

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	1846259	1846259	1846259	1846259
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	714
L50	2	4	1	437
LG50	2	4	1	483
L75	4	8	2	884
LG75	4	7	2	992
# misassemblies	42	19	71	3
# misassembled contigs	8	13	6	3
Misassembled contigs length	1721469	1421925	1605372	3435
# local misassemblies	61	46	39	8
# unaligned contigs	1 + 1 part	11 + 6 part	0 + 3 part	269 + 75 part
Unaligned length	3719	82042	110373	303050
Genome fraction (%)	86.108	92.835	57.415	72.180
Duplication ratio	1.145	1.097	1.603	1.077
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2567.27	1783.23	3578.98	1212.56
# indels per 100 kbp	69.25	54.03	90.09	23.26
Largest alignment	110422	240672	68819	5936
NA50	53133	111118	10059	1020
NGA50	53133	113786	9245	964
NA75	25521	35945	-	579
NGA75	24033	44112	-	522
LA50	11	6	40	501
LGA50	11	5	42	555
LA75	23	14	-	1070
LGA75	24	12	-	1217

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

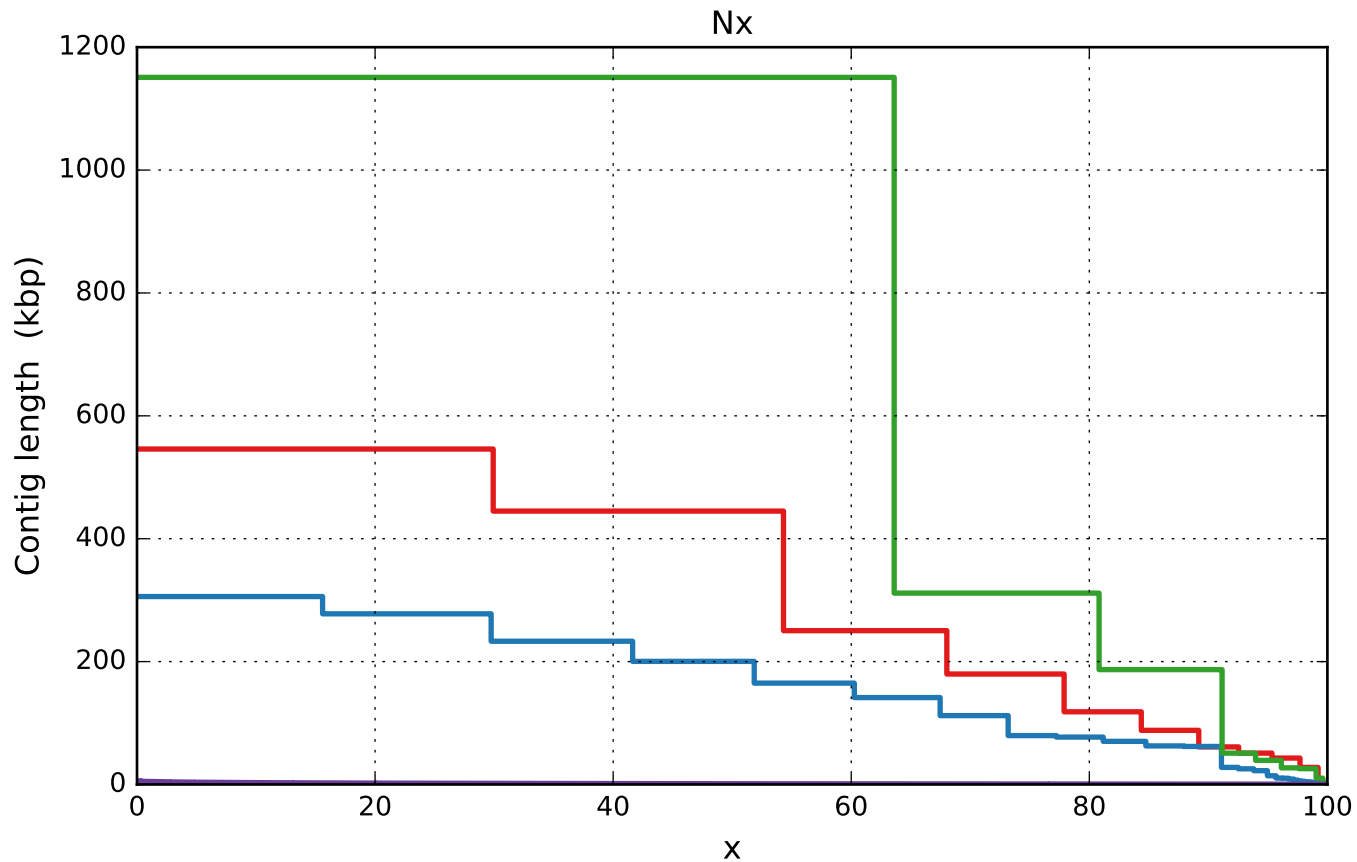
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	42	19	71	3
# relocations	42	19	69	3
# translocations	0	0	0	0
# inversions	0	0	2	0
# misassembled contigs	8	13	6	3
Misassembled contigs length	1721469	1421925	1605372	3435
# local misassemblies	61	46	39	8
# mismatches	40814	30564	37938	16159
# indels	1101	926	955	310
# short indels	972	818	855	277
# long indels	129	108	100	33
Indels length	3496	3043	2524	879

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).

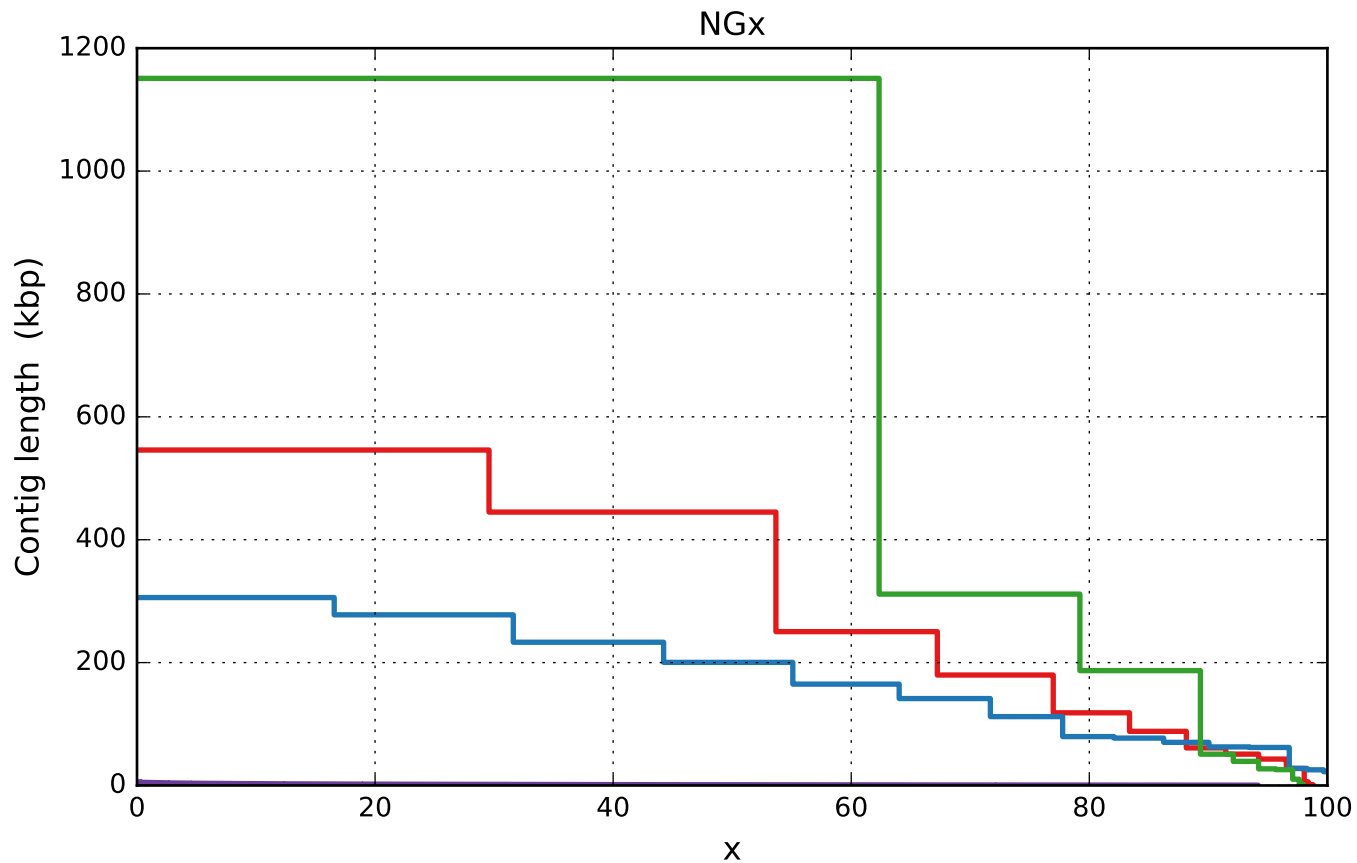
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	1	11	0	269
Fully unaligned length	2293	67969	0	274460
# partially unaligned contigs	1	6	3	75
# with misassembly	0	0	2	4
# both parts are significant	1	2	1	5
Partially unaligned length	1426	14073	110373	28590
# 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

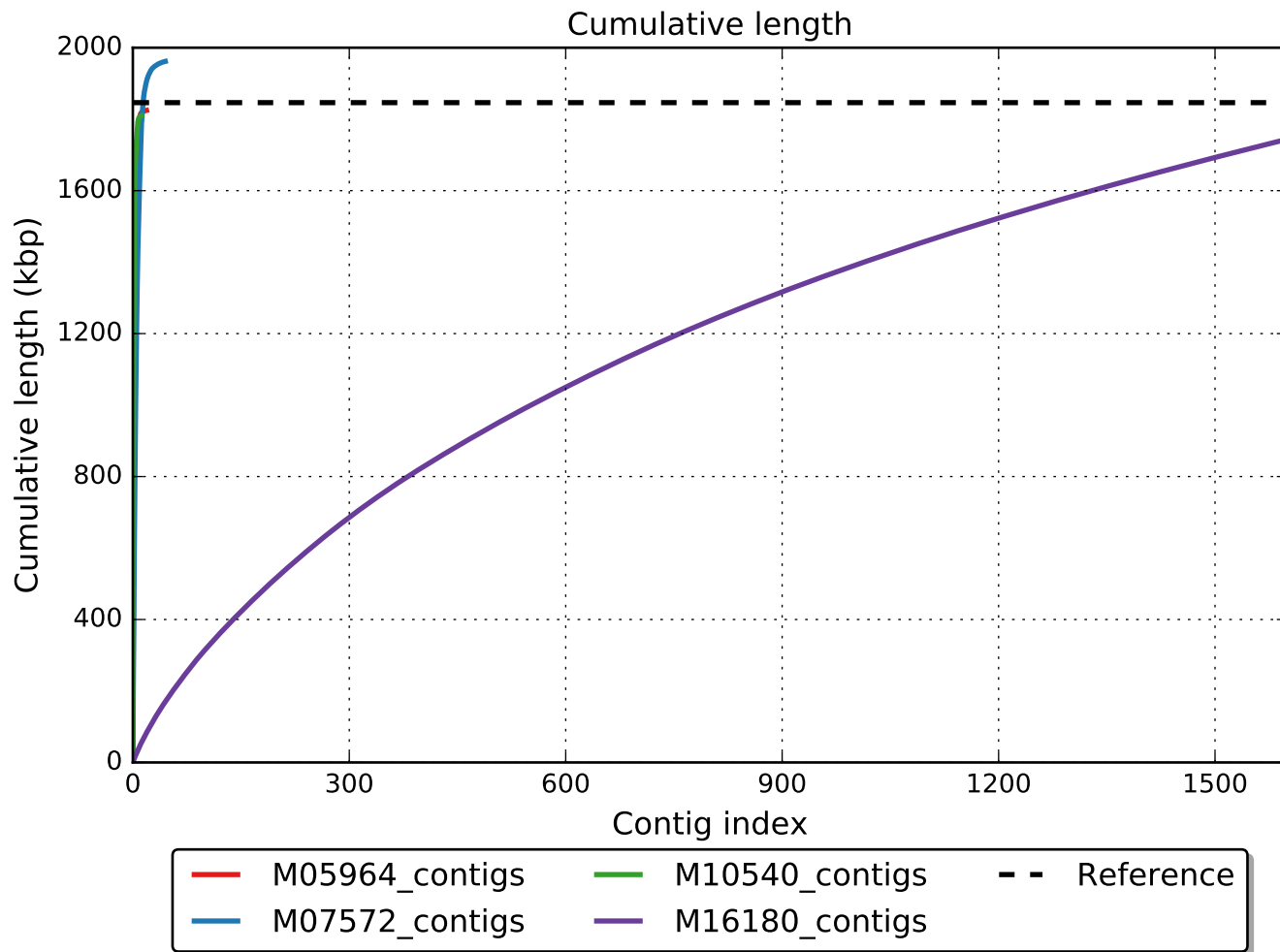


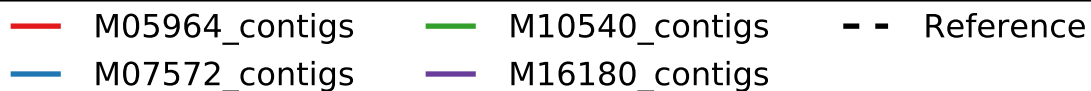
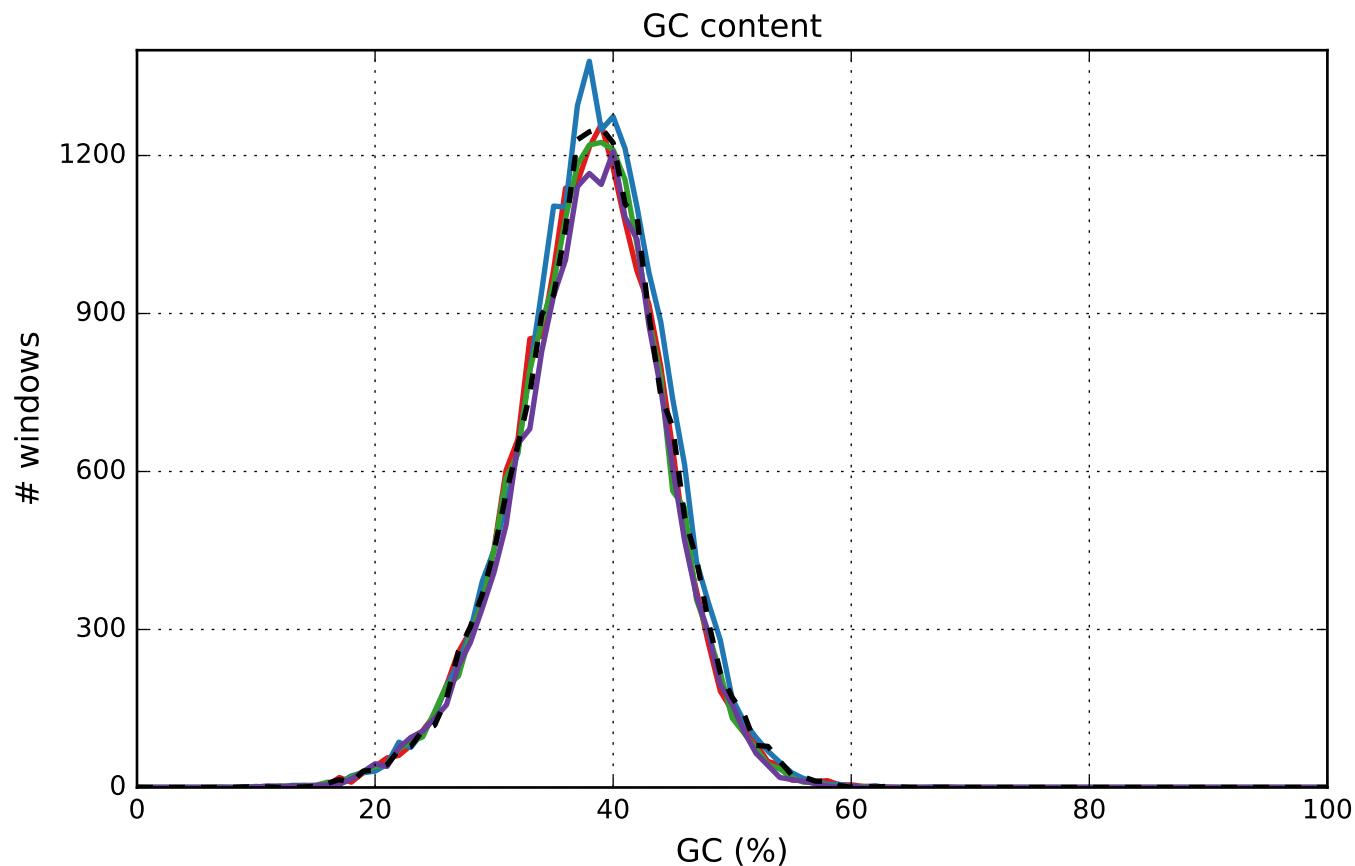
M05964_contigs

M10540_contigs

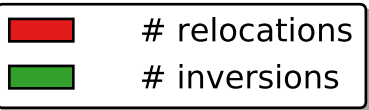
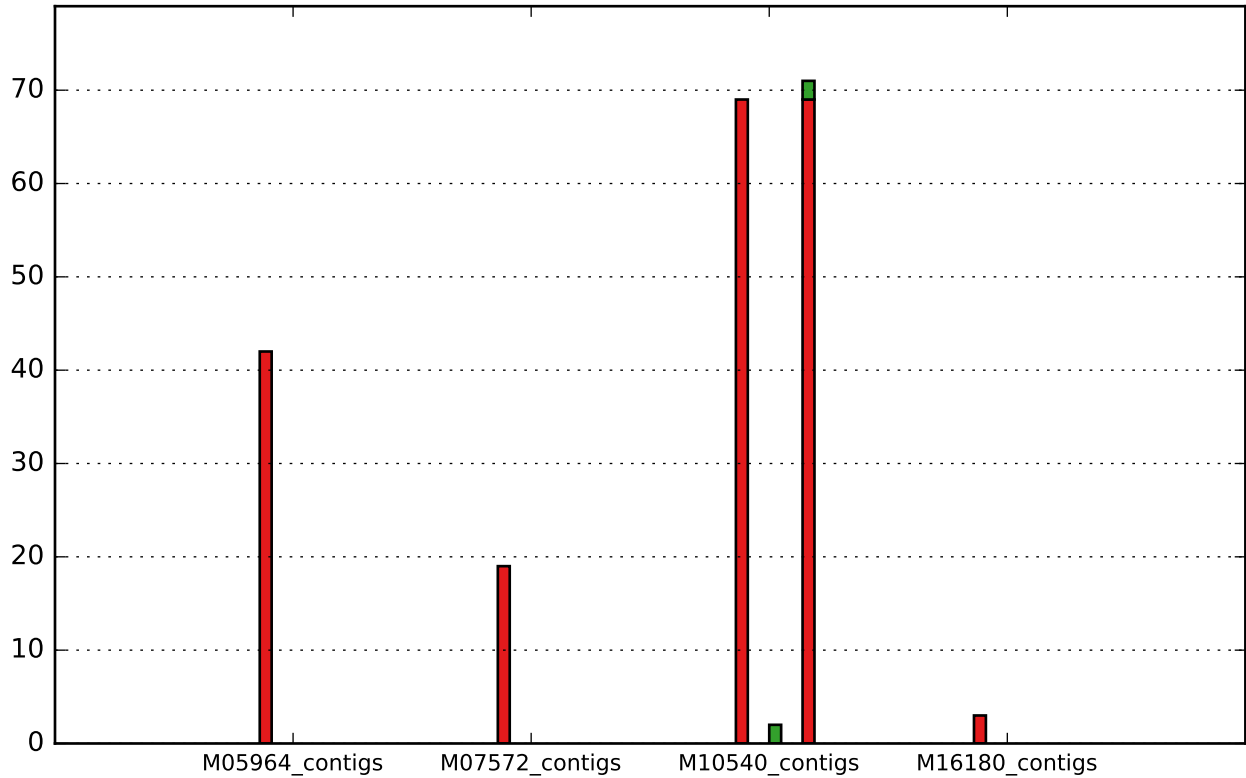
M16180_contigs

M07572_contigs

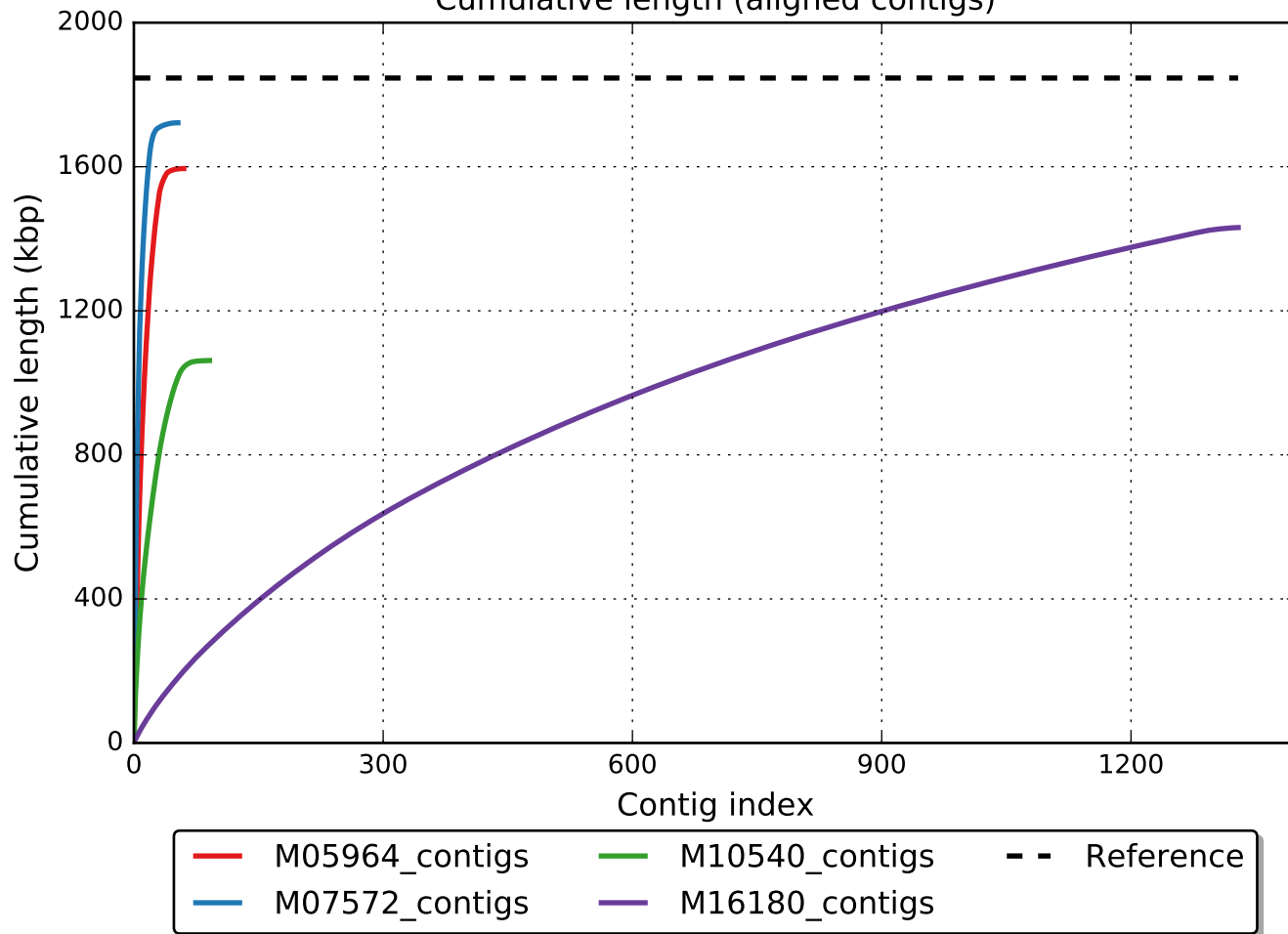




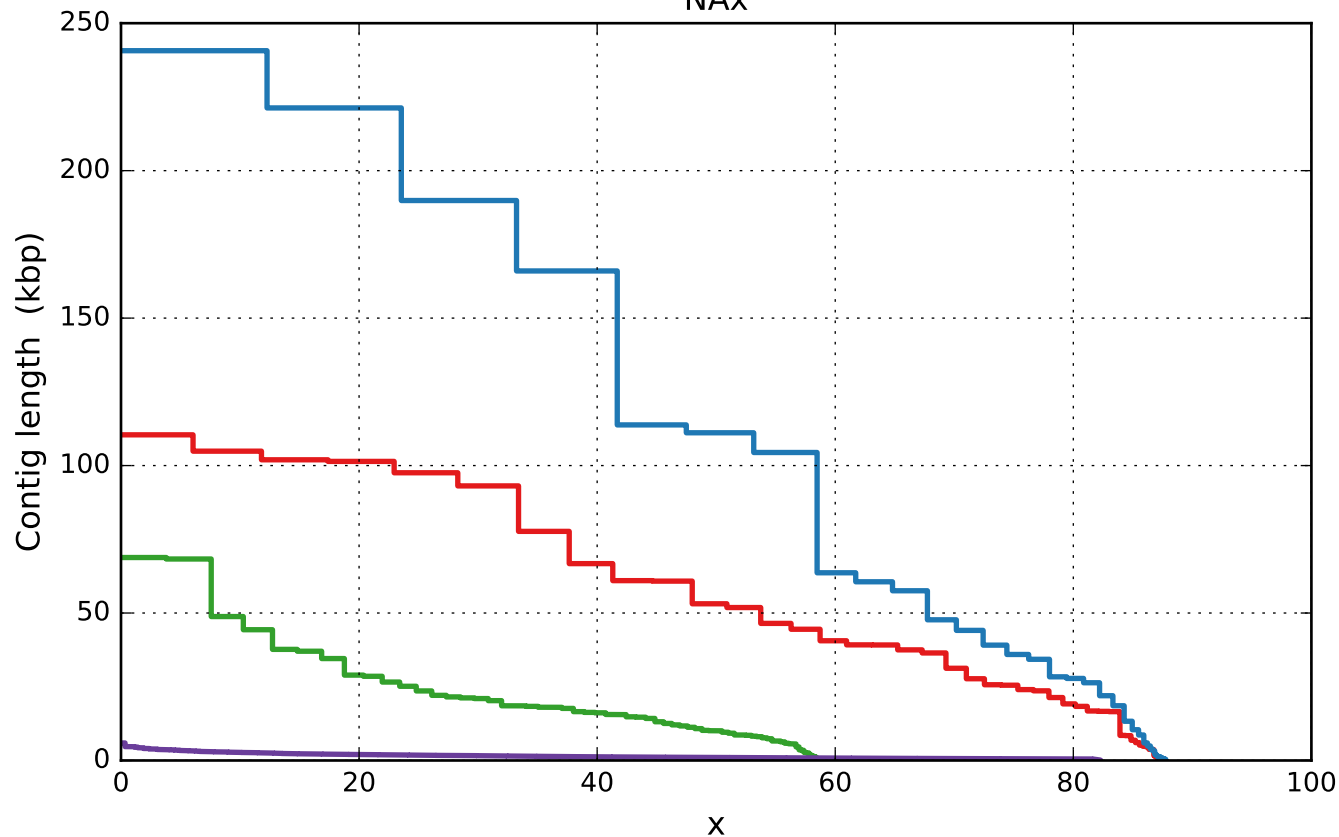
Misassemblies



Cumulative length (aligned contigs)

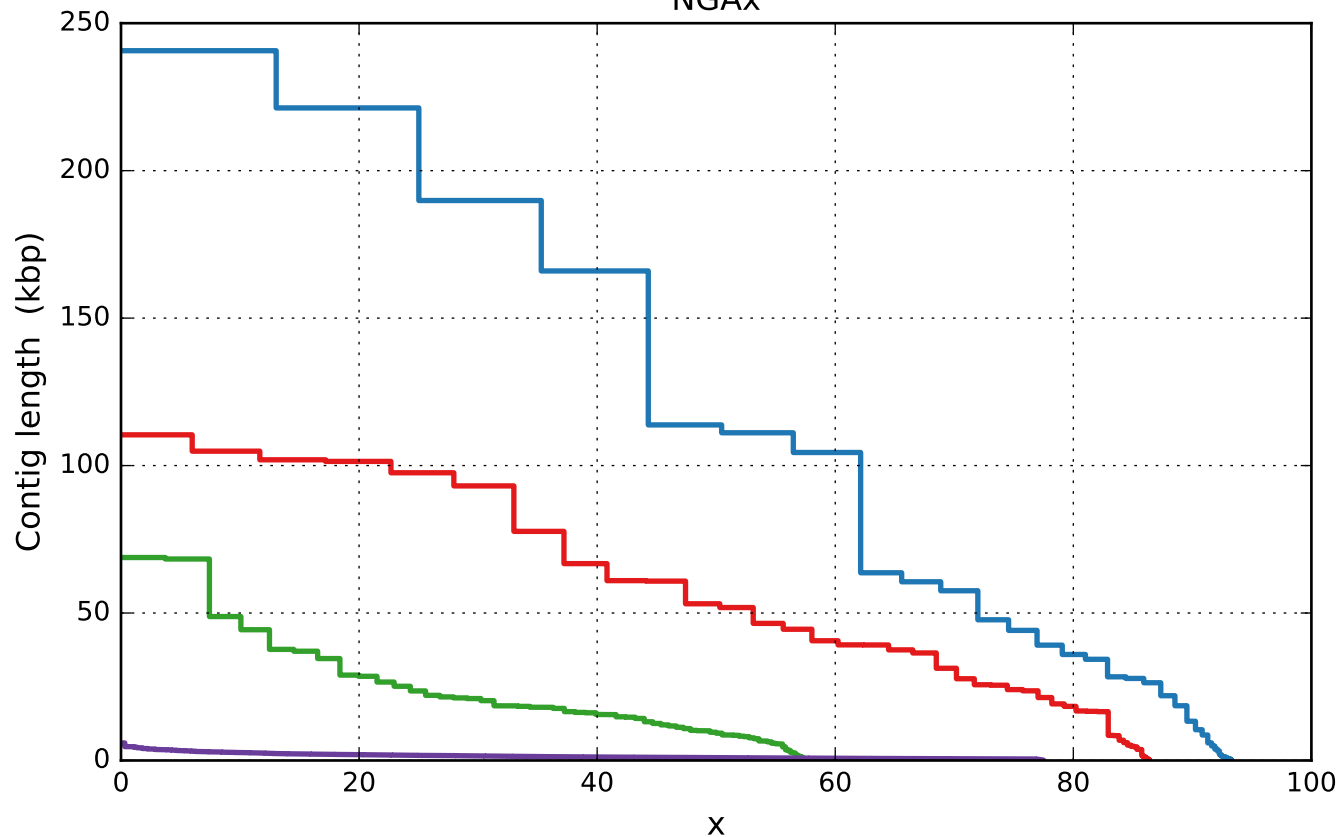


NAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

