

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	1830138	1830138	1830138	1830138
GC (%)	41.19	41.57	37.84	37.98
Reference GC (%)	38.15	38.15	38.15	38.15
N50	120793	120675	1150417	165472
NG50	179983	140698	1150417	291100
N75	28168	5904	311604	100510
NG75	117636	111326	311604	134943
L50	5	7	1	4
LG50	3	5	1	3
L75	12	23	2	8
LG75	6	8	2	6
# misassemblies	45	44	76	42
# misassembled contigs	11	14	7	12
Misassembled contigs length	1736208	1754955	1726481	1807642
# local misassemblies	64	64	37	62
# unaligned contigs	738 + 0 part	746 + 4 part	67 + 22 part	135 + 22 part
Unaligned length	588237	704732	121754	188716
Genome fraction (%)	86.292	88.235	56.949	90.454
Duplication ratio	1.150	1.136	1.732	1.153
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	2435.64	2270.65	3628.61	2199.29
# indels per 100 kbp	74.15	74.37	94.60	73.82
Largest alignment	146760	113208	74272	125826
NA50	25832	26525	3509	39003
NGA50	40061	40982	6271	46355
NA75	-	-	-	7560
NGA75	13843	22421	-	25910
LA50	21	24	53	14
LGA50	13	13	44	11
LA75	-	-	-	40
LGA75	29	28	-	24

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

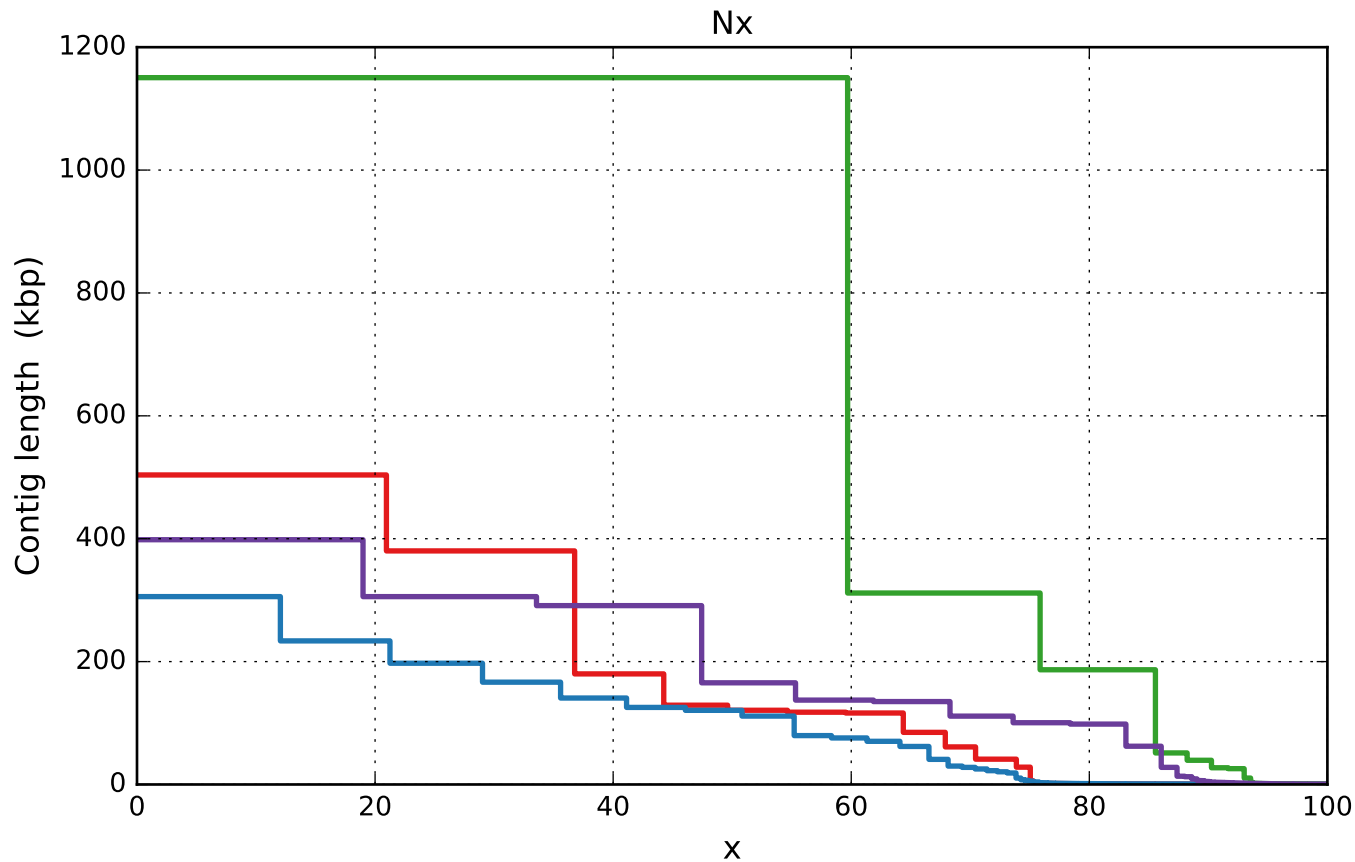
	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	45	44	76	42
# relocations	45	44	76	42
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	11	14	7	12
Misassembled contigs length	1736208	1754955	1726481	1807642
# local misassemblies	64	64	37	62
# mismatches	38465	36667	37819	36408
# indels	1171	1201	986	1222
# short indels	1053	1089	909	1108
# long indels	118	112	77	114
Indels length	3170	3321	2139	3653

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	738	746	67	135
Fully unaligned length	588237	680390	54901	152024
# partially unaligned contigs	0	4	22	22
# with misassembly	0	1	4	2
# both parts are significant	0	1	3	7
Partially unaligned length	0	24342	66853	36692
# 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).

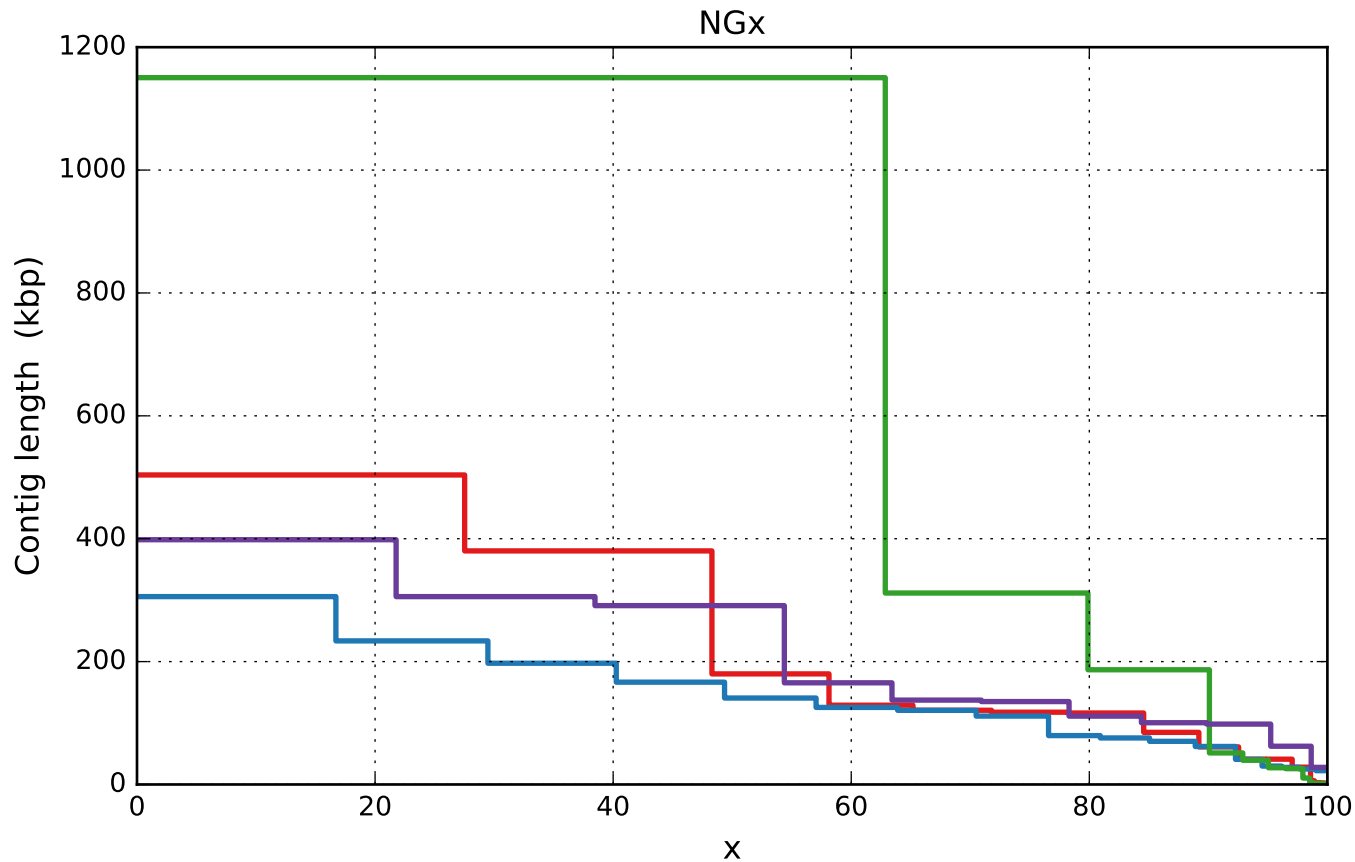


M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

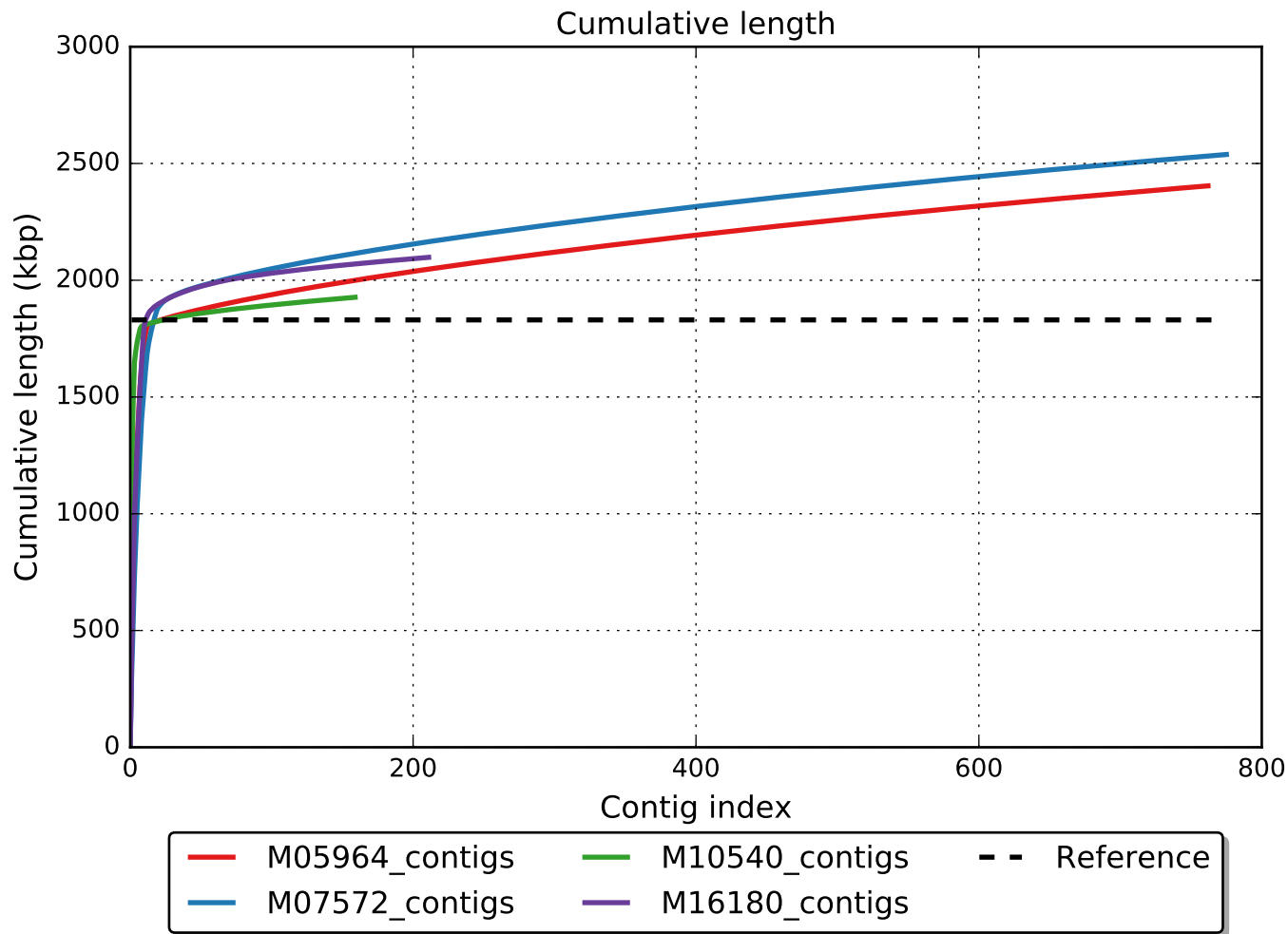


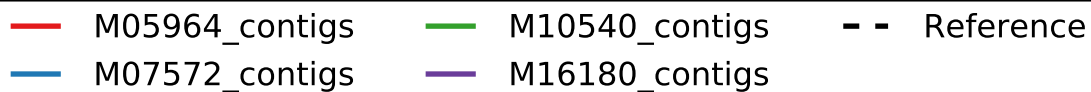
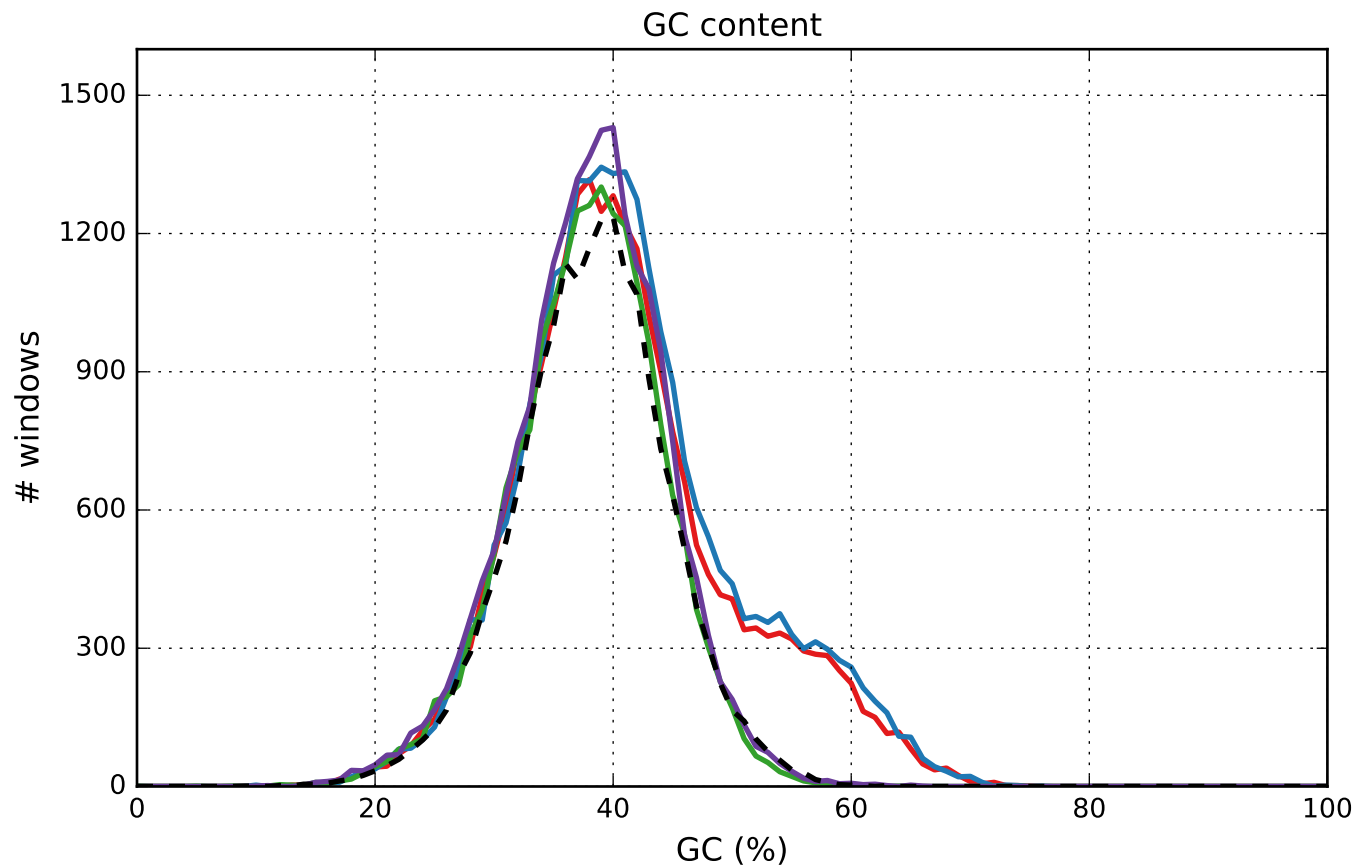
M05964_contigs

M10540_contigs

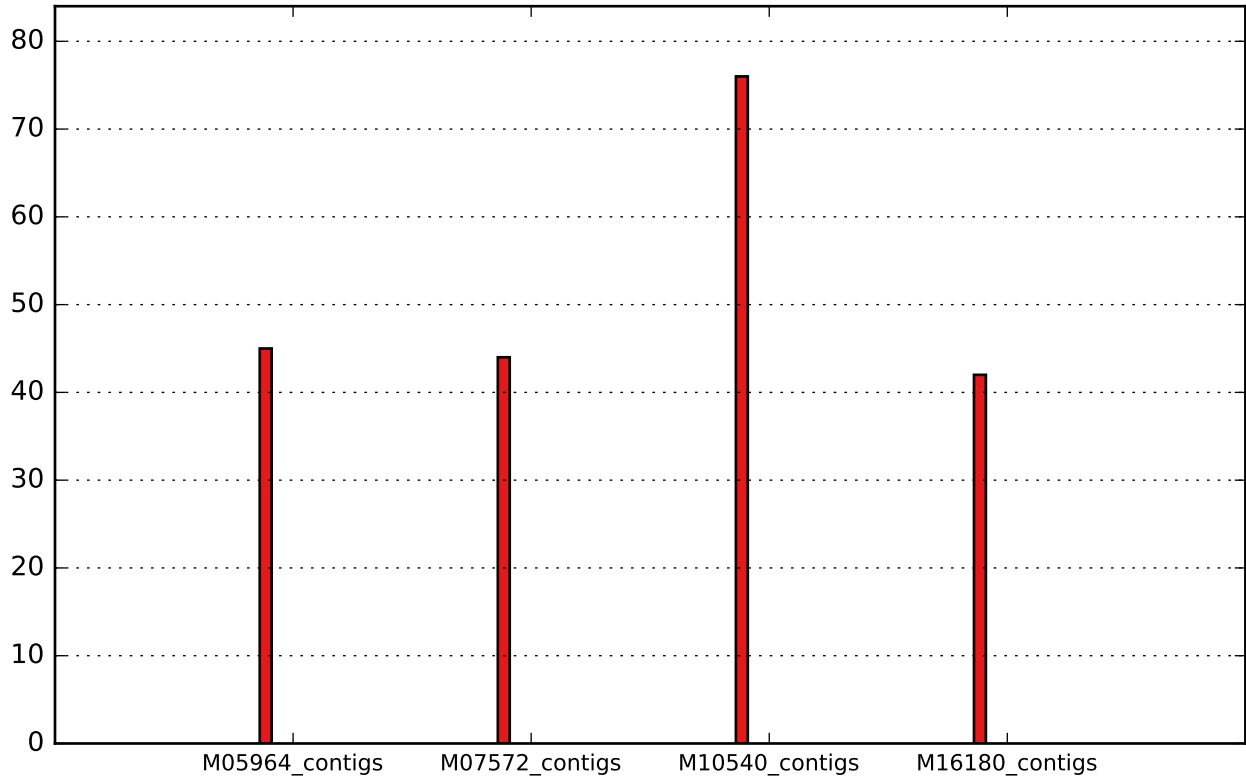
M16180_contigs

M07572_contigs



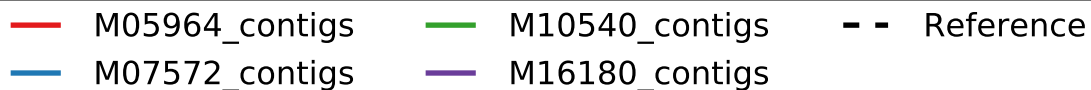
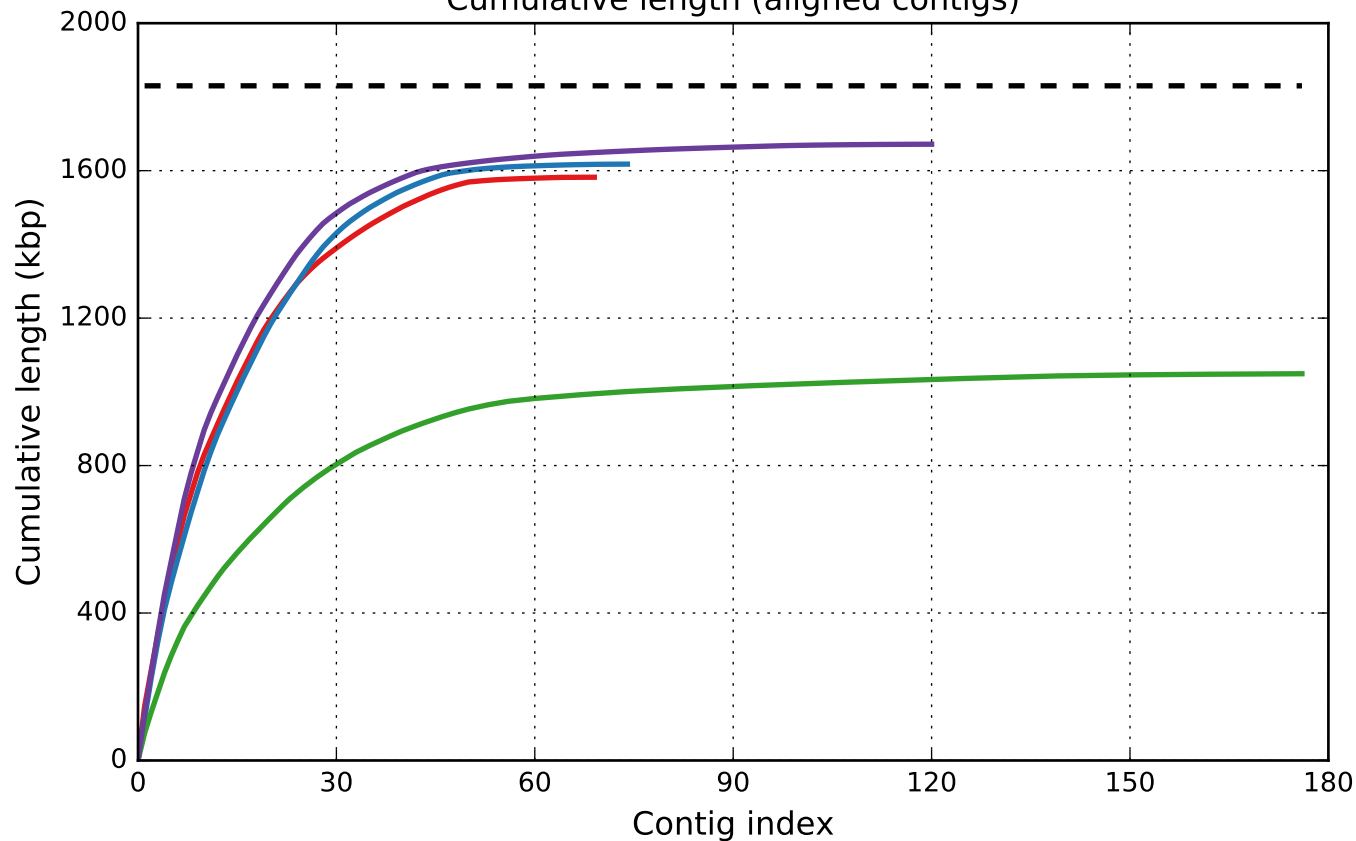


Misassemblies

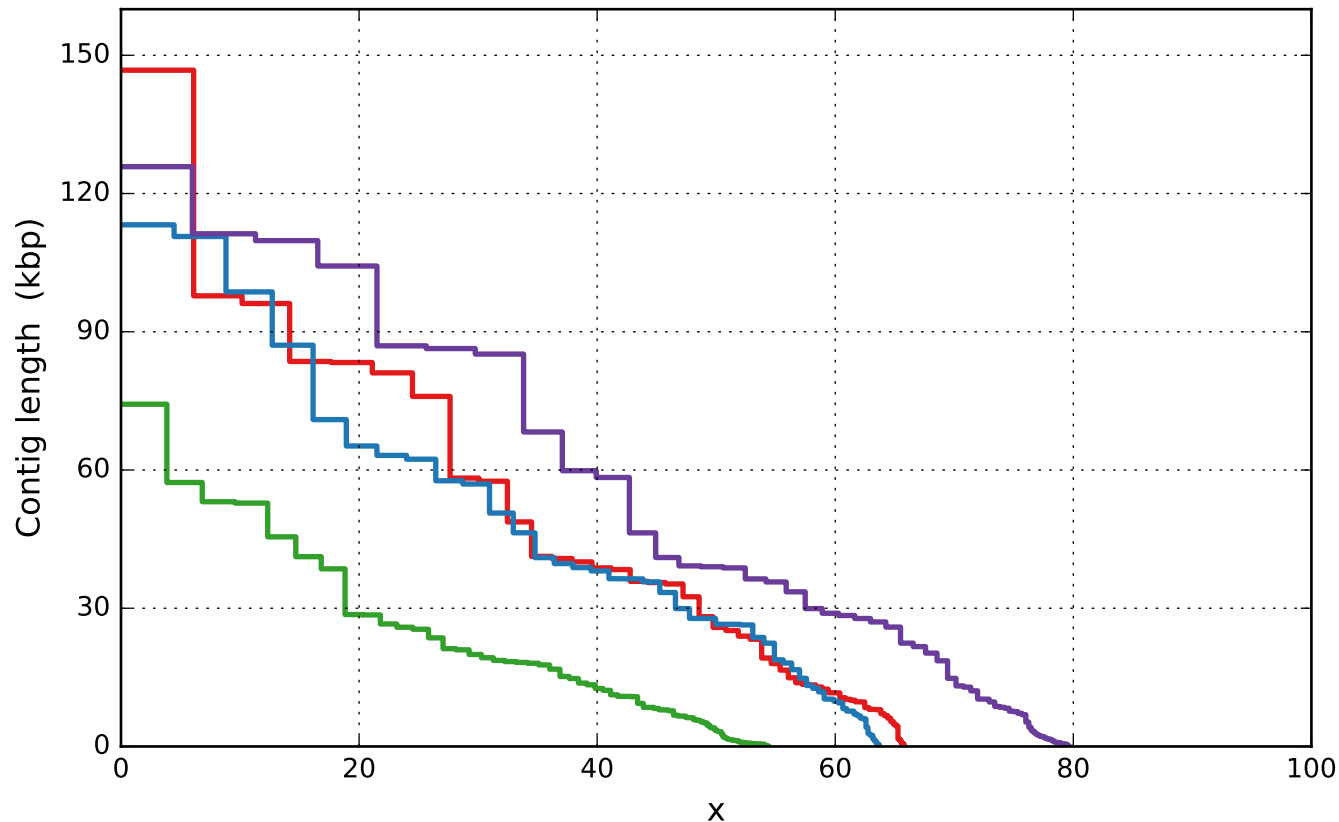


 # relocations

Cumulative length (aligned contigs)



NAx



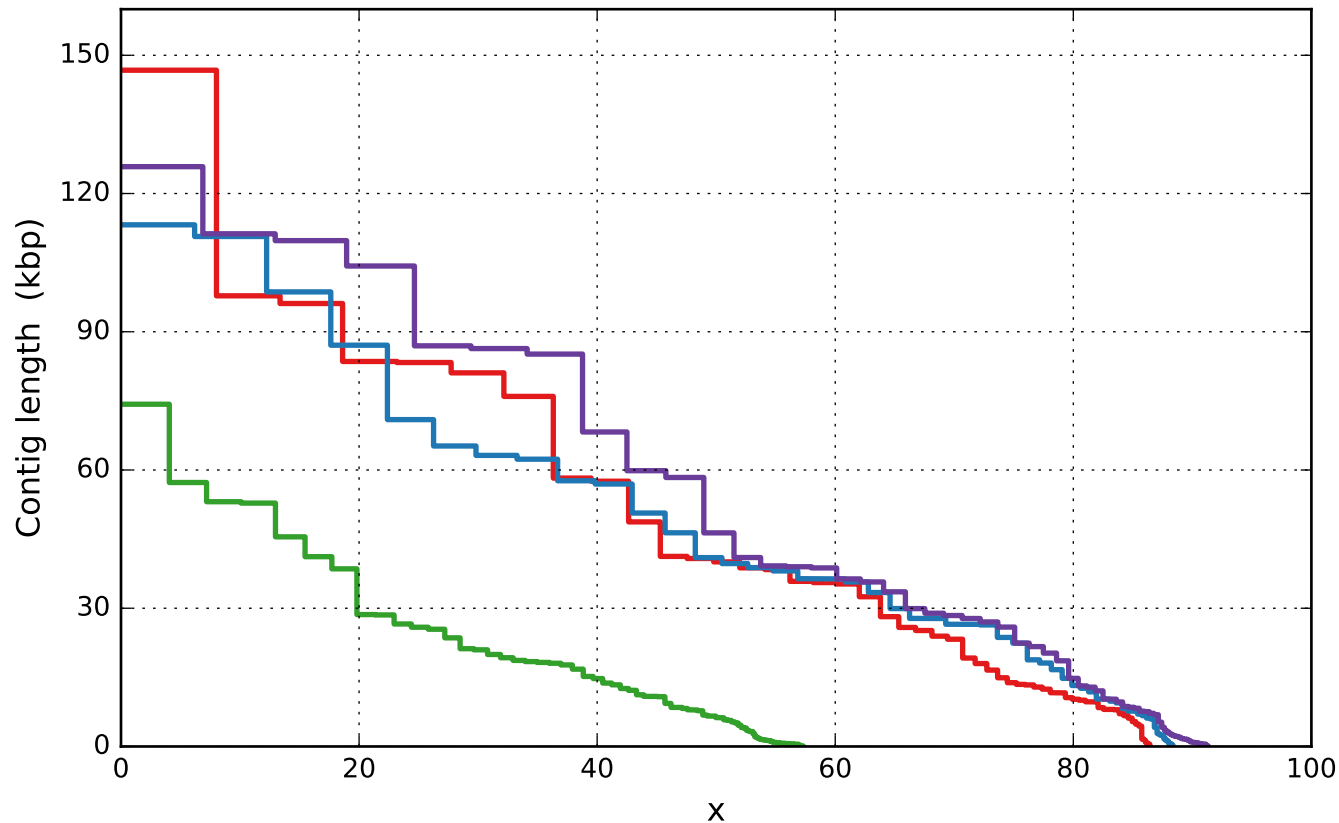
M05964_contigs

M10540_contigs

M16180_contigs

M07572_contigs

NGAx



— M05964_contigs — M10540_contigs — M16180_contigs
— M07572_contigs

