Report

	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# contigs (>= 0 bp)	134	261	69	141	84	126	38	69	41	55	19	36	61	72	23	42
# contigs (>= 1000 bp)	36	72	29	49	36	51	21	33	35	43	15	26	36	42	17	28
# contigs (>= 5000 bp)	31	47	27	39	27	34	20	31	21	35	14	22	23	36	15	26
# contigs (>= 10000 bp)	25	36	24	30	23	29	18	25	18	23	12	17	19	25	13	20
# contigs (>= 25000 bp)	19	26	16	22	18	20	13	21	16	17	10	15	15	18	11	18
# contigs (>= 50000 bp)	9	13	9	12	9	13	9	13	10	12	7	13	8	11	7	14
Total length (>= 0 bp)	1856487	2018561	1846668	1875236	1861765	2033998	1843463	1877718	1943458	2047751	1839699	1890630	1868767	2042415	1834414	1893788
Total length (>= 1000 bp)	1843001	1993863	1841807	1860135	1852825	2015592	1840271	1870234	1941913	2044301	1838715	1887625	1863738	2032406	1832278	1889956
Total length (>= 5000 bp)	1828185	1920860	1837035	1838044	1832670	1957892	1836531	1865087	1912787	2021558	1836960	1877331	1836604	2013233	1826810	1884609
Total length (>= 10000 bp)	1778633	1849422	1816581	1771774	1800812	1923302	1825488	1825390	1890847	1931796	1826417	1843900	1805426	1934655	1816267	1845458
Total length (>= 25000 bp)	1686546	1676512	1703942	1624648	1727524	1769021	1765750	1755503	1863980	1826189	1801233	1812508	1751712	1808181	1794781	1810534
Total length (>= 50000 bp)	1298668	1254806	1445343	1313950	1393482	1533445	1618312	1496920	1632852	1659461	1701763	1755696	1485927	1564002	1649111	1681577
# contigs	41	74	30	56	38	59	22	37	35	43	16	27	37	46	19	30
Largest contig	473423	217183	334836	369249	343779	312213	400731	369262	550439	312376	409689	401071	550431	312355	400825	401071
Total length	1846118	1995099	1842389	1864193	1854153	2022140	1840807	1872401	1941913	2044301	1839251	1888140	1864279	2035777	1833634	1891040
Reference length	1887192	1887192	1887192	1887192	1887192	1887192	1887192	1887192	1887192	1887192	1887192	1887192	1887192	1887192	1887192	1887192
GC (%)	37.95	38.36	38.10	38.08	37.95	38.40	38.10	38.09	38.00	38.44	38.07	38.18	38.00	38.44	38.04	38.18
Reference GC (%)	38.01	38.01	38.01	38.01	38.01	38.01	38.01	38.01	38.01	38.01	38.01	38.01	38.01	38.01	38.01	38.01
N50	97979	80448	157960	82364	144973	103159	285281	100164	183050	141208	333934	138055	182978	141152	311520	125281
NG50	97979	80448	157960	82364	122974	103159	285281	93358	183050	141208	333934	138055	182978	141152	311520	125281
N75	44883	33152	63553	33896	60895	52032	83976	52751	75809	77394	191716	96606	79438	53598	189976	73822
NG75	44231	35070	52654	33896	49193	67108	83976	52751	81560	81370	191716	96606	79438	81353	189976	73822
L50	5	9	4	7	4	6	3	5	3	5	3	5	3	5	3	5
LG50	5	9	4	7	5	6	3	6	3	5	3	5	3	5	3	5
L75	11	20	8	15	9	13	6	12	8	10	5	9	7	11	5	10
LG75	12	18	9	15	10	11	6	12	7	9	5	9	7	9	5	10
# misassemblies	35	32	68	26	44	39	77	37	53	41	75	38	47	41	71	39
# misassembled contigs	16	18	17	16	19	17	15	20	17	15	12	14	17	16	11	18
Misassembled contigs length	1492273	1275865	1341777	1361745	1634046	1599122	1421522	1633746	1789890	1769765	1417058	1751188	1696104	1741761	1353317	1753269
# local misassemblies	73	51	35	58	71	58	38	61	73	58	40	66	72	58	39	64
# unaligned contigs	5 + 3 part	22 + 17 part	2 + 9 part	7 + 14 part	5 + 1 part	20 + 8 part	1 + 5 part	4 + 5 part	3 + 2 part	10 + 10 part	1 + 2 part	3 + 2 part	5 + 2 part	12 + 10 part	2 + 5 part	3 + 2 part
Unaligned length	75768	215491	315859	94954	22912	175865	269093	60317	15414	167664	245616	24798	23955	185069	292166	24704
Genome fraction (%)	84.673	88.767	55.955	86.437	84.552	89.189	56.447	86.695	85.001	89.557	55.253	87.364	84.768	89.499	55.181	87.544
Duplication ratio	1.108	1.062	1.446	1.085	1.148	1.097	1.475	1.108	1.201	1.110	1.528	1.130	1.150	1.096	1.480	1.130
# N's per 100 kbp	8.29	8.32	0.05	1.45	1.19	0.49	0.00	0.80	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.05
# mismatches per 100 kbp	2520.68	2437.12	3657.57	2405.17	2531.49	2421.39	3681.53	2403.89	2523.79	2379.96	3662.04	2397.36	2495.54	2395.70	3663.66	2397.81
# indels per 100 kbp	88.93	90.79	117.14	85.21	89.49	92.56	117.15	85.81	90.77	92.18	115.56	86.25	89.64	92.18	115.81	86.01
Largest alignment	167217	128175	66377	124715	167250	138984	66377	124728	178056	138984	66377	135526	178056	138984	66377	135526
NA50	34675	34020	6729	42195	35066	37329	8250	49023	35066	45438	7674	49023	35542	43504	7204	49023
NGA50	34675	37296	6591	42195	34998	37656	7204	48450	35066	48622	6374	49023	35066	48622	6374	49023
NA75	14848	11694	-	16250	13879	14791	-	16584	15247	14749	-	17458	15307	14791	-	17458
NGA75	13739	15948	-	15940	13582	20552	-	16316	16509	26496	-	17458	15247	22639	-	17458
LA50	16	16	51	14	15	15	47	12	15	13	48	12	14	14	47	12
LGA50	16	14	54	14	16	14	50	13	15	12	52	12	15	12	51	12
LA75	36	38	-	32	35	35	-	30	36	33	-	27	33	33	-	28
LGA75	38	33	-	34	37	29	-	31	33	26	-	27	34	27	-	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

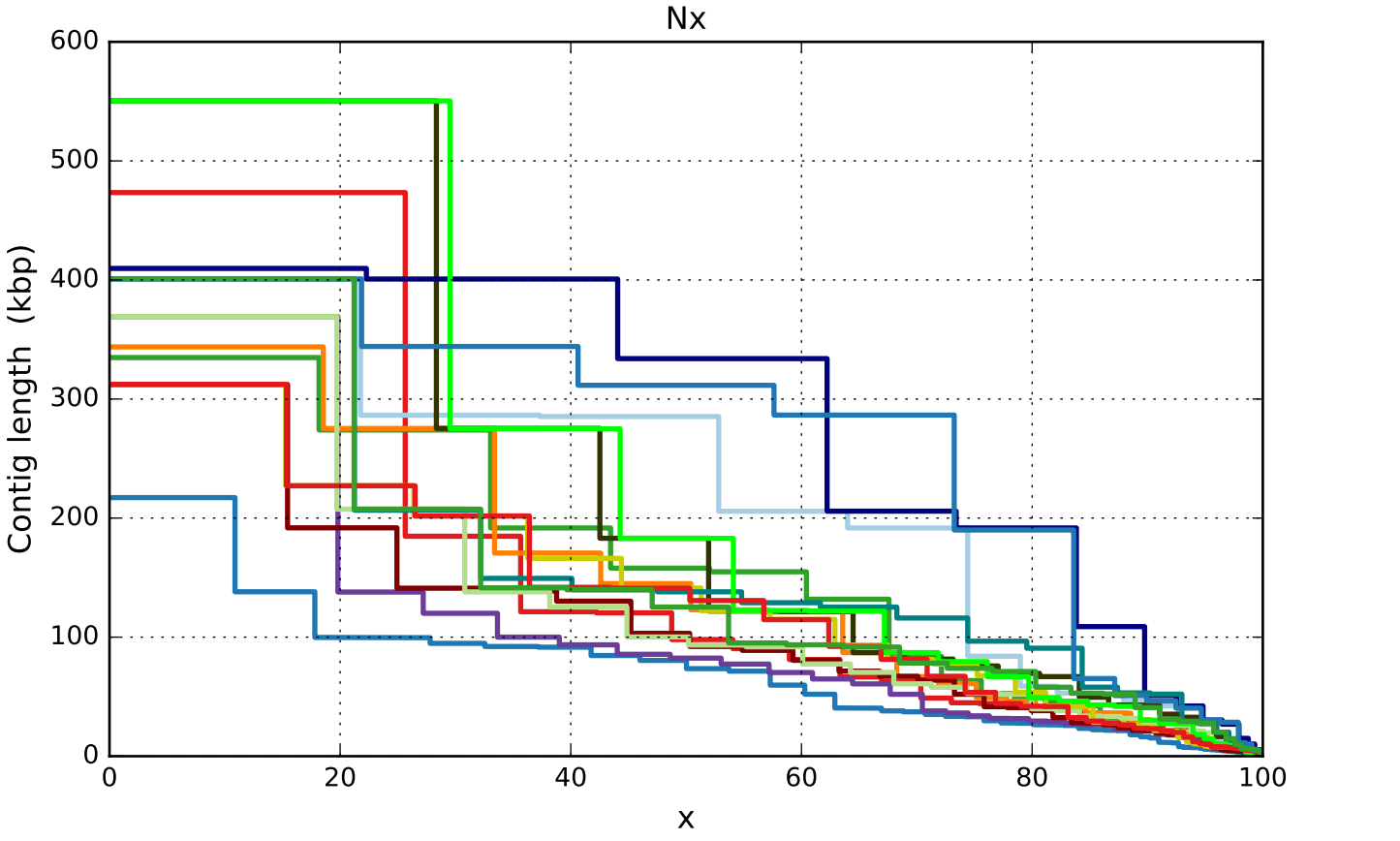
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# misassemblies	35	32	68	26	44	39	77	37	53	41	75	38	47	41	71	39
# relocations	34	32	68	26	44	39	77	37	52	41	73	38	46	41	70	39
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	1	0	0	0	0	0	0	0	1	0	2	0	1	0	1	0
# misassembled contigs	16	18	17	16	19	17	15	20	17	15	12	14	17	16	11	18
Misassembled contigs length	1492273	1275865	1341777	1361745	1634046	1599122	1421522	1633746	1789890	1769765	1417058	1751188	1696104	1741761	1353317	1753269
# local misassemblies	73	51	35	58	71	58	38	61	73	58	40	66	72	58	39	64
# mismatches	40279	40827	38623	39234	40394	40756	39218	39330	40485	40224	38185	39526	39922	40464	38152	39615
# indels	1421	1521	1237	1390	1428	1558	1248	1404	1456	1558	1205	1422	1434	1557	1206	1421
# short indels	1306	1397	1150	1274	1315	1426	1160	1278	1334	1420	1118	1296	1315	1424	1118	1294
# long indels	115	124	87	116	113	132	88	126	122	138	87	126	119	133	88	127
Indels length	3487	3917	2622	3409	3483	4311	2709	3606	3685	4431	2633	3625	3610	4320	2639	3637

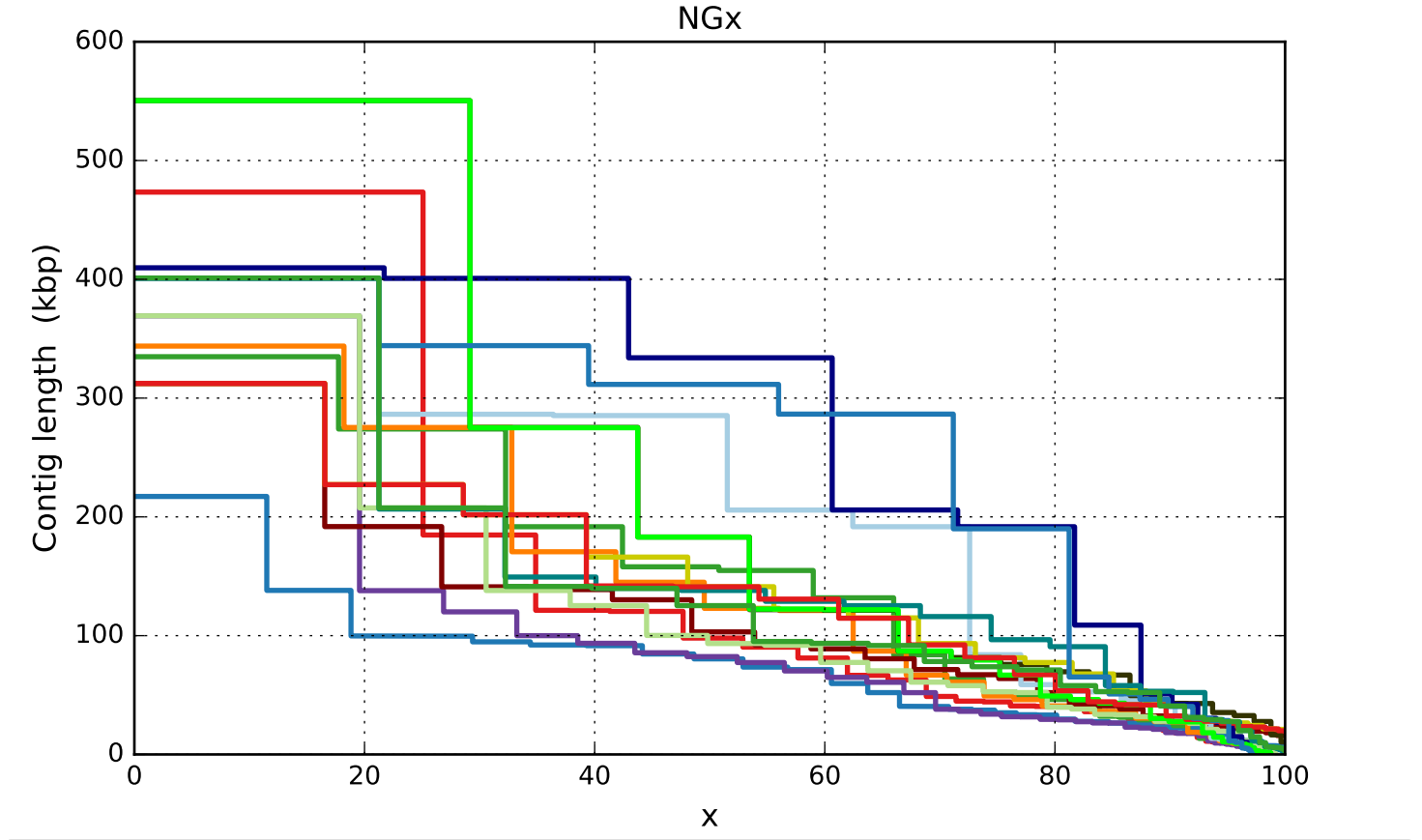
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

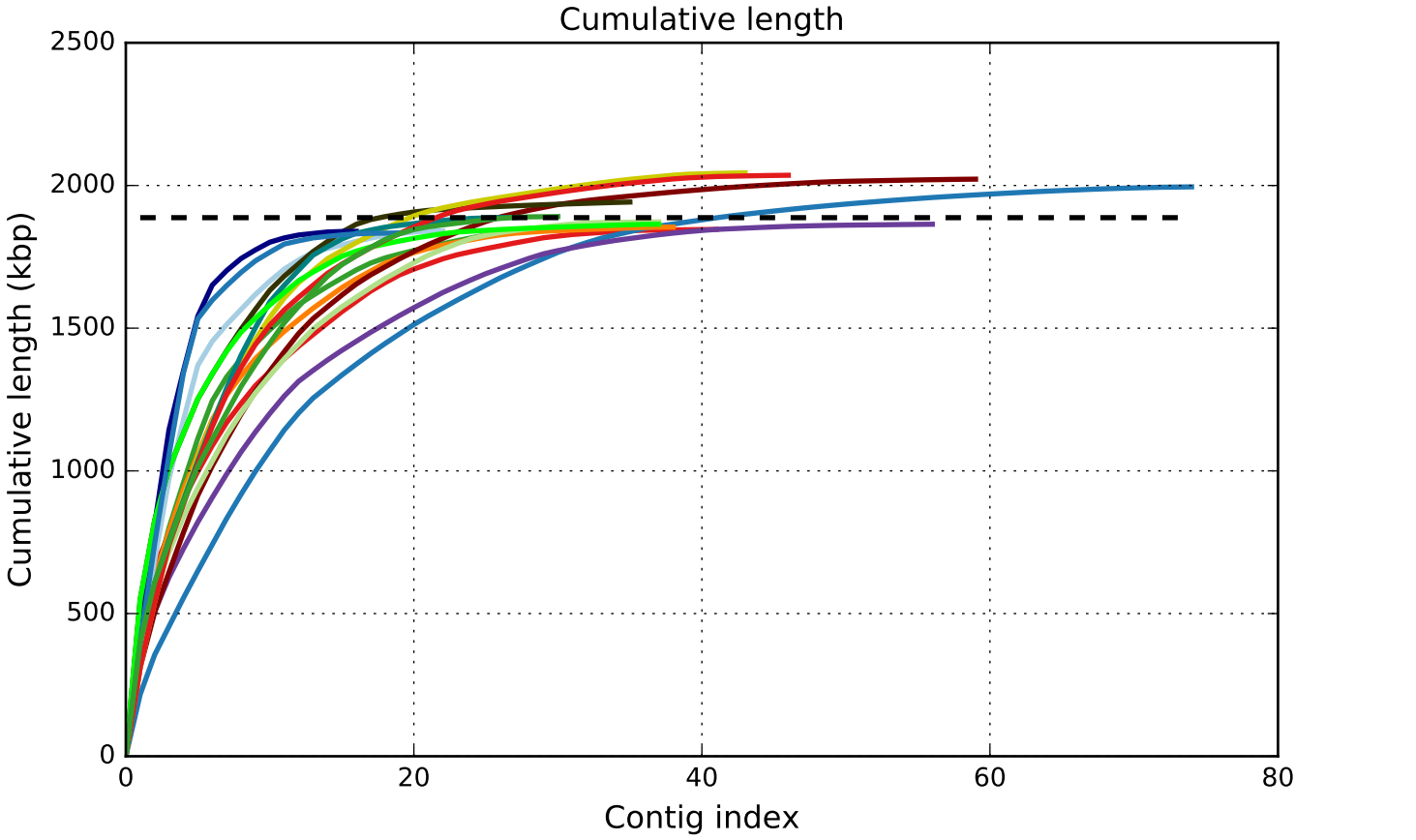
Unaligned report

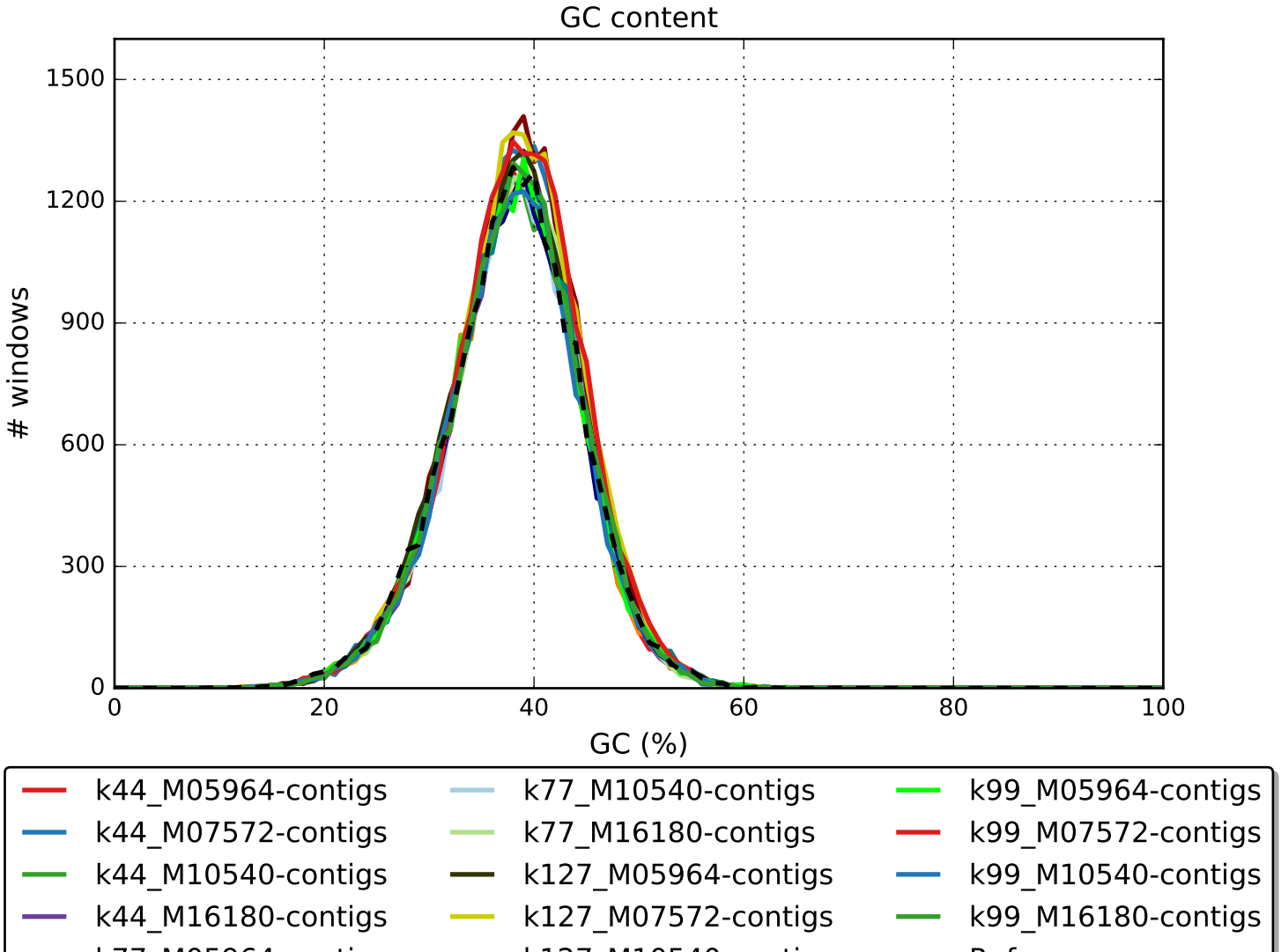
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	5	22	2	7	5	20	1	4	3	10	1	3	5	12	2	3
Fully unaligned length	65316	157632	1614	25712	22076	110544	536	19081	12276	85920	536	17772	22862	81288	1356	17707
# partially unaligned contigs	3	17	9	14	1	8	5	5	2	10	2	2	2	10	5	2
# with misassembly	2	1	5	2	0	2	2	0	0	3	1	0	0	5	3	0
# both parts are significant	2	7	9	10	1	4	5	5	1	8	2	2	1	6	5	2
Partially unaligned length	10452	57859	314245	69242	836	65321	268557	41236	3138	81744	245080	7026	1093	103781	290810	6997
# N's	153	166	1	27	22	10	0	15	0	0	0	0	0	0	1	1

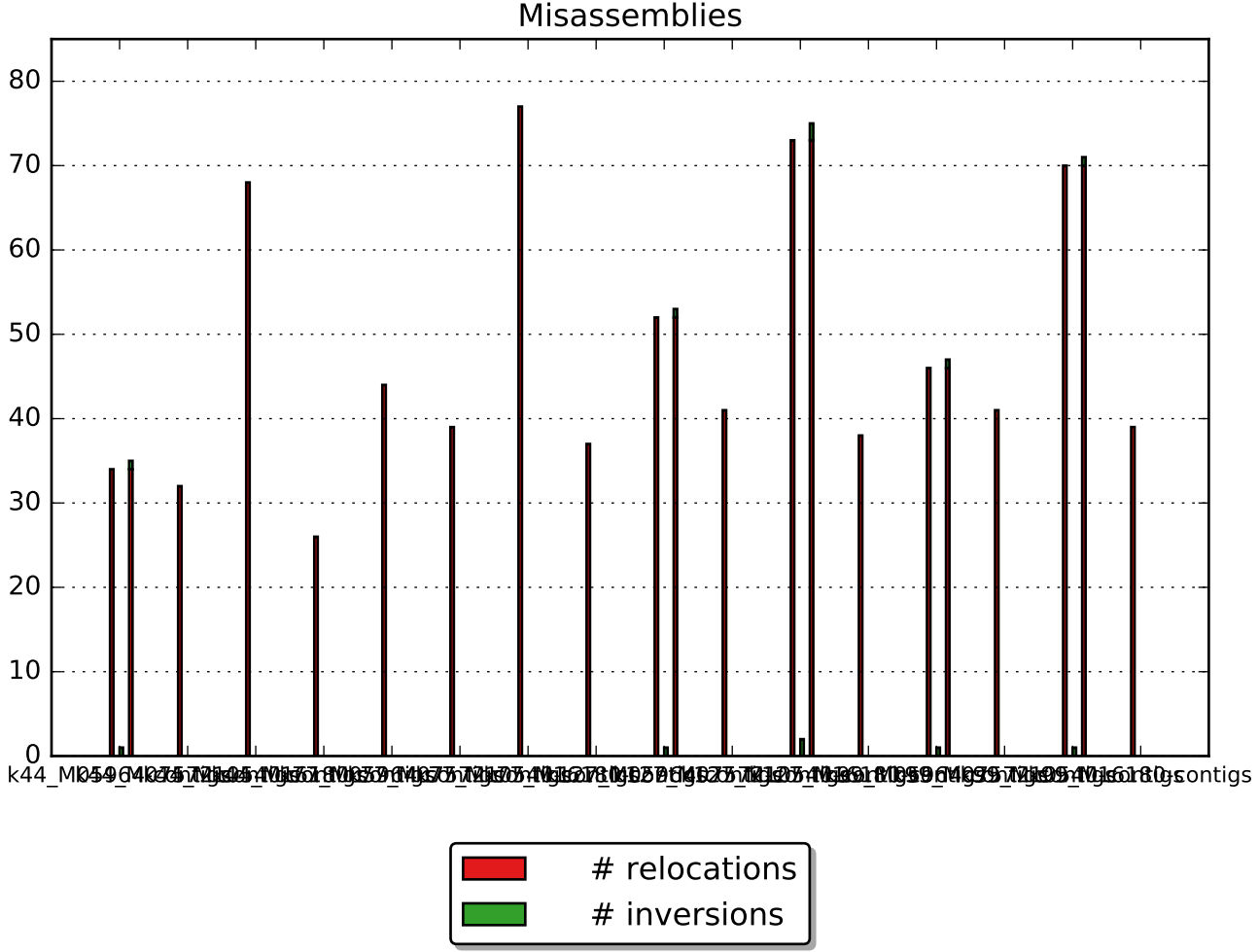
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

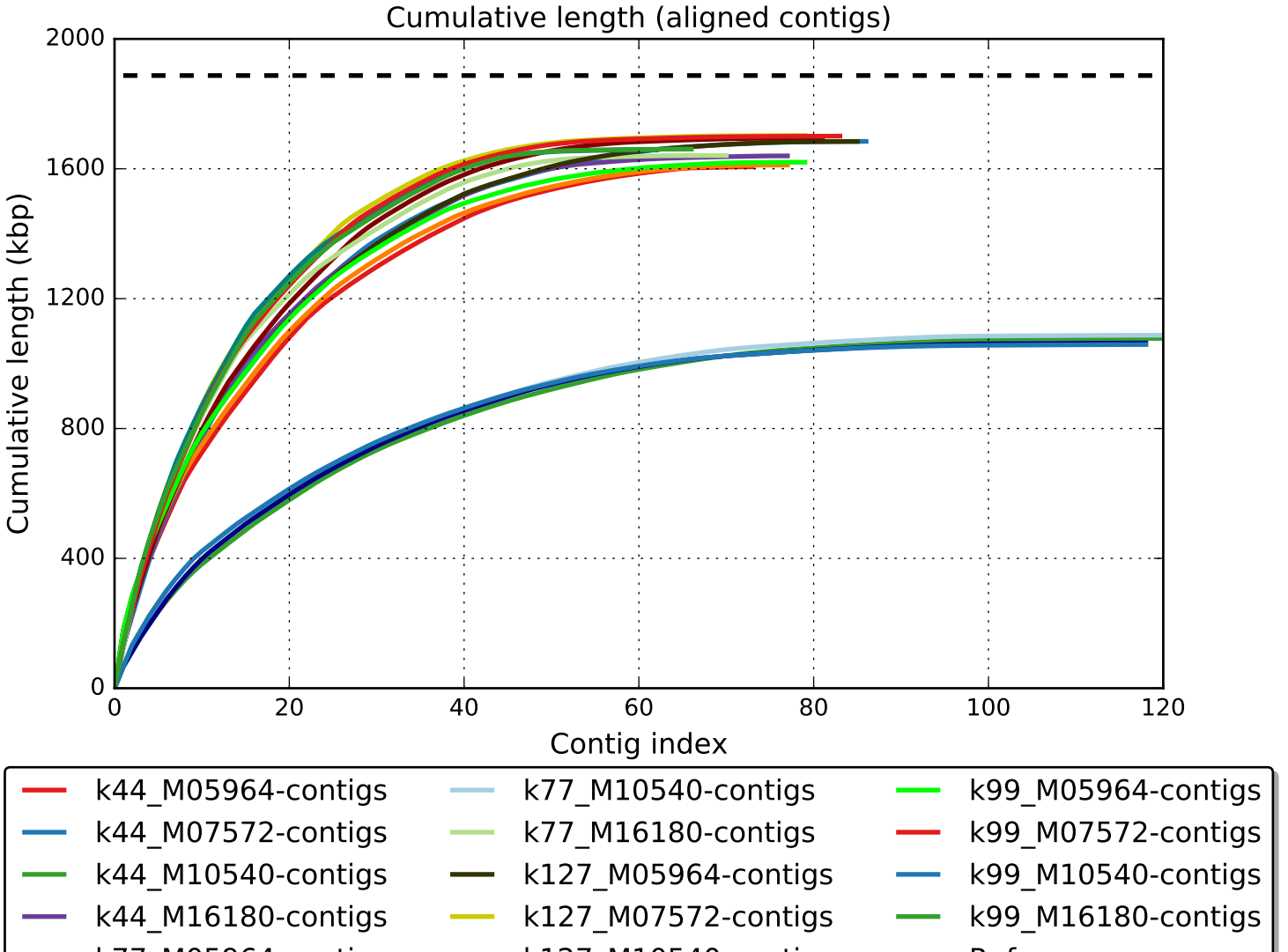

Nx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs

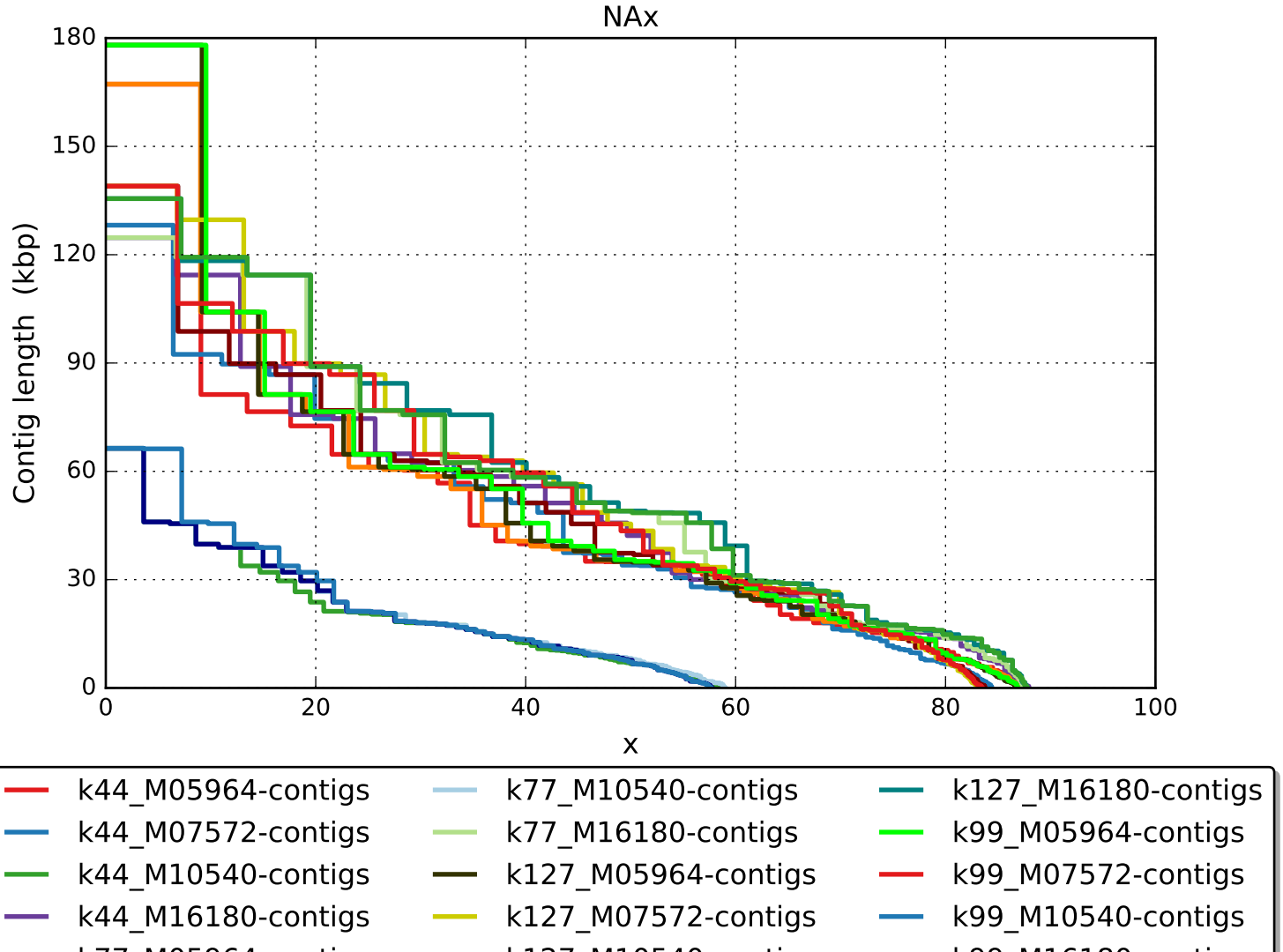

NGx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs

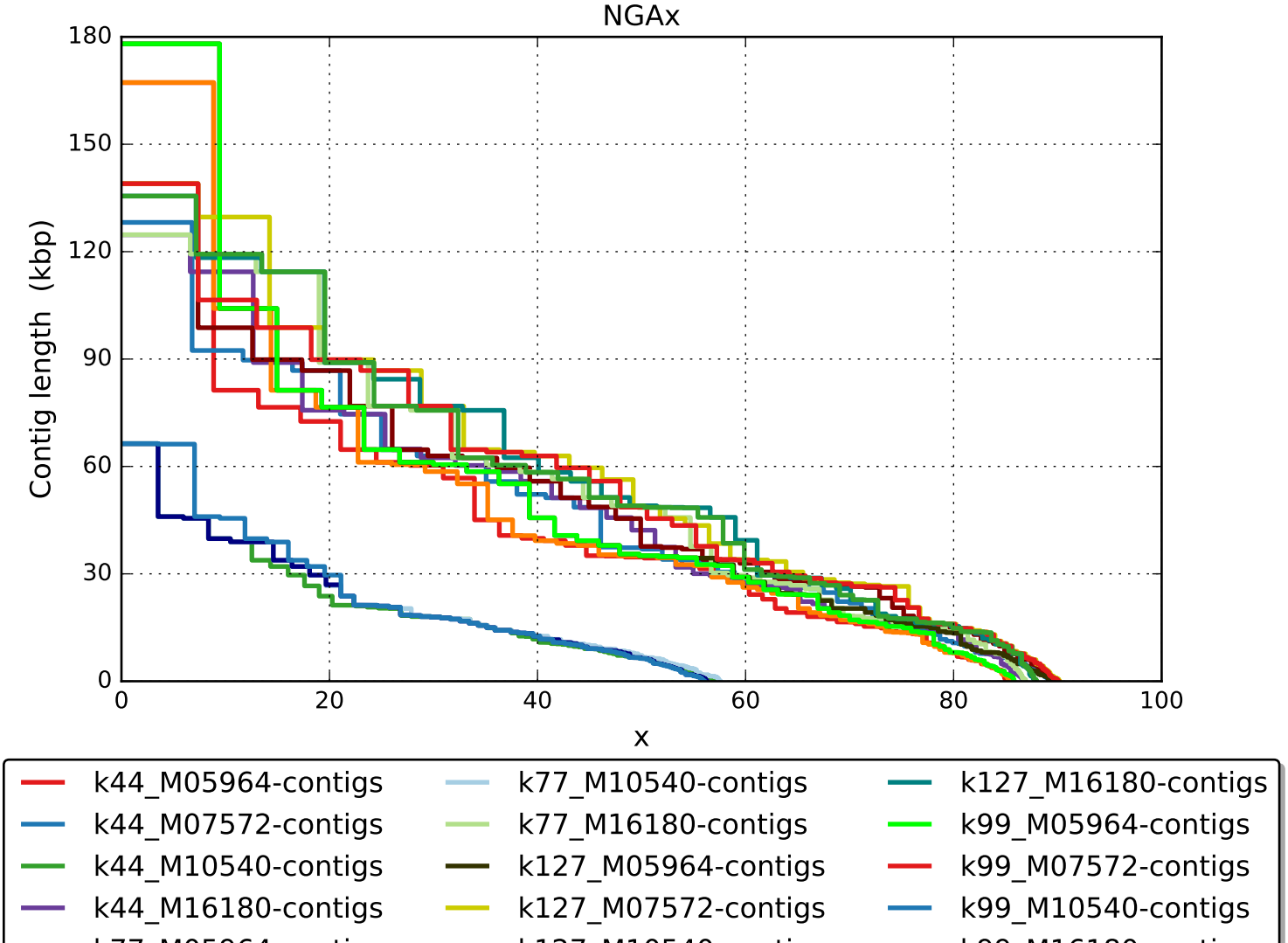

Cumulative length
Cumulative length (kbp)
Contig index
2500
2000
1500
1000
500
0
0
20
40
60
80
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs
k99_M16180-contigs

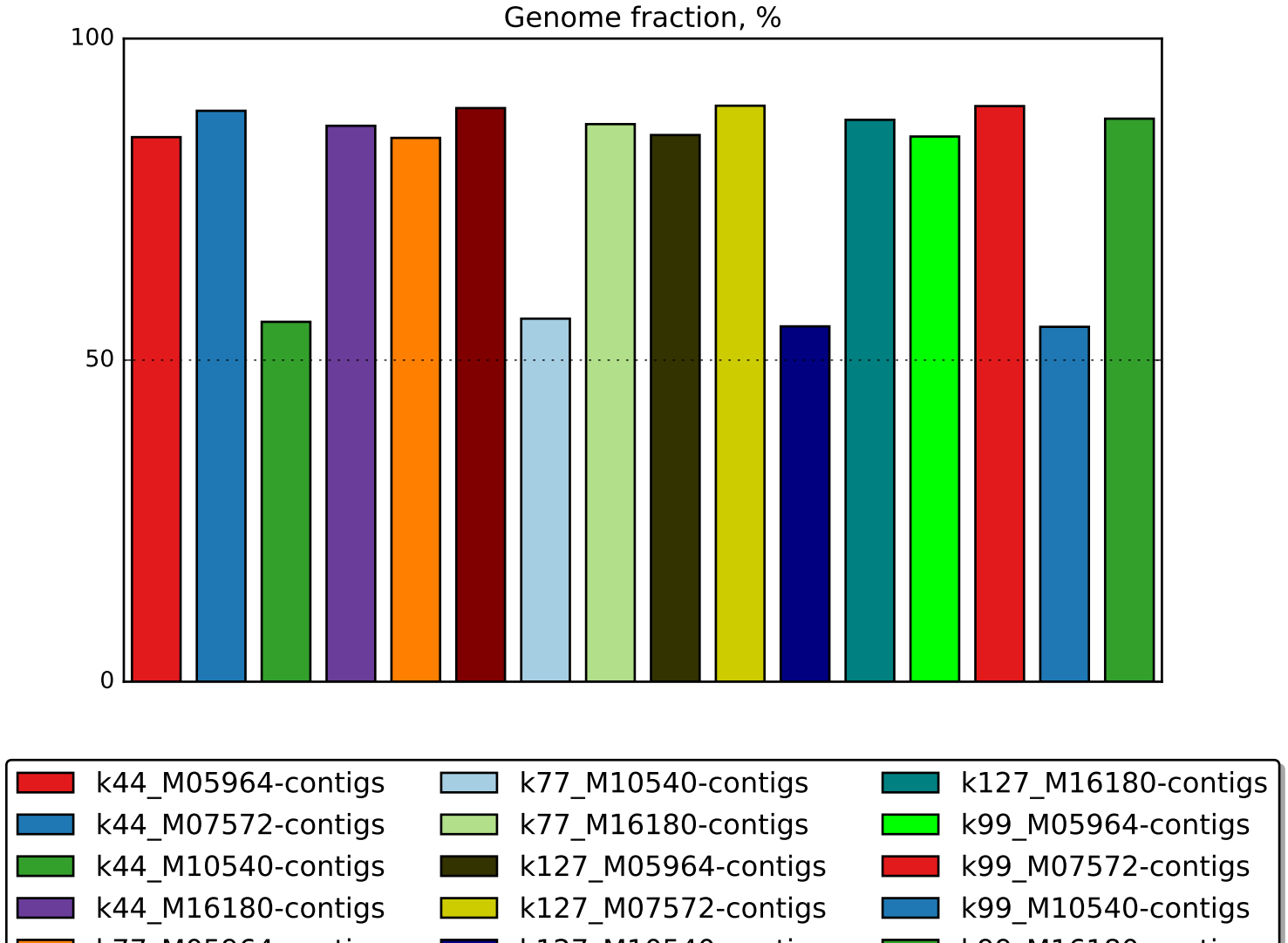

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs
k99_M16180-contigs


Misassemblies
80
70
60
50
40
30
20
10
0
k44_M
contigs
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
Contig index
0
400
800
1200
1600
2000
0
20
40
60
80
100
120
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs
k99_M16180-contigs


NAx
Contig length (kbp)
x
0
30
60
90
120
150
180
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs


NGAx
Contig length (kbp)
x
0
30
60
90
120
150
180
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs


Genome fraction, %
100
50
0
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs