

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	1932306	1932306	1932306	1932306
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.08	38.08	38.08	38.08
N50	120793	120675	1150417	165472
NG50	179983	140698	1150417	291100
N75	28168	5904	311604	100510
NG75	116324	79549	311604	111243
L50	5	7	1	4
LG50	3	5	1	3
L75	12	23	2	8
LG75	7	9	2	7
# misassemblies	56	31	98	42
# misassembled contigs	12	14	9	12
Misassembled contigs length	1684750	1741936	1796578	1845738
# local misassemblies	57	59	35	59
# unaligned contigs	733 + 2 part	739 + 7 part	84 + 15 part	140 + 19 part
Unaligned length	585897	719960	75041	190882
Genome fraction (%)	84.686	84.112	58.966	86.146
Duplication ratio	1.111	1.119	1.625	1.146
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2545.34	2363.49	3589.08	2426.41
# indels per 100 kbp	62.58	62.20	86.19	64.88
Largest alignment	207278	139314	58344	139056
NA50	27083	29534	7127	39213
NGA50	39404	40868	7127	41161
NA75	-	-	-	7297
NGA75	15308	21831	-	17572
LA50	19	21	48	14
LGA50	11	13	48	12
LA75	-	-	-	39
LGA75	30	28	-	28

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

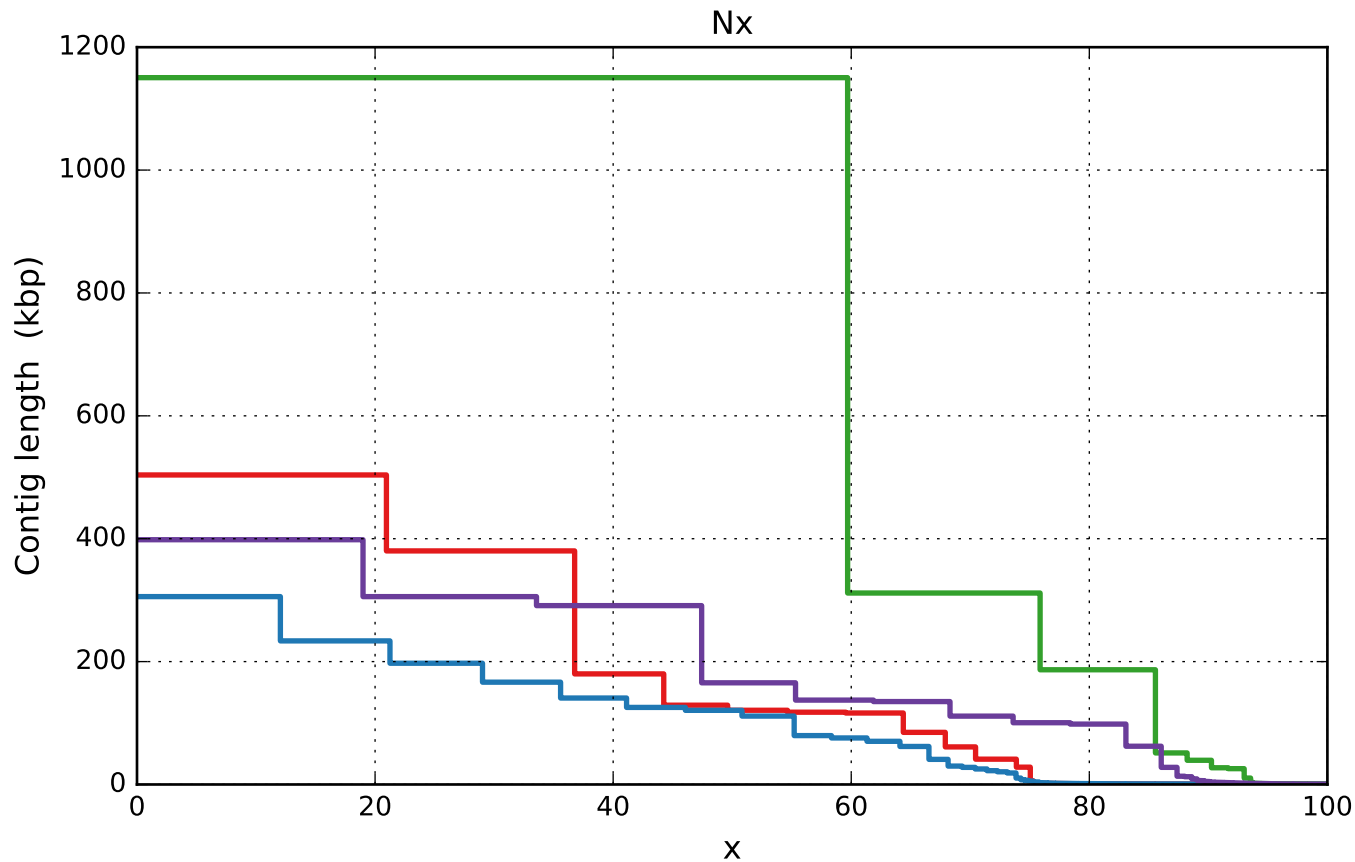
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	56	31	98	42
# relocations	54	31	98	42
# translocations	0	0	0	0
# inversions	2	0	0	0
# misassembled contigs	12	14	9	12
Misassembled contigs length	1684750	1741936	1796578	1845738
# local misassemblies	57	59	35	59
# mismatches	41652	38414	40894	40390
# indels	1024	1011	982	1080
# short indels	911	882	897	950
# long indels	113	129	85	130
Indels length	3258	3410	2488	3362

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	733	739	84	140
Fully unaligned length	584729	653873	68502	165675
# partially unaligned contigs	2	7	15	19
# with misassembly	0	1	1	1
# both parts are significant	0	1	0	1
Partially unaligned length	1168	66087	6539	25207
# 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).

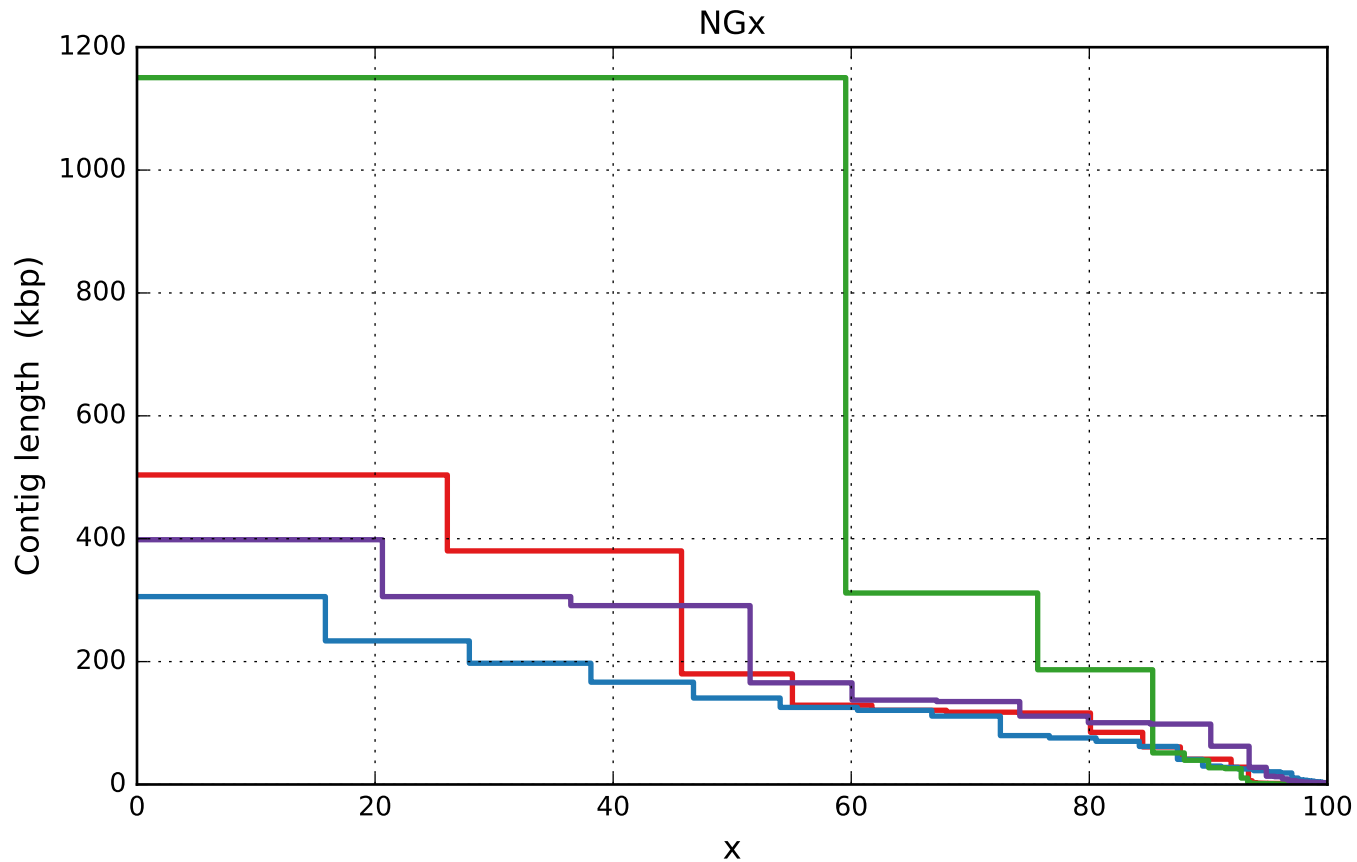


M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

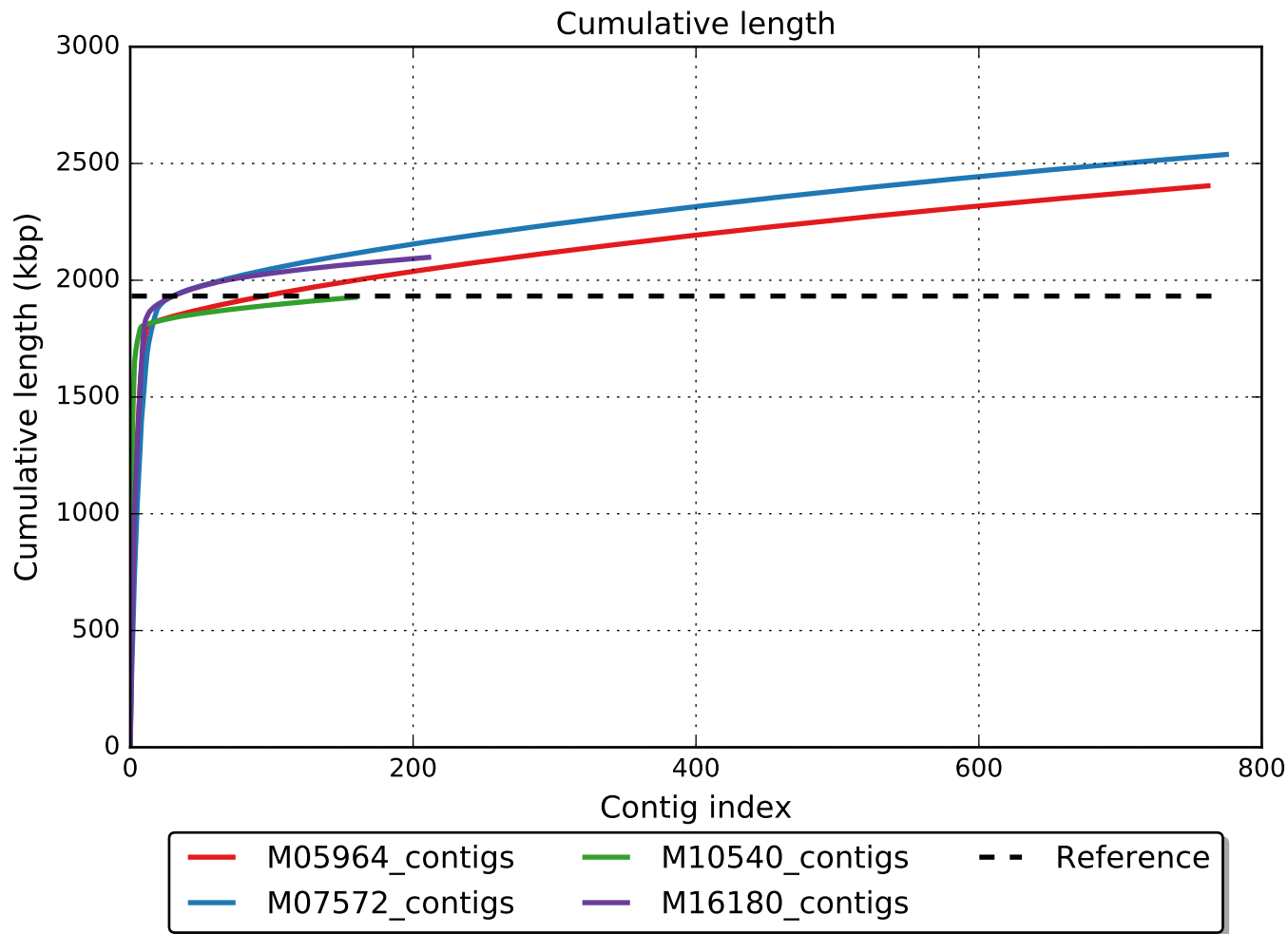


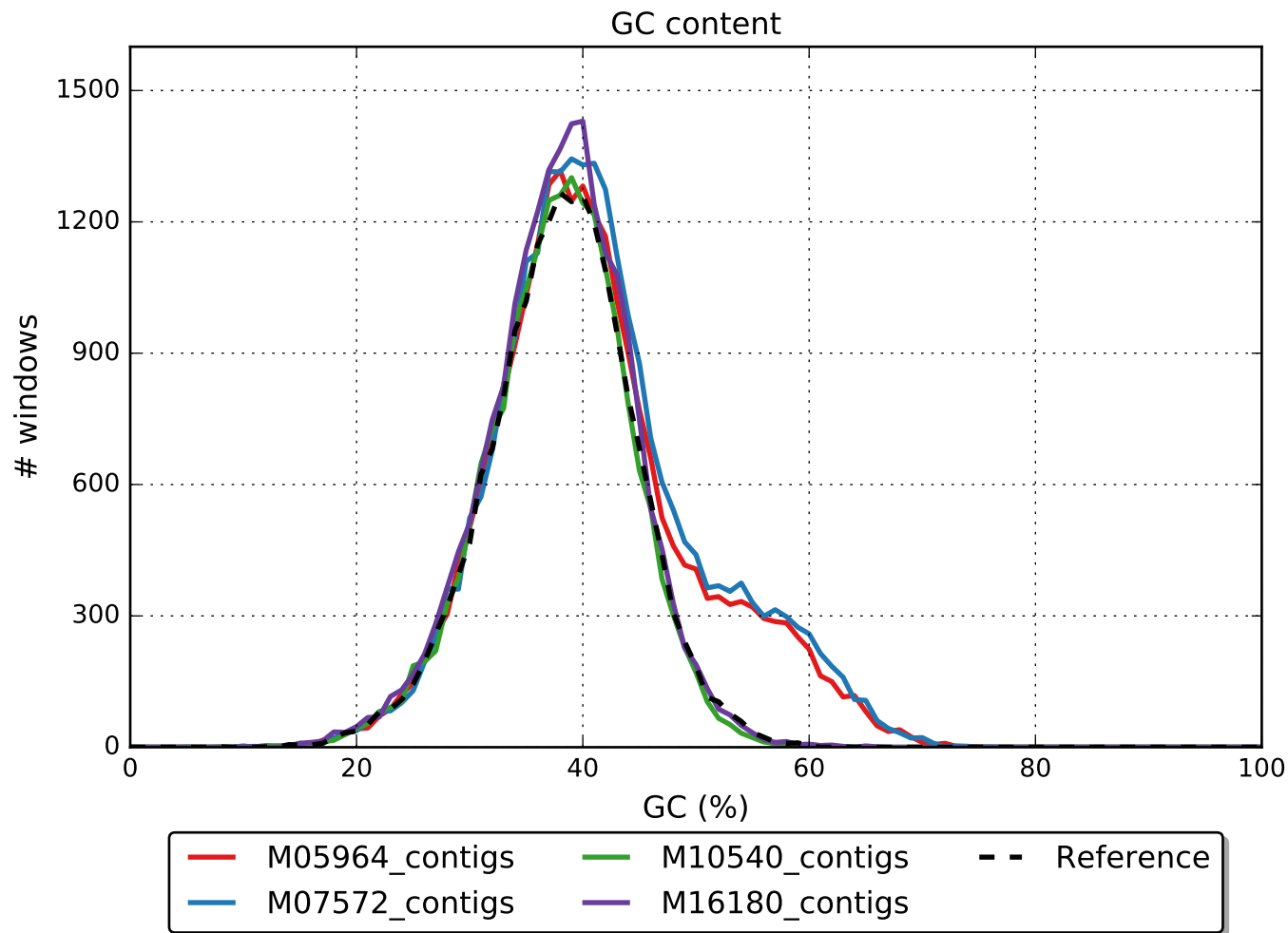
M05964_contigs

M10540_contigs

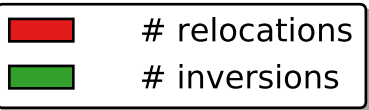
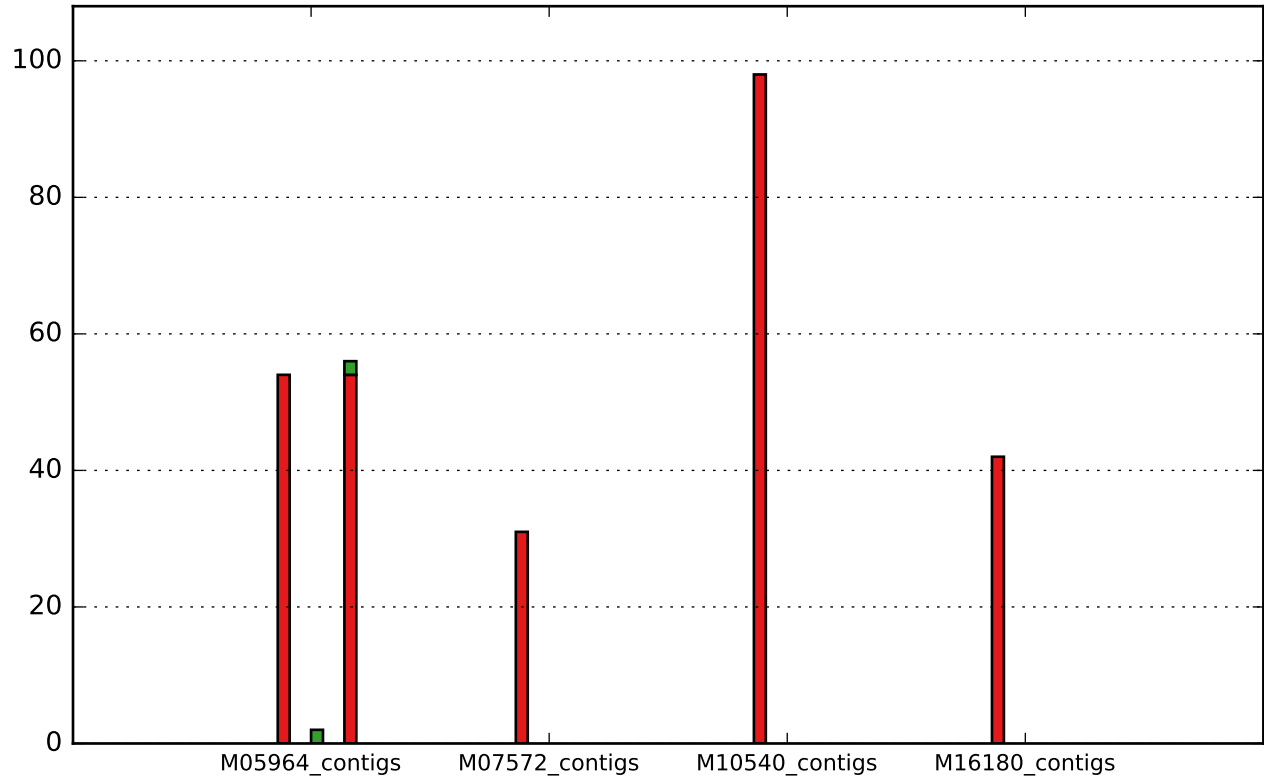
M16180_contigs

M07572_contigs

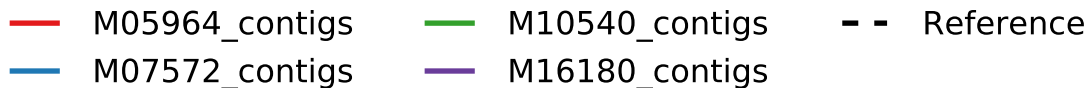
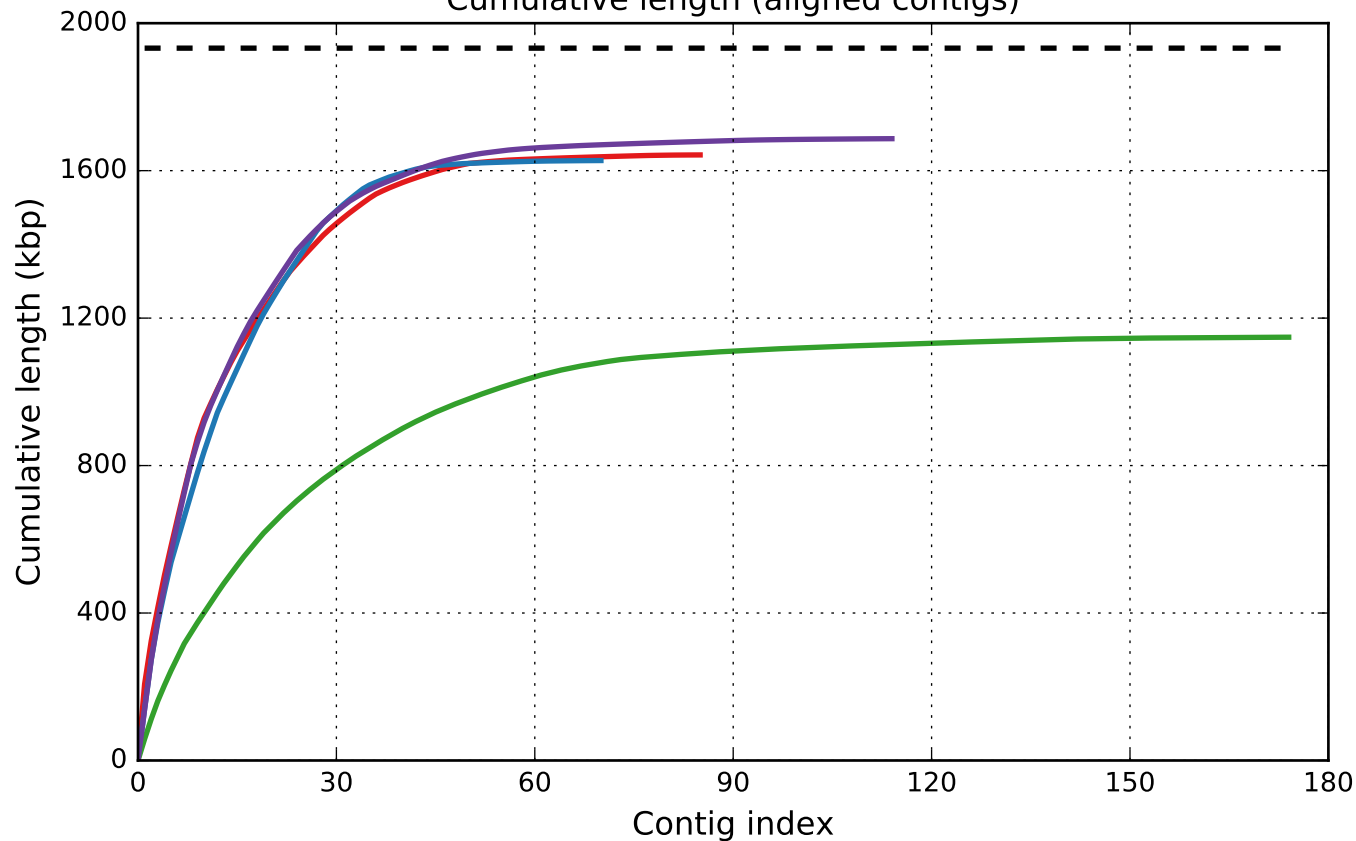




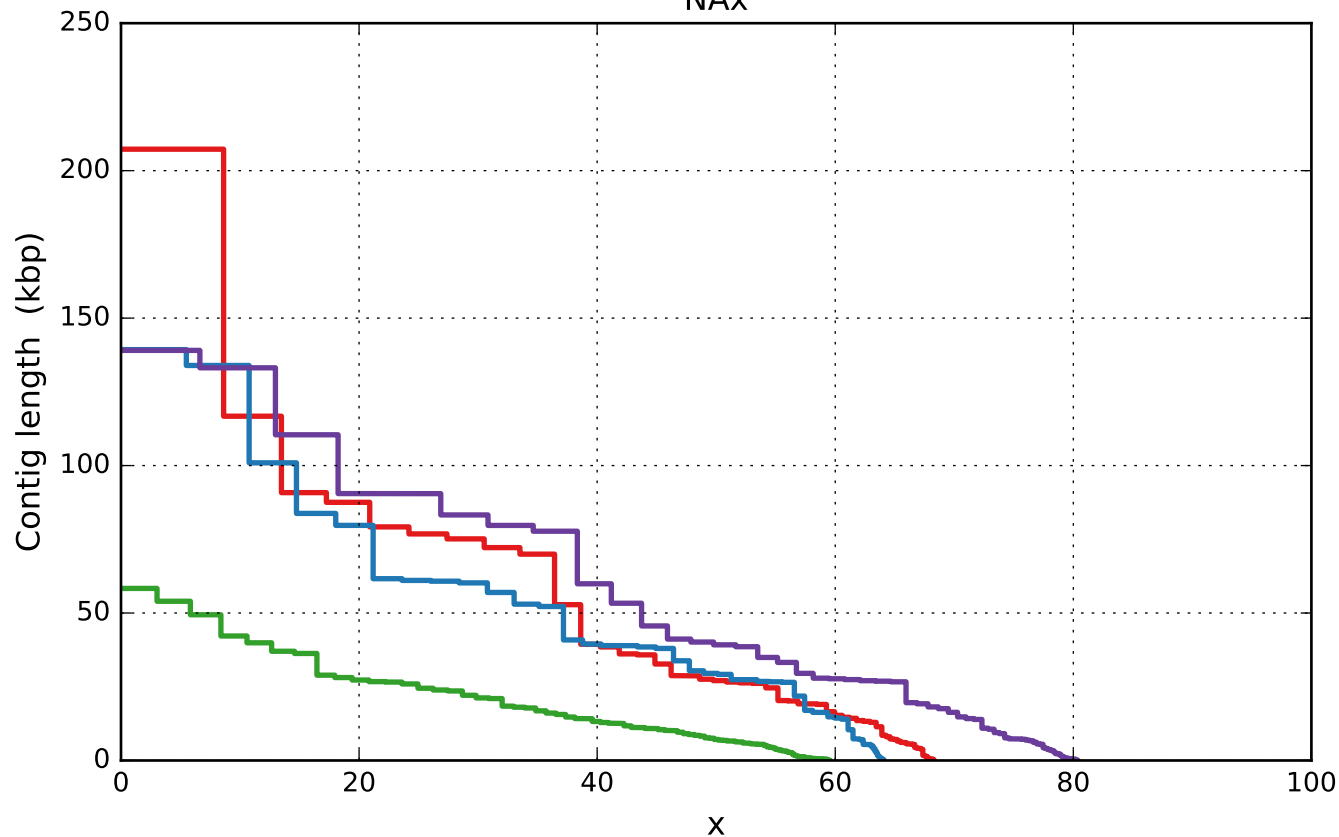
Misassemblies



Cumulative length (aligned contigs)



NAx



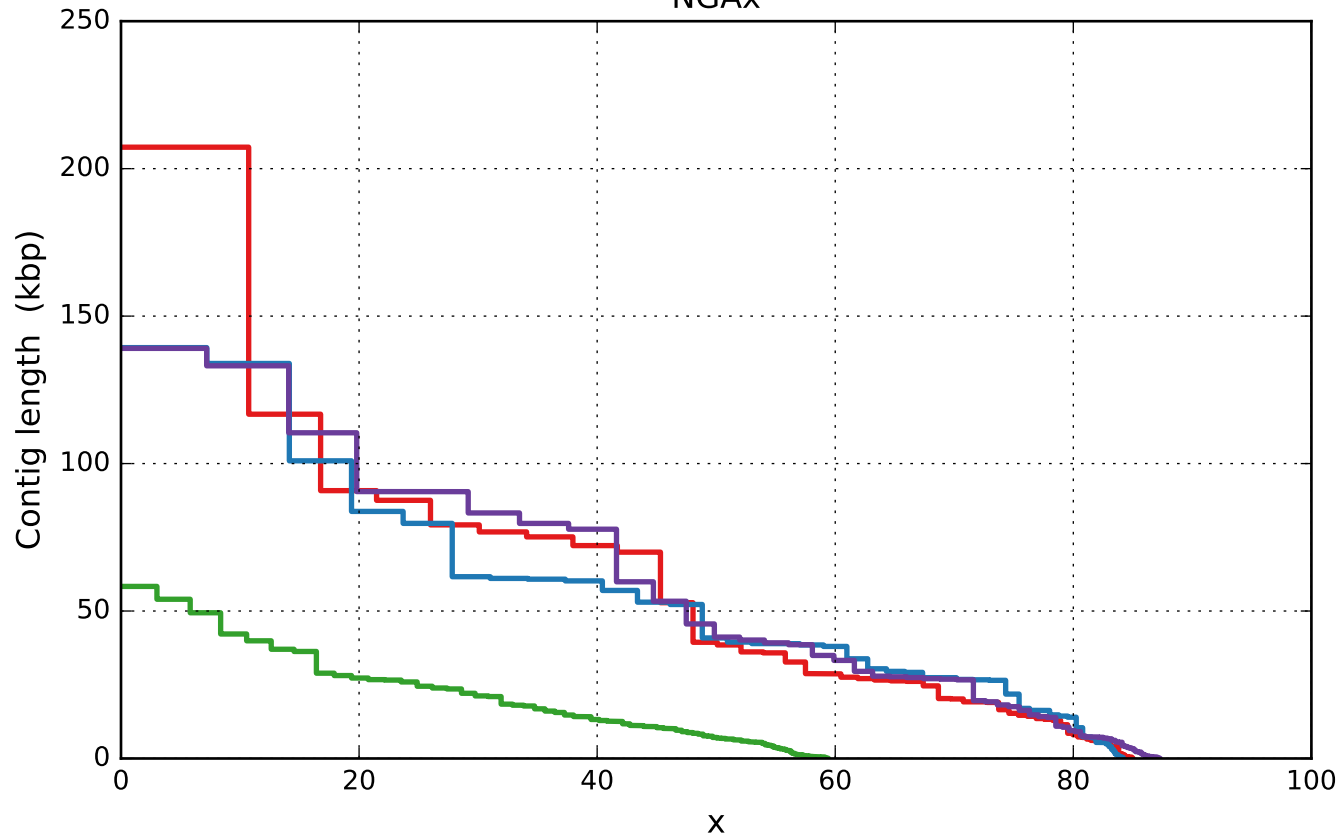
M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

