

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	1969659	1969659	1969659	1969659
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.31	38.31	38.31	38.31
N50	120793	120675	1150417	165472
NG50	179983	140698	1150417	291100
N75	28168	5904	311604	100510
NG75	116324	79549	186707	111243
L50	5	7	1	4
LG50	3	5	1	3
L75	12	23	2	8
LG75	7	9	3	7
# misassemblies	50	44	84	56
# misassembled contigs	12	14	7	14
Misassembled contigs length	1777375	1759644	1725018	1812948
# local misassemblies	59	62	42	70
# unaligned contigs	728 + 4 part	735 + 14 part	78 + 24 part	147 + 25 part
Unaligned length	580682	700910	106988	209567
Genome fraction (%)	82.024	80.887	53.675	84.701
Duplication ratio	1.129	1.153	1.722	1.132
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2442.32	2283.14	3412.26	2482.32
# indels per 100 kbp	68.77	58.31	77.85	68.99
Largest alignment	178366	153177	51310	154272
NA50	36146	25298	5581	35073
NGA50	59822	34879	3284	36053
NA75	-	-	-	10984
NGA75	14907	14907	-	18310
LA50	15	23	57	16
LGA50	10	14	62	14
LA75	-	-	-	37
LGA75	28	33	-	31

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

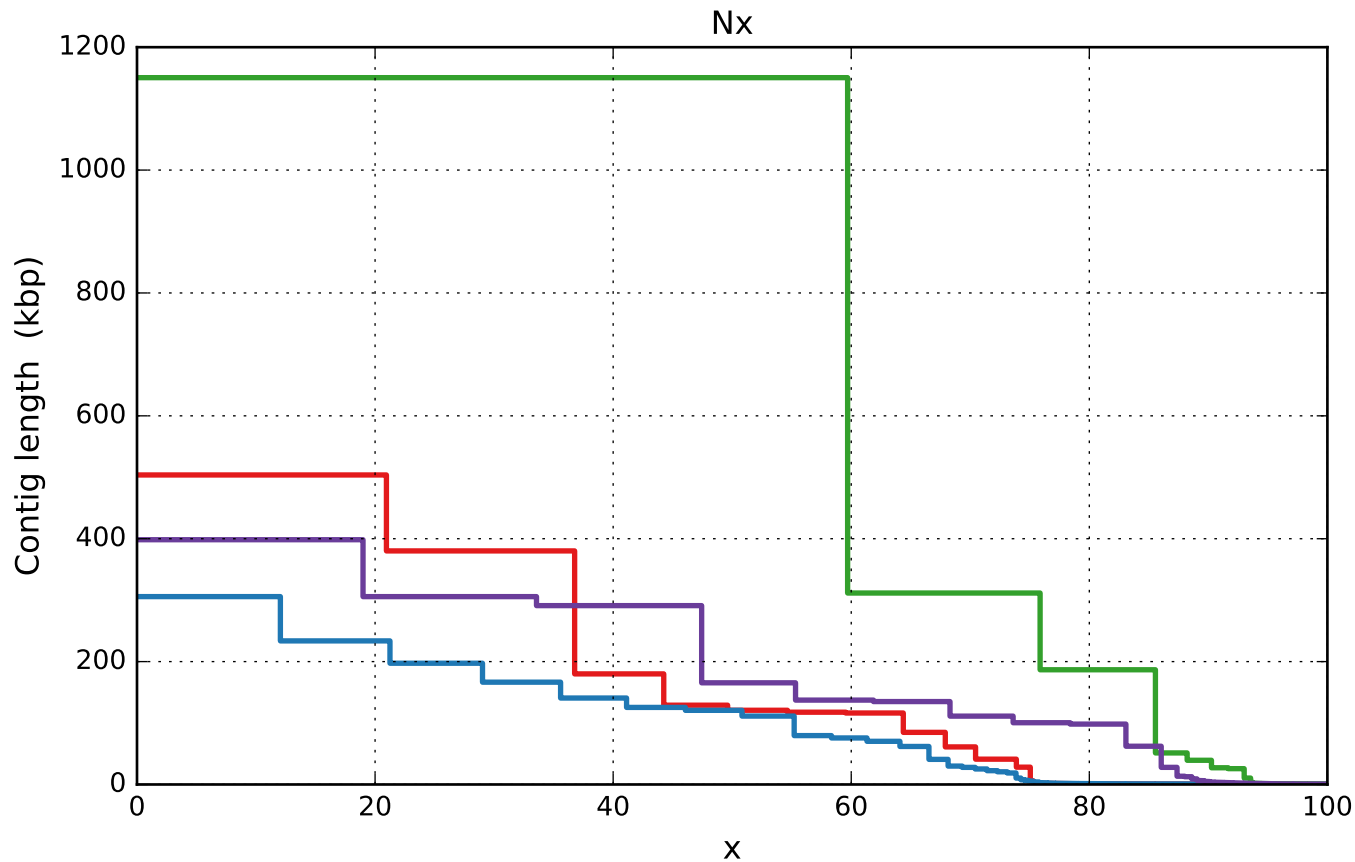
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	50	44	84	56
# relocations	50	43	83	54
# translocations	0	0	0	0
# inversions	0	1	1	2
# misassembled contigs	12	14	7	14
Misassembled contigs length	1777375	1759644	1725018	1812948
# local misassemblies	59	62	42	70
# mismatches	39458	36375	36075	41413
# indels	1111	929	823	1151
# short indels	970	830	760	1032
# long indels	141	99	63	119
Indels length	3500	2793	1917	3132

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	728	735	78	147
Fully unaligned length	575129	631290	61815	175782
# partially unaligned contigs	4	14	24	25
# with misassembly	0	4	2	2
# both parts are significant	1	6	2	6
Partially unaligned length	5553	69620	45173	33785
# 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).

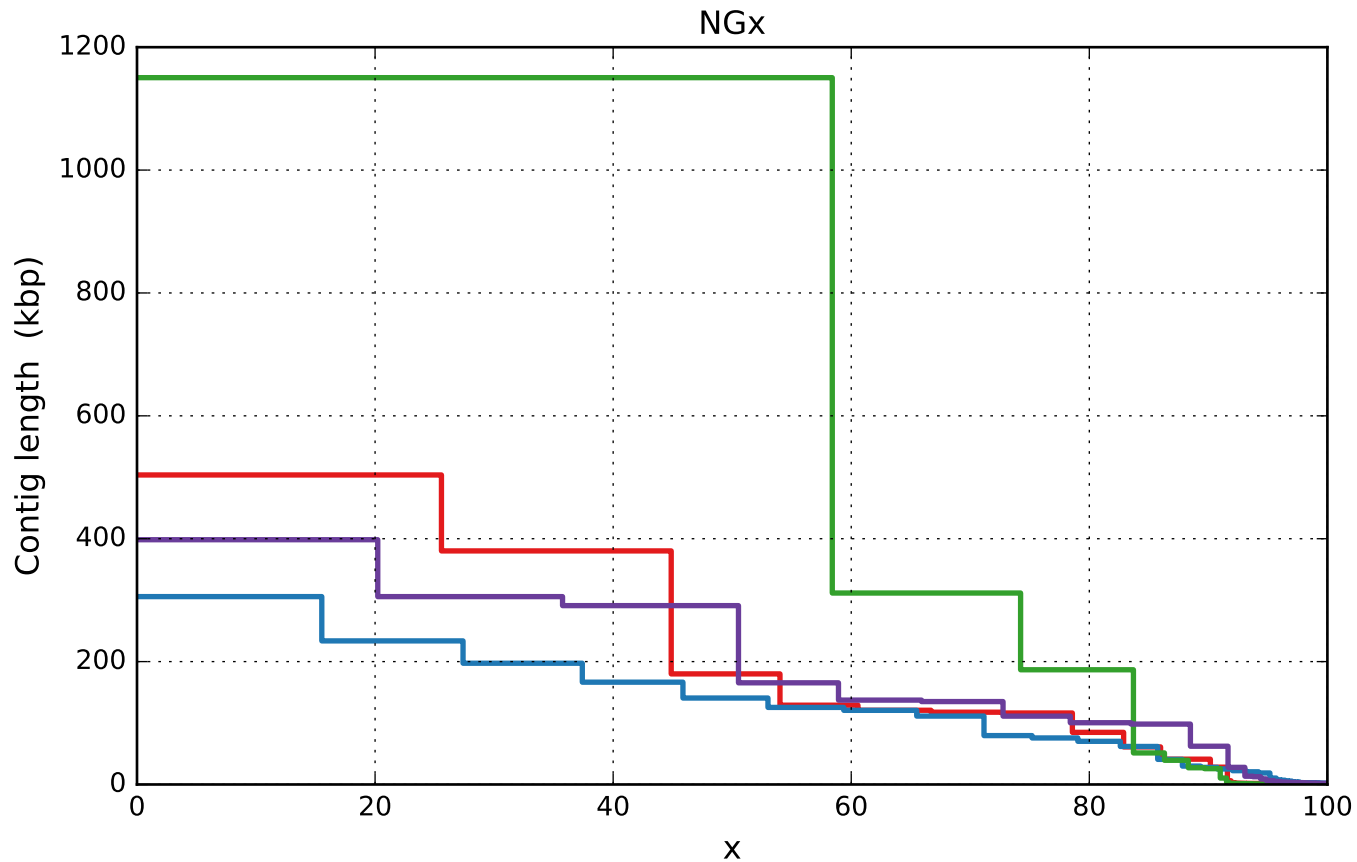


M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

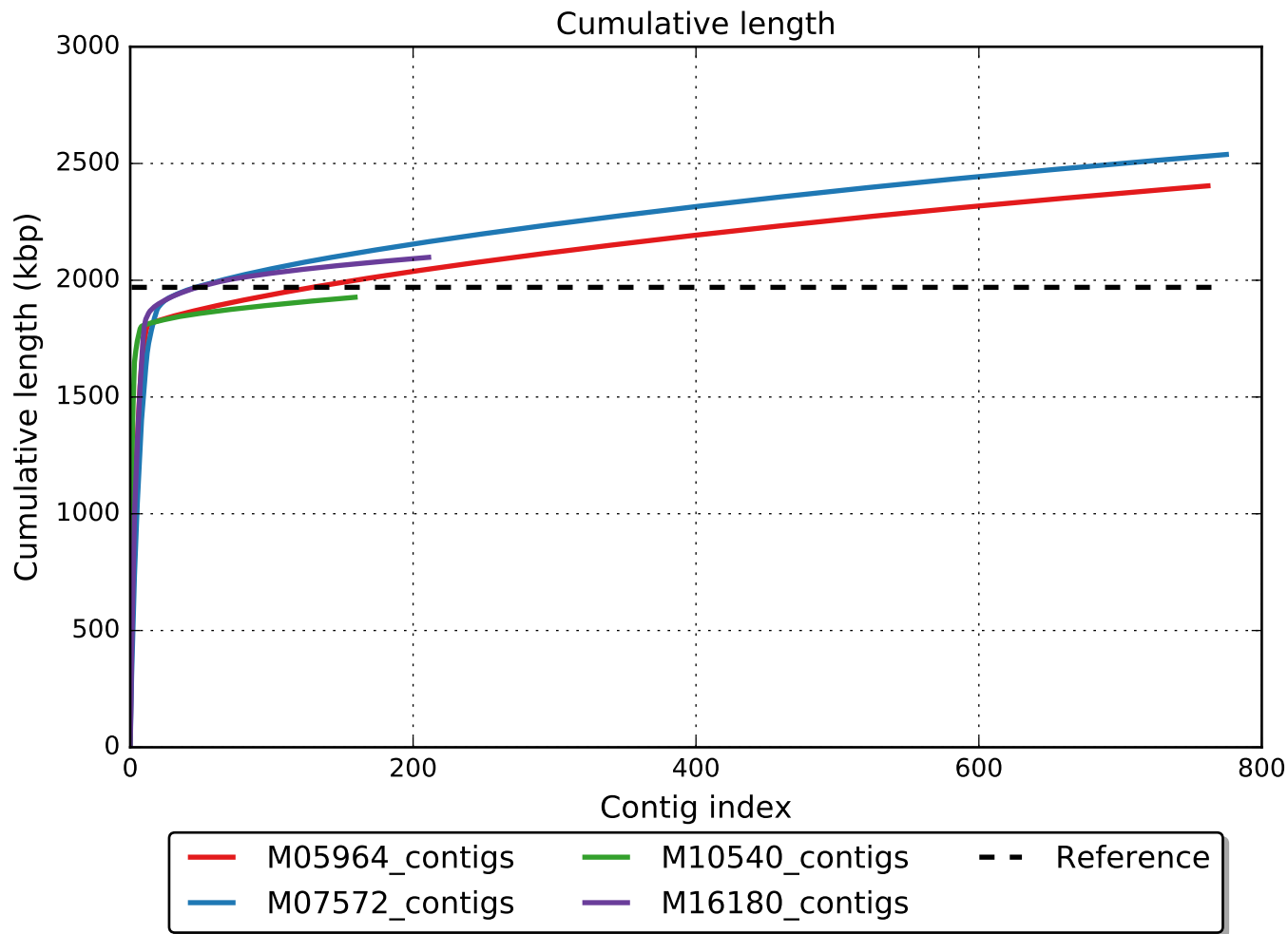


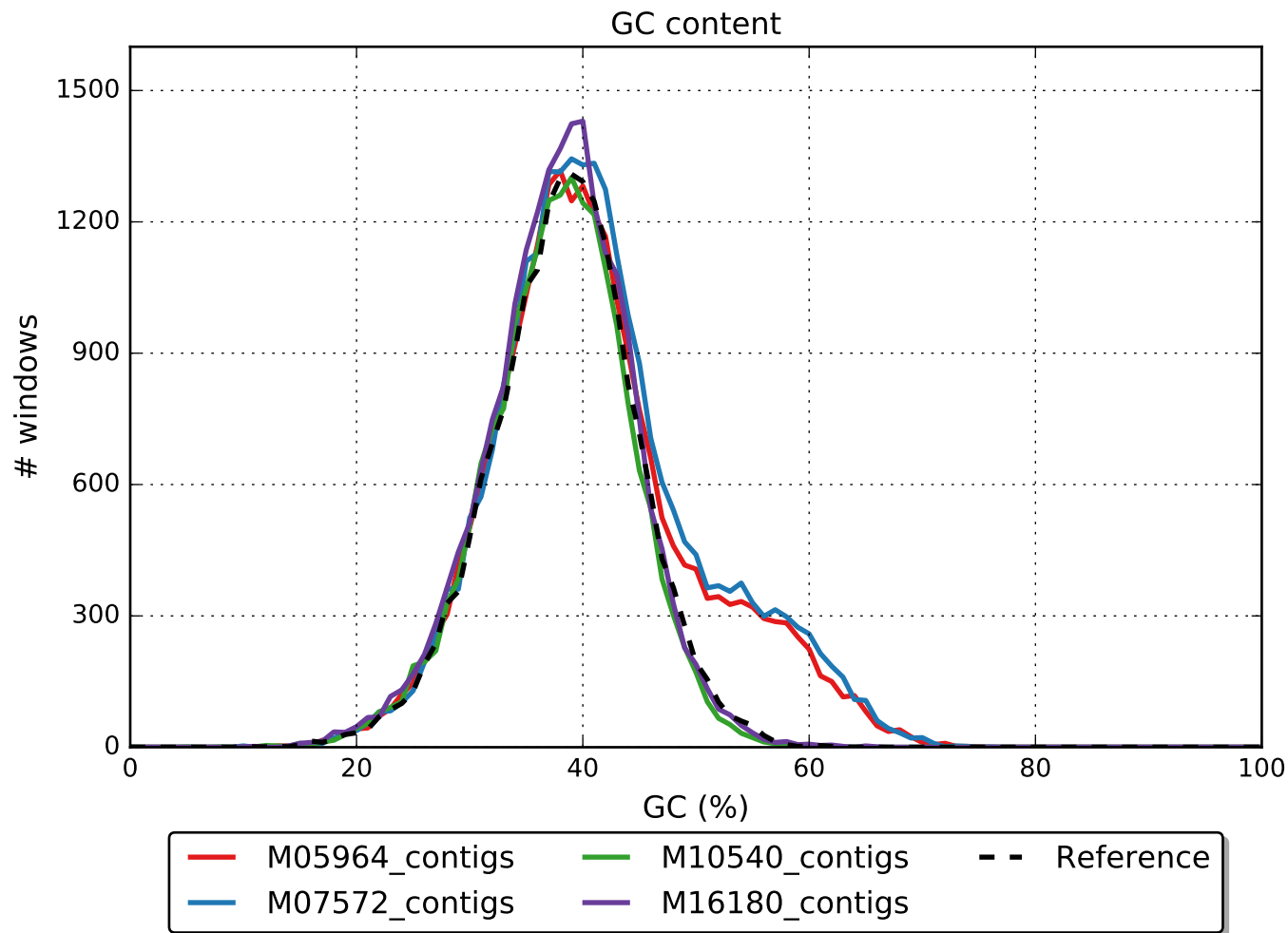
M05964_contigs

M10540_contigs

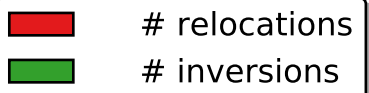
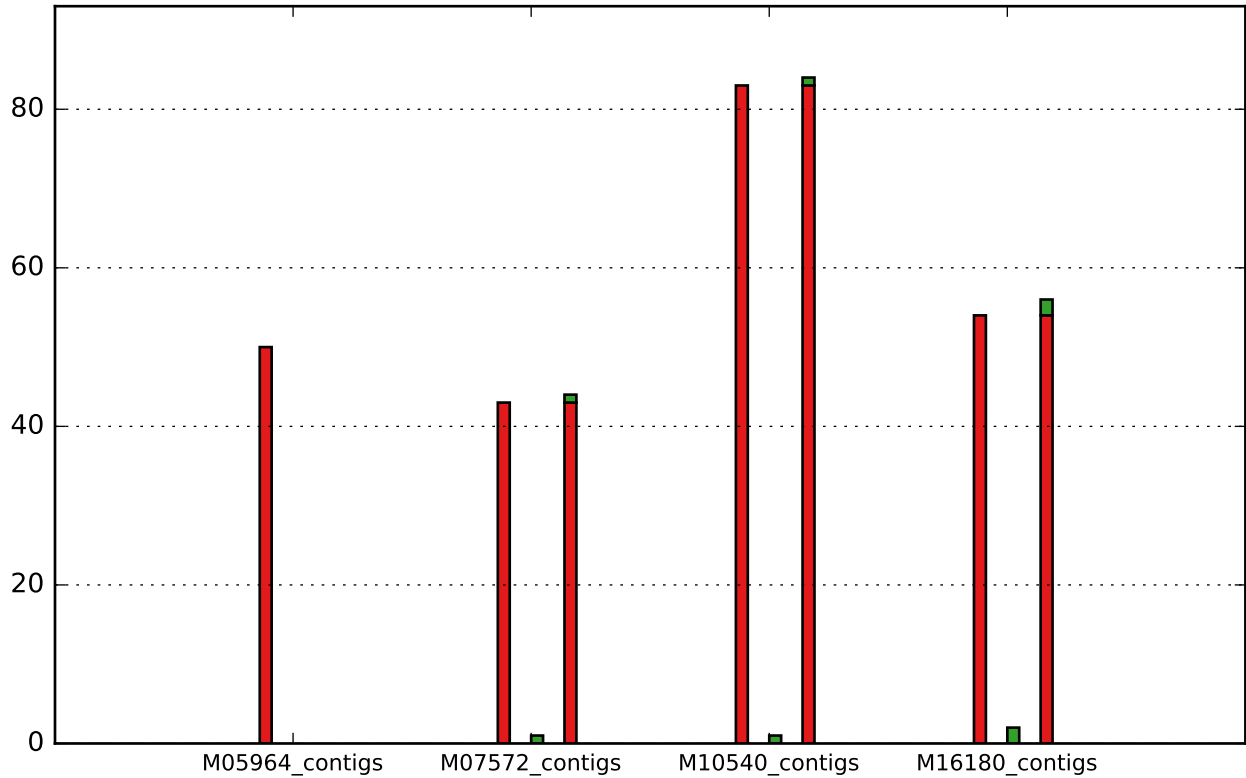
M16180_contigs

M07572_contigs

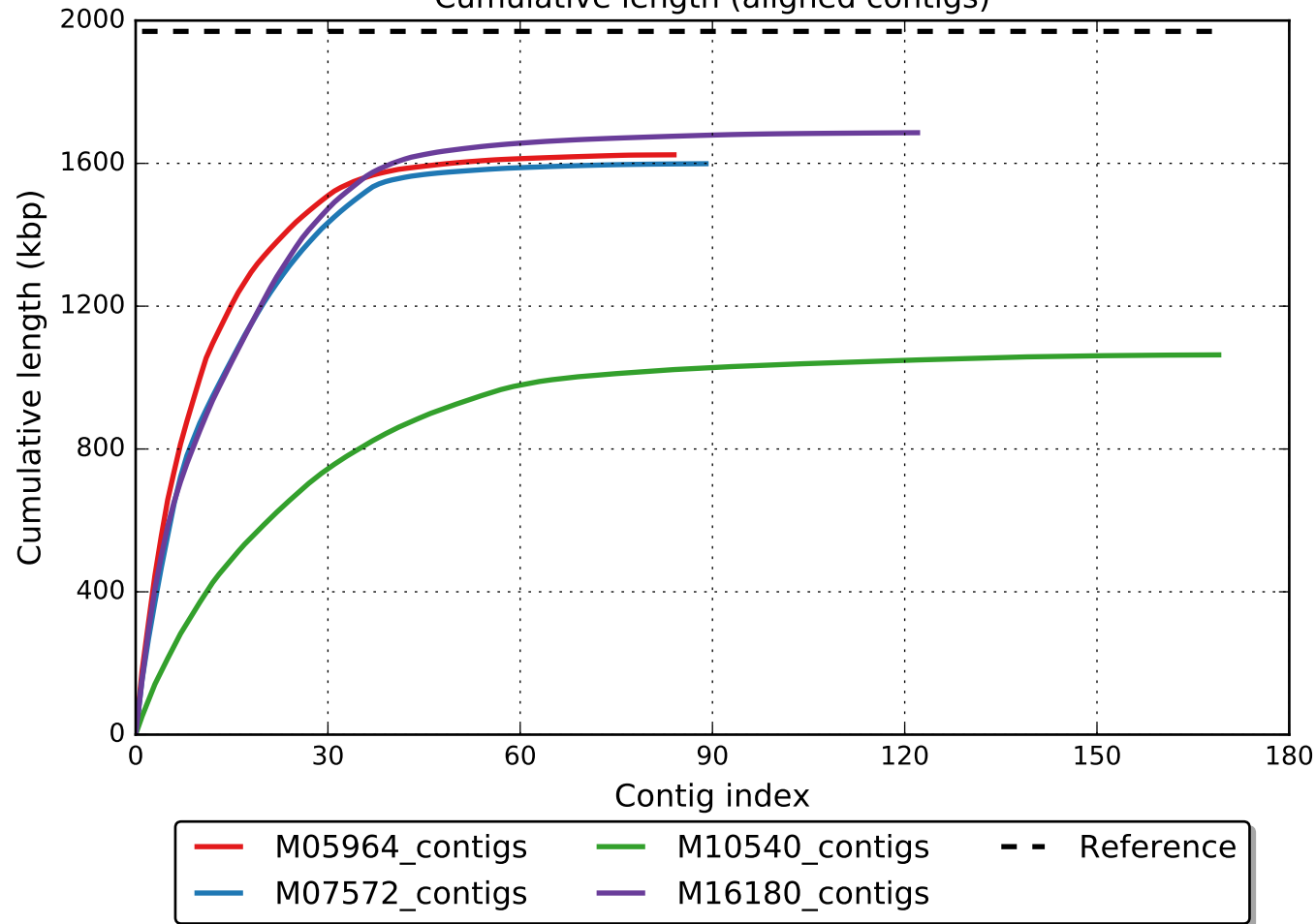




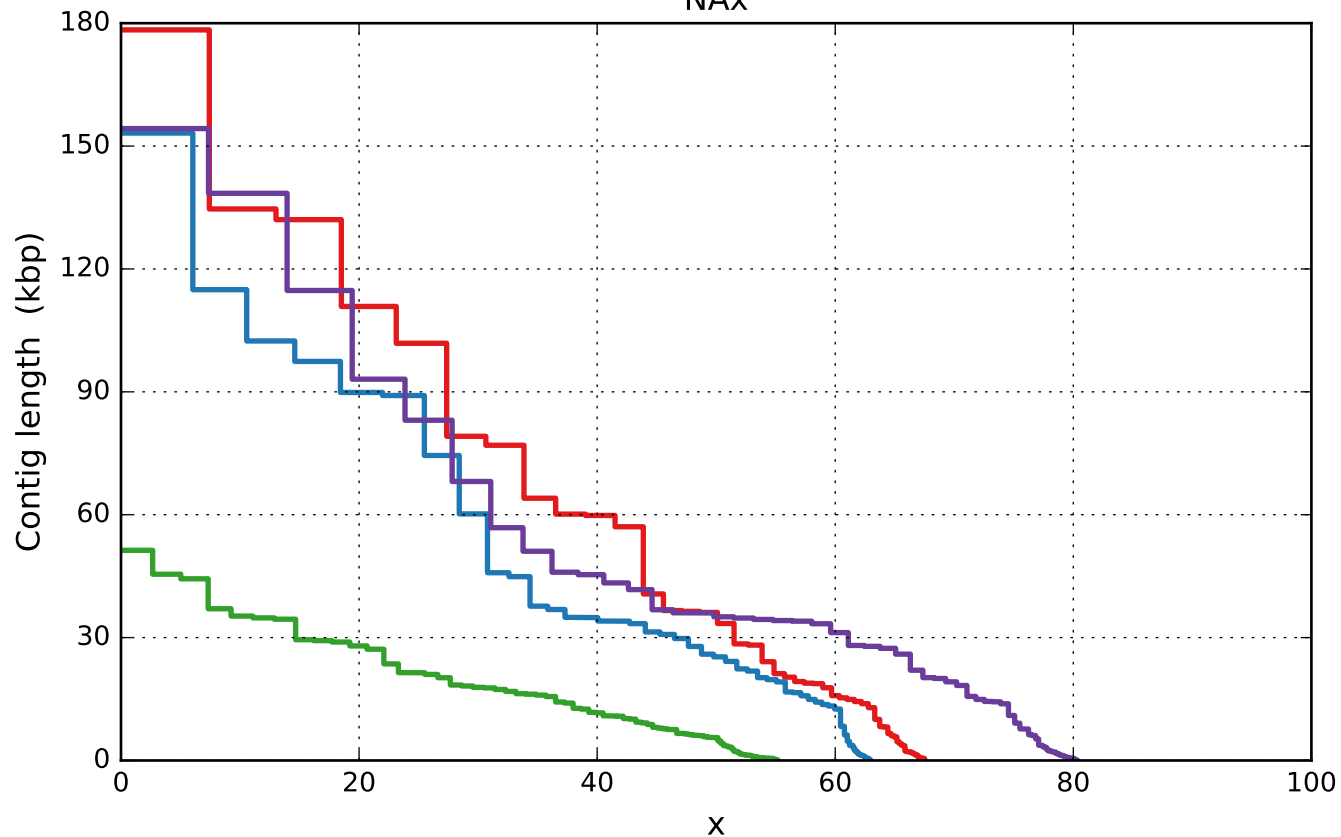
Misassemblies



Cumulative length (aligned contigs)



NAx



M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

NGAx

