

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	1850897	1850897	1850897	1850897
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	1149
N75	179754	79547	311459	786
NG75	179754	112073	311459	709
L50	2	4	1	437
LG50	2	4	1	485
L75	4	8	2	884
LG75	4	7	2	997
# misassemblies	47	7	84	1
# misassembled contigs	9	6	6	1
Misassembled contigs length	1782615	902633	1741348	982
# local misassemblies	66	24	43	10
# unaligned contigs	2 + 1 part	5 + 7 part	0 + 3 part	306 + 85 part
Unaligned length	4970	53728	34736	364041
Genome fraction (%)	86.802	95.975	60.264	68.644
Duplication ratio	1.133	1.074	1.591	1.082
# N's per 100 kbp	59.52	57.45	38.30	84.60
# mismatches per 100 kbp	2478.49	744.82	3589.10	1429.26
# indels per 100 kbp	63.11	24.83	85.80	28.18
Largest alignment	157918	251457	51332	5936
NA50	44468	140605	10860	961
NGA50	44468	140605	10283	884
NA75	25261	48366	-	532
NGA75	24858	61870	-	-
LA50	12	5	38	520
LGA50	12	5	40	581
LA75	25	11	-	1136
LGA75	26	9	-	-

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

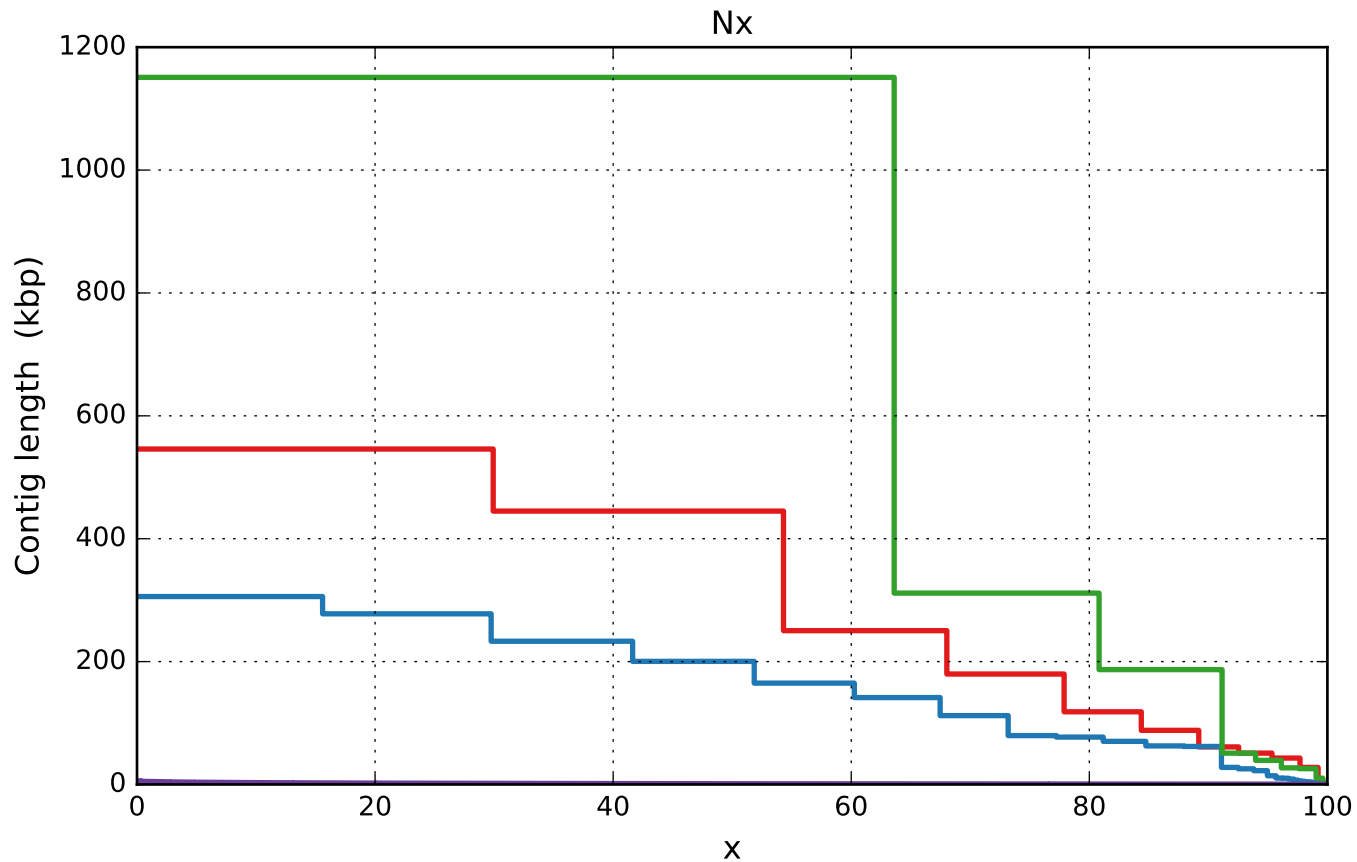
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	47	7	84	1
# relocations	46	7	84	1
# translocations	0	0	0	0
# inversions	1	0	0	0
# misassembled contigs	9	6	6	1
Misassembled contigs length	1782615	902633	1741348	982
# local misassemblies	66	24	43	10
# mismatches	39820	13231	40034	18159
# indels	1014	441	957	358
# short indels	898	360	866	313
# long indels	116	81	91	45
Indels length	3243	2164	2250	1196

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).

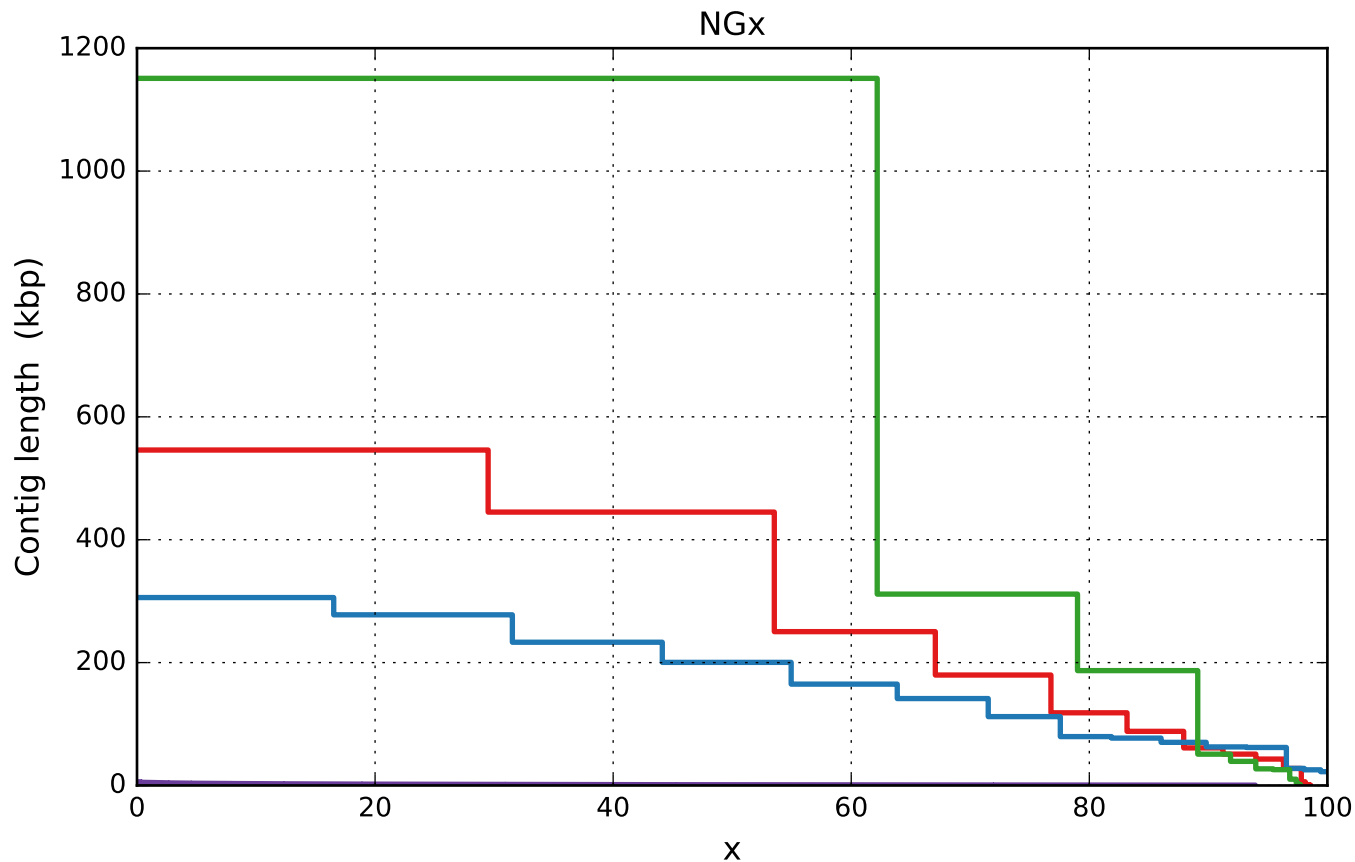
Unaligned report

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	2	5	0	306
Fully unaligned length	3605	30703	0	322661
# partially unaligned contigs	1	7	3	85
# with misassembly	0	3	2	2
# both parts are significant	1	3	1	8
Partially unaligned length	1365	23025	34736	41380
# N's	1086	1127	693	1471

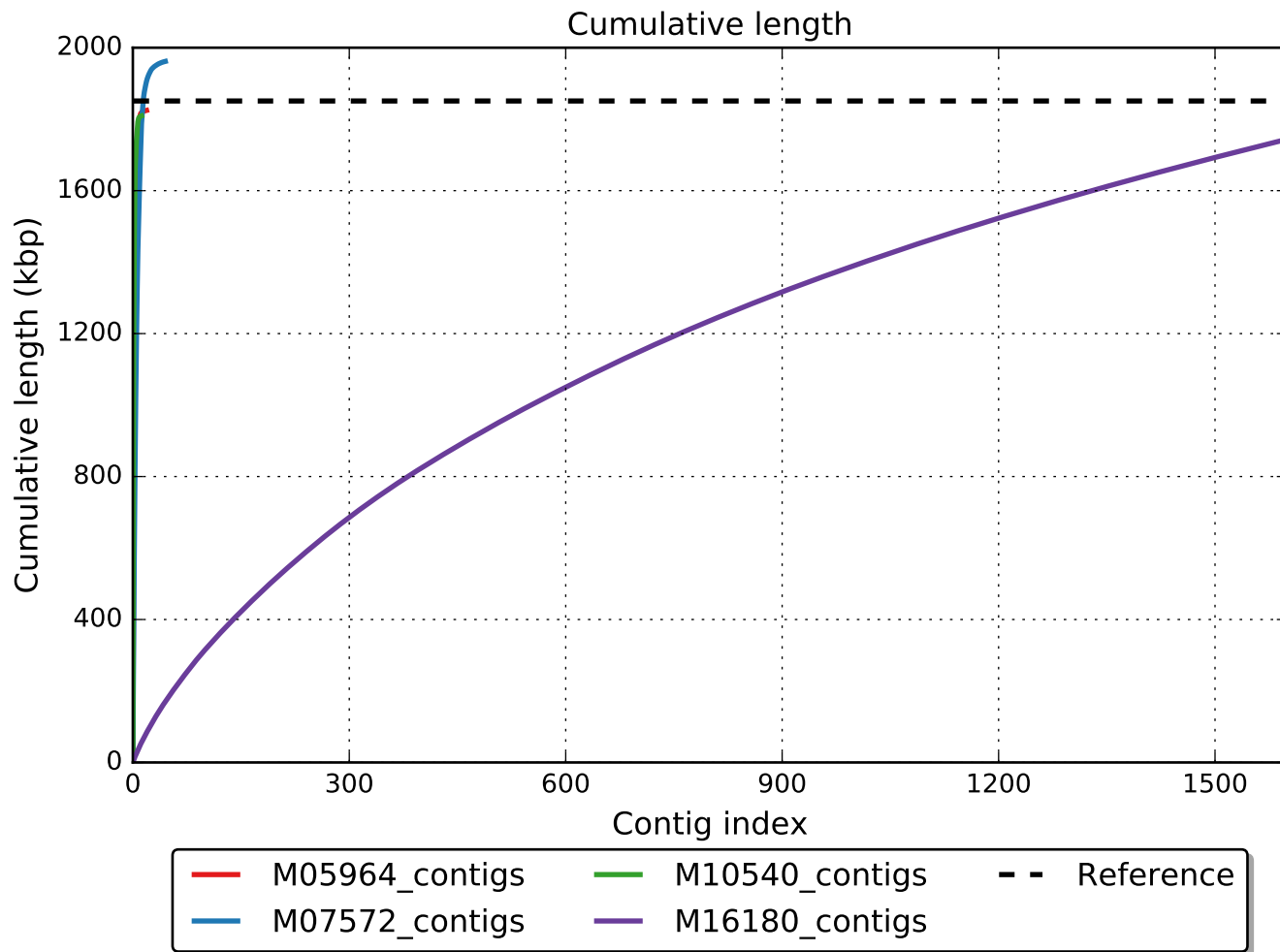
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

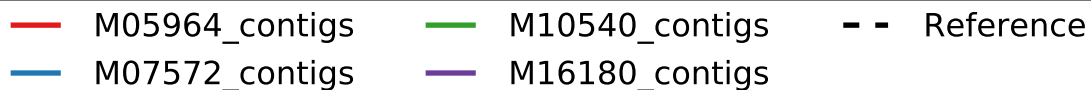
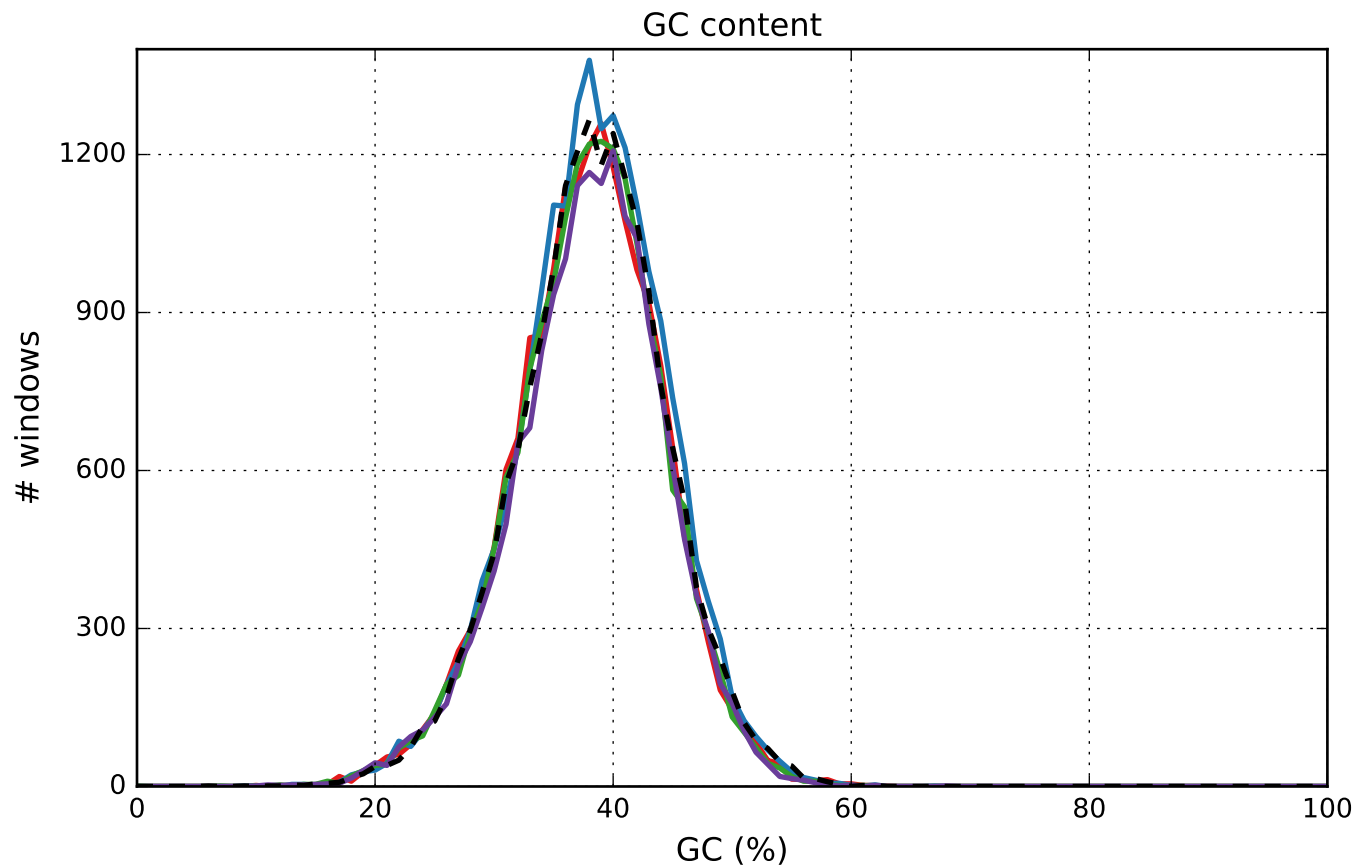


— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

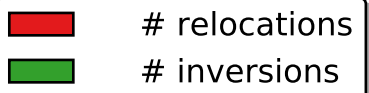
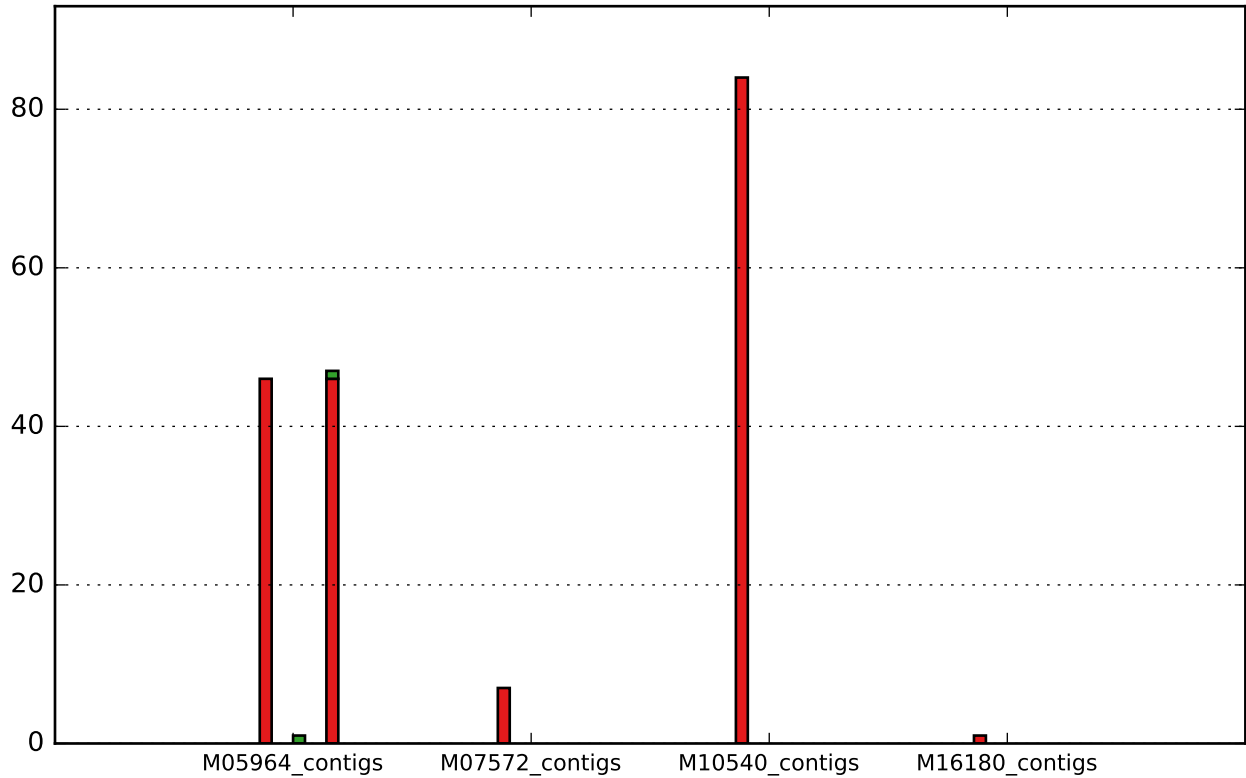


M05964_contigs M10540_contigs M16180_contigs
M07572_contigs

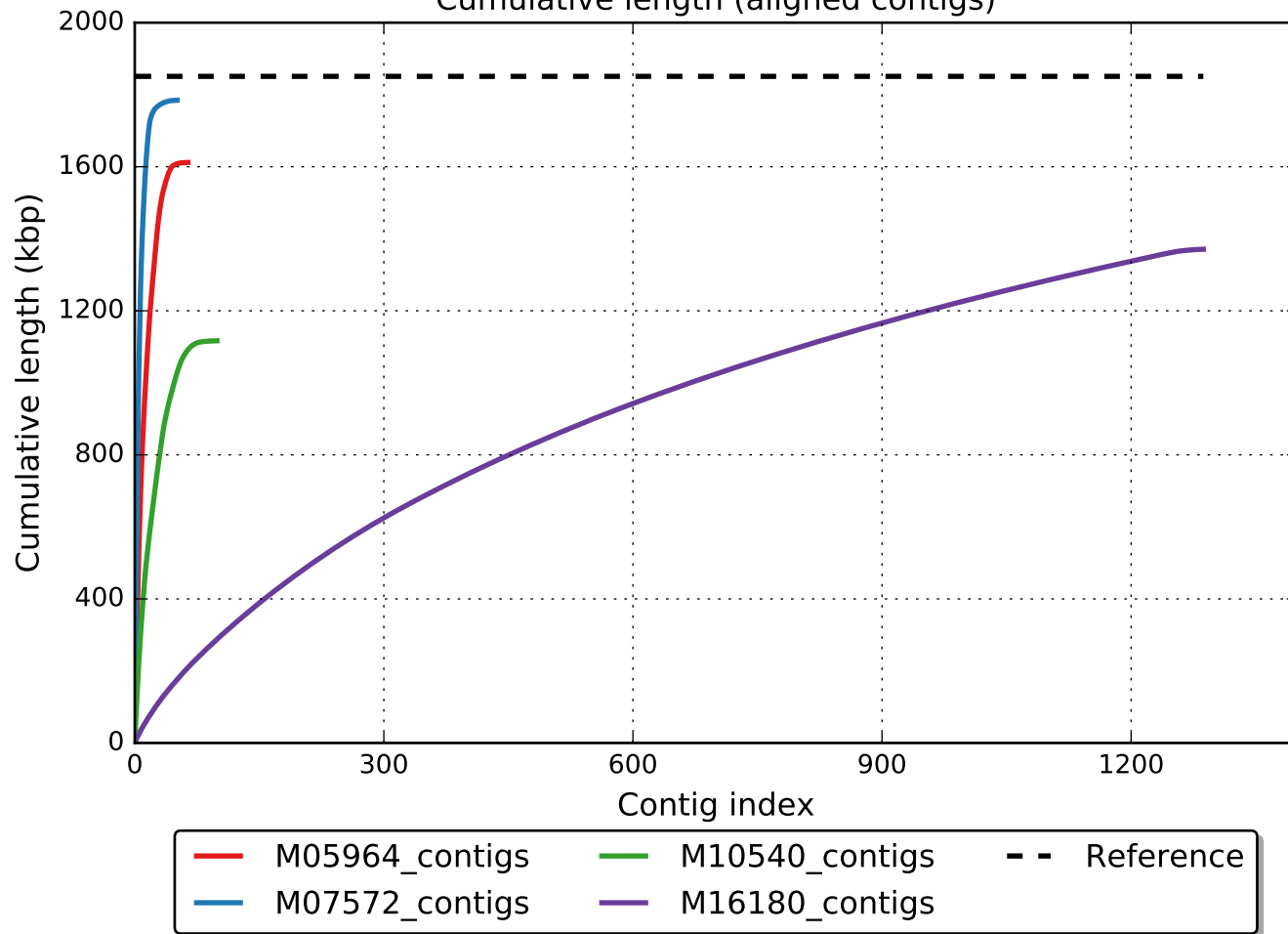




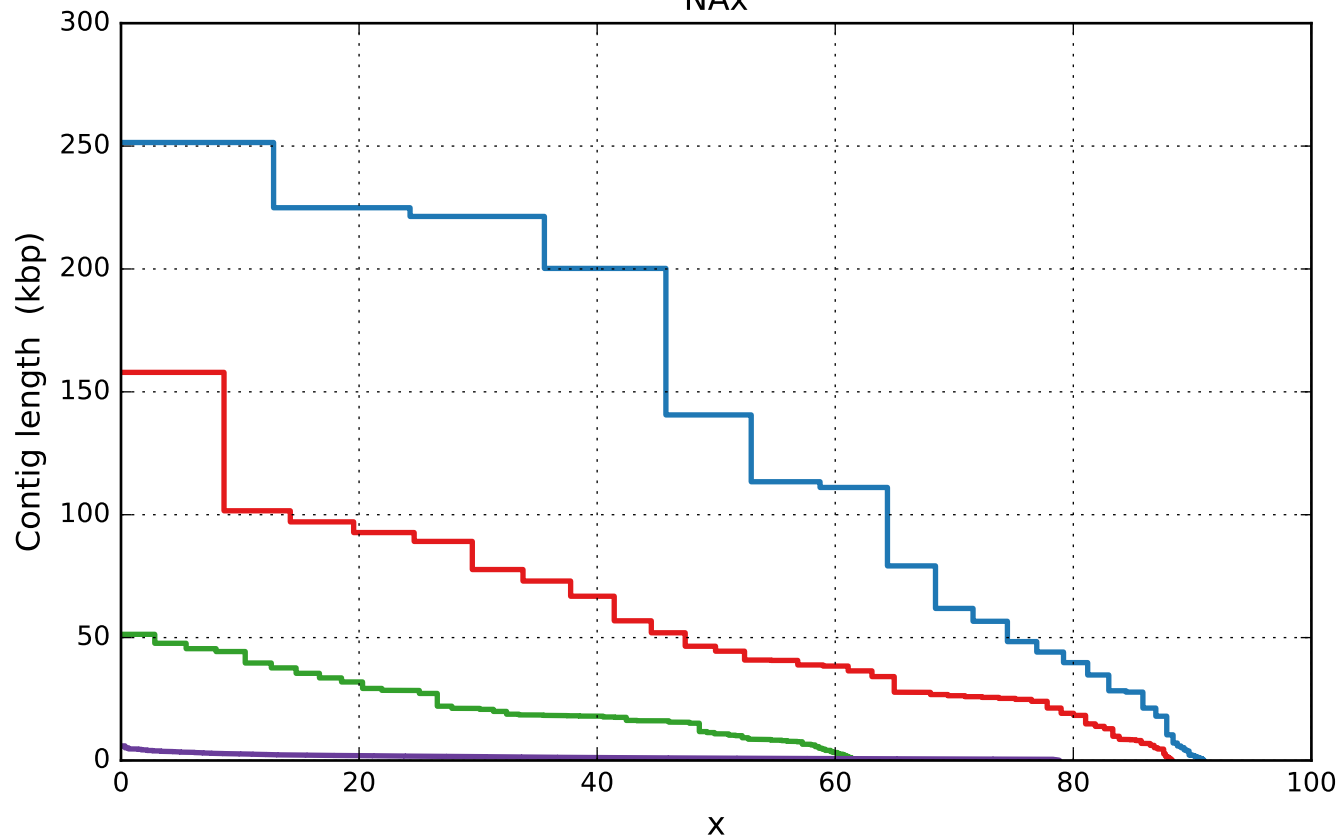
Misassemblies



Cumulative length (aligned contigs)



NAx



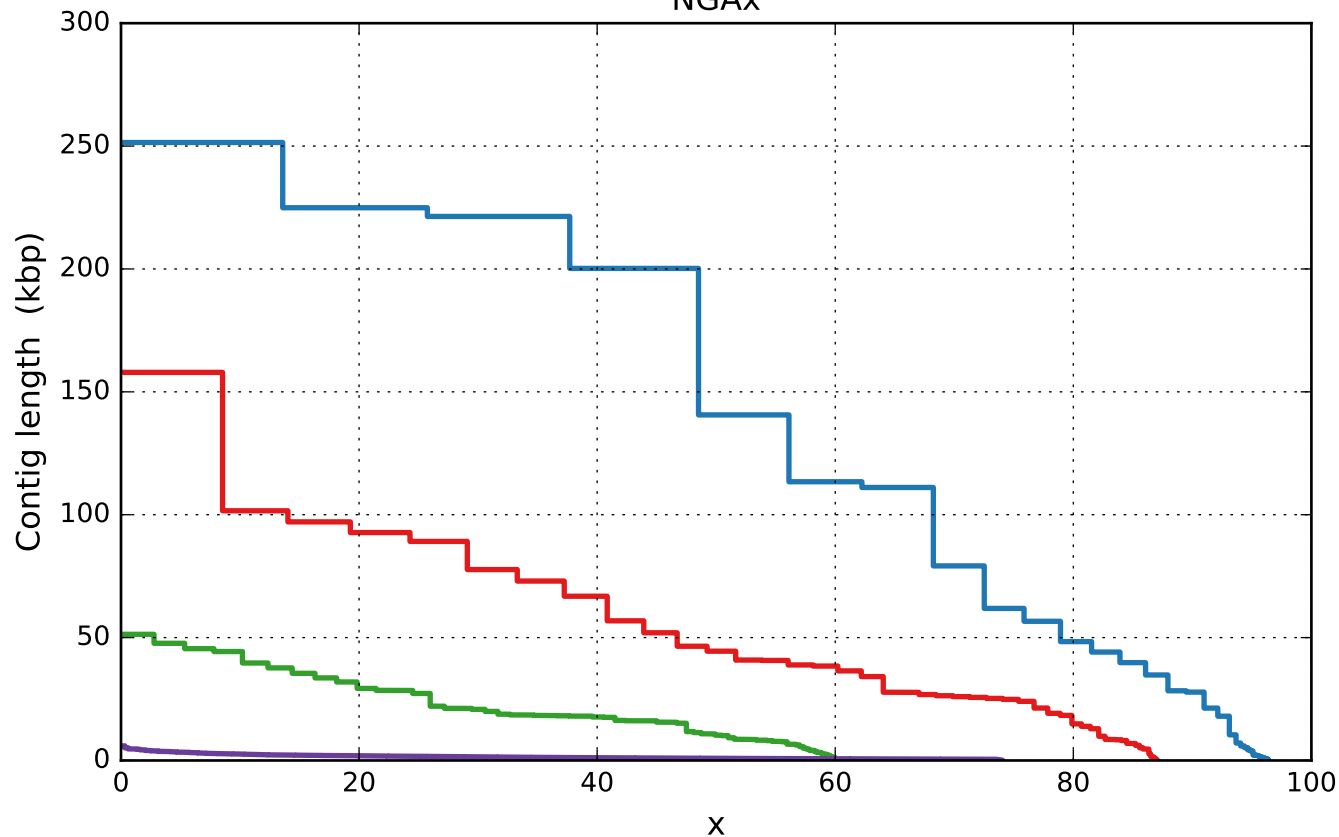
M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

NGAx



M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

