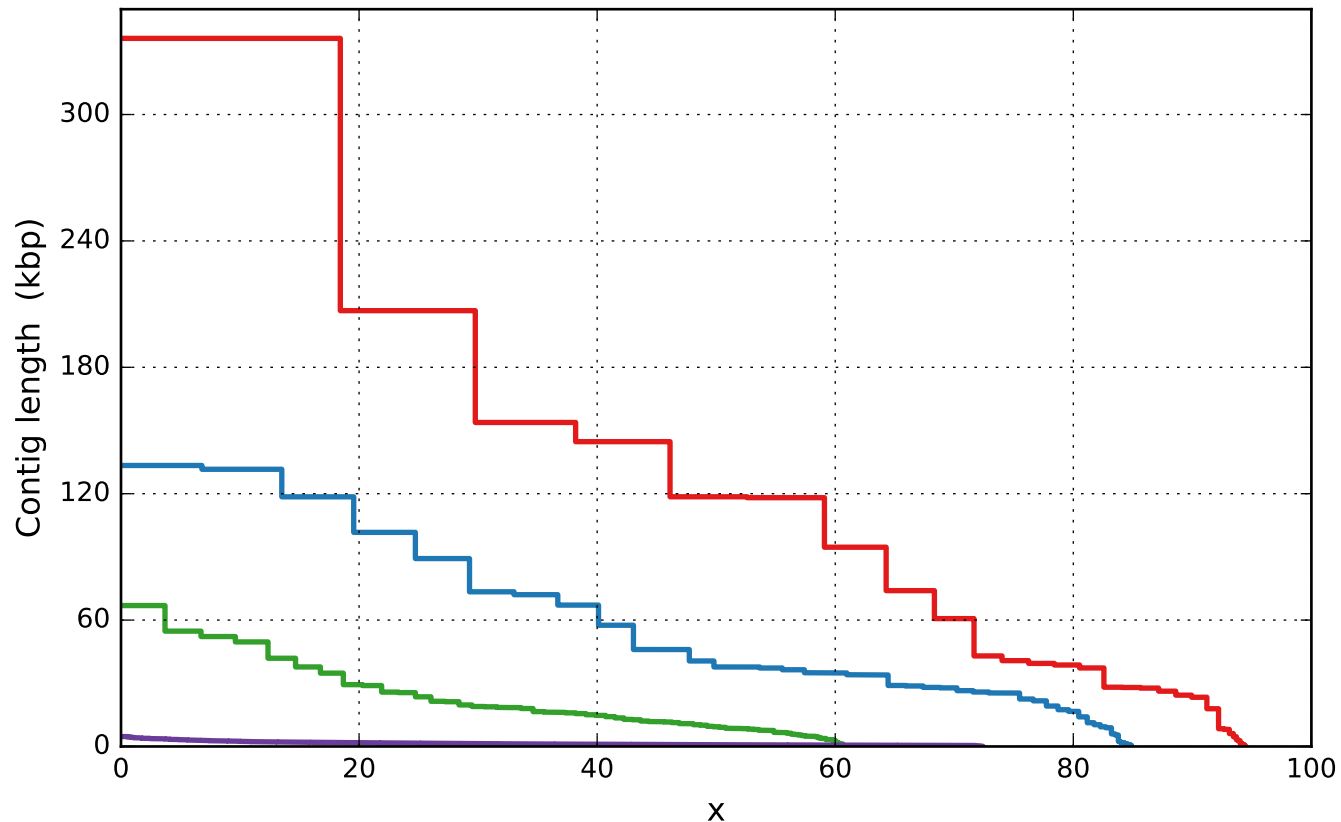
Misassemblies



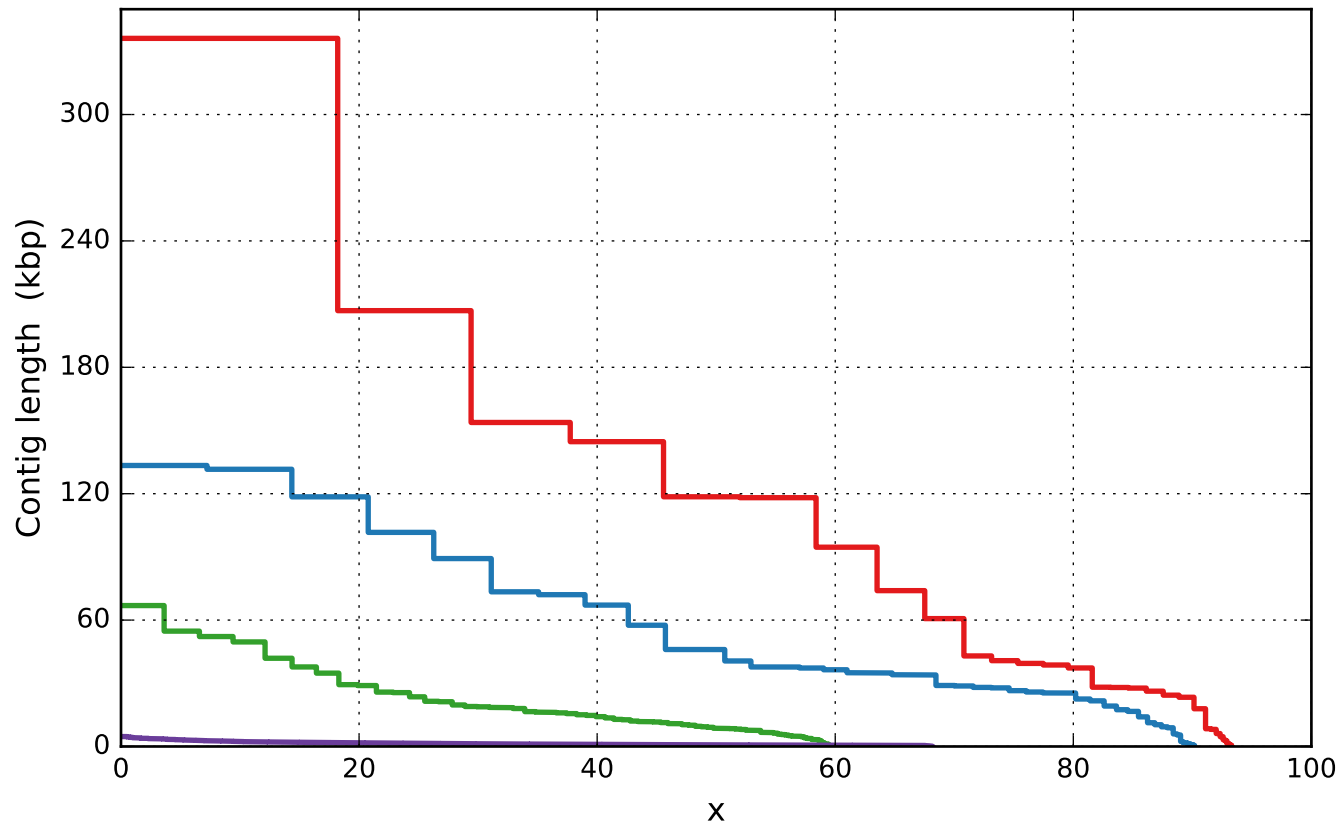
Cumulative length (aligned contigs)



NAx



NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

