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	1846503	1846503	1846503	1846503	1846503	1846503	1846503	1846503	1846503	1846503	1846503	1846503	1846503	1846503	1846503	1846503
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 (%)	38.16	38.16	38.16	38.16	38.16	38.16	38.16	38.16	38.16	38.16	38.16	38.16	38.16	38.16	38.16	38.16
N50	97979	80448	157960	82364	144973	103159	285281	100164	183050	141208	333934	138055	182978	141152	311520	125281
NG50	97979	80448	157960	82364	144973	103159	285281	100164	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	44883	37295	63553	36285	60895	67108	83976	57916	81560	81370	191716	116061	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	4	6	3	5	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	11	17	8	14	9	11	6	11	7	9	5	8	7	9	5	10
# misassemblies	15	25	63	21	16	34	68	25	18	32	89	30	15	34	86	29
# misassembled contigs	8	17	13	11	9	16	11	14	9	13	11	12	7	14	10	14
Misassembled contigs length	961558	1156595	1310520	1154003	1243858	1510870	1393238	1368538	1382066	1583790	1816204	1617128	1281759	1547851	1748400	1579530
# local misassemblies	27	58	36	53	25	59	41	57	27	60	48	60	26	61	45	61
# unaligned contigs	3 + 3 part	19 + 14 part	3 + 7 part	13 + 12 part	2 + 4 part	18 + 10 part	2 + 5 part	7 + 4 part	2 + 3 part	11 + 7 part	2 + 0 part	3 + 3 part	3 + 3 part	10 + 8 part	3 + 2 part	3 + 4 part
Unaligned length	56473	197885	232287	124986	12525	180057	215447	92188	11749	159344	10749	52263	14380	177096	39749	57372
Genome fraction (%)	92.843	90.387	61.026	87.611	93.238	90.600	61.238	87.534	94.080	90.677	60.841	88.380	93.992	90.584	60.766	88.190
Duplication ratio	1.044	1.077	1.429	1.075	1.070	1.101	1.437	1.101	1.111	1.126	1.628	1.125	1.066	1.111	1.599	1.126
# 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	1450.18	2452.55	3606.96	2478.45	1442.87	2444.50	3607.39	2453.74	1450.39	2441.65	3613.85	2450.28	1454.28	2438.84	3615.37	2456.49
# indels per 100 kbp	42.23	60.58	86.79	68.06	43.10	61.99	87.11	68.92	44.96	63.43	86.97	71.69	44.31	61.82	86.98	71.79
Largest alignment	183610	118530	54754	118493	257760	131858	54754	151369	258107	133385	54754	150384	257830	133385	82226	151369
NA50	73979	34975	9098	40791	79514	35008	9573	44375	80740	38650	10088	47380	80712	37745	9721	46341
NGA50	73979	36425	9098	40791	79514	37667	9098	44375	80740	41844	9573	54354	80712	41844	9573	46341
NA75	34239	18041	-	18436	34272	18236	-	19057	37257	19189	-	23734	40740	19189	-	22478
NGA75	34239	21568	-	19035	34272	23073	-	19207	41793	26463	-	27665	40740	25362	-	26745
LA50	8	17	47	14	7	16	44	12	7	14	42	12	7	14	42	12
LGA50	8	15	47	14	7	14	45	12	7	12	43	11	7	12	43	12
LA75	18	37	-	31	16	36	-	28	16	32	-	26	15	32	-	27
LGA75	18	31	-	30	16	29	-	27	14	25	-	24	15	26	-	25

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

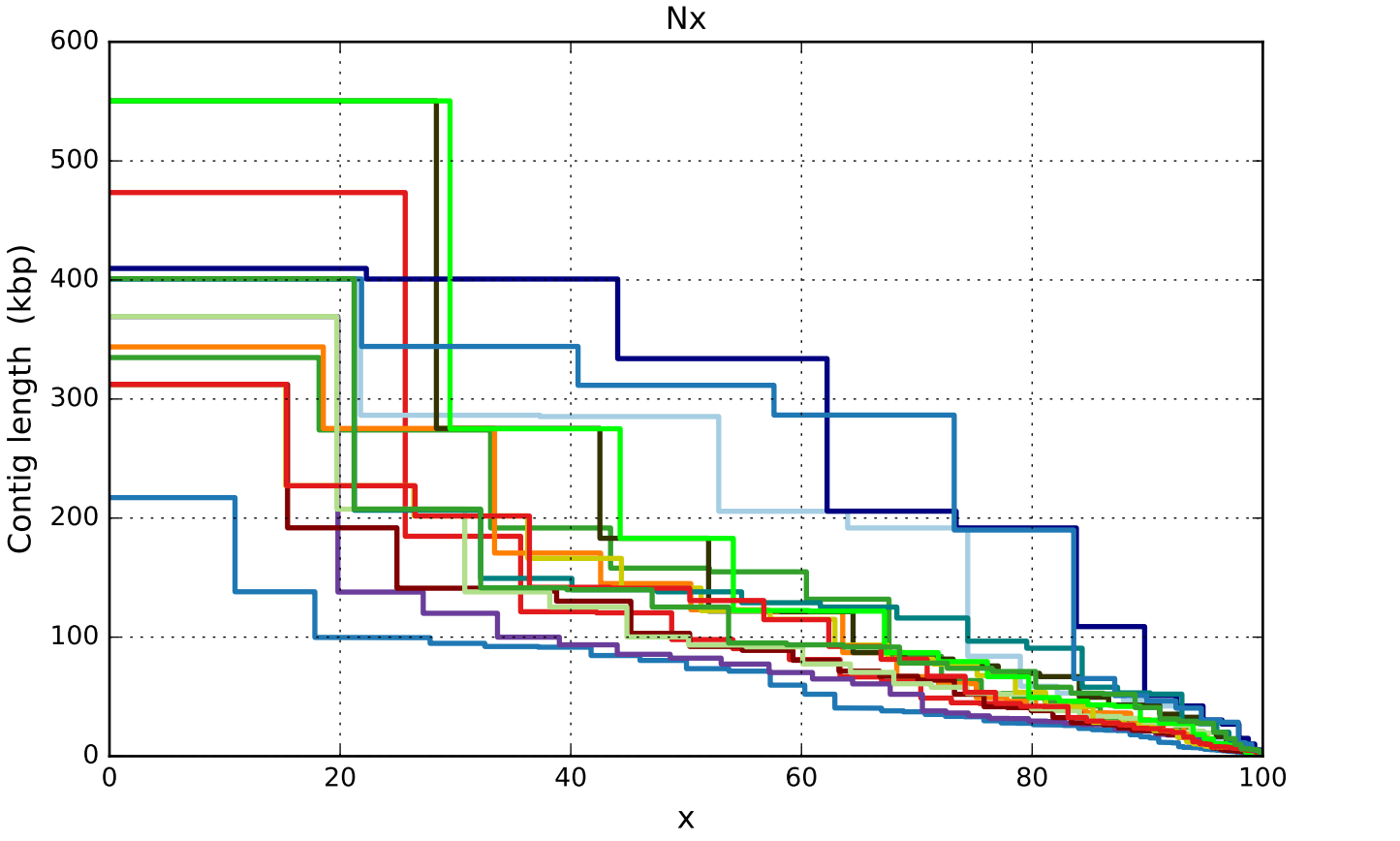
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# misassemblies	15	25	63	21	16	34	68	25	18	32	89	30	15	34	86	29
# relocations	15	24	63	20	16	33	68	24	18	31	87	29	15	33	84	29
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	0	1	0	1	0	1	0	1	0	1	2	1	0	1	2	0
# misassembled contigs	8	17	13	11	9	16	11	14	9	13	11	12	7	14	10	14
Misassembled contigs length	961558	1156595	1310520	1154003	1243858	1510870	1393238	1368538	1382066	1583790	1816204	1617128	1281759	1547851	1748400	1579530
# local misassemblies	27	58	36	53	25	59	41	57	27	60	48	60	26	61	45	61
# mismatches	24861	40933	40645	40095	24841	40895	40791	39660	25196	40882	40599	39987	25240	40793	40566	40002
# indels	724	1011	978	1101	742	1037	985	1114	781	1062	977	1170	769	1034	976	1169
# short indels	644	894	895	975	655	916	903	982	691	940	895	1029	681	914	891	1027
# long indels	80	117	83	126	87	121	82	132	90	122	82	141	88	120	85	142
Indels length	2275	3356	2508	3390	2596	3529	2501	3449	2711	3563	2468	3717	2759	3469	2570	3737

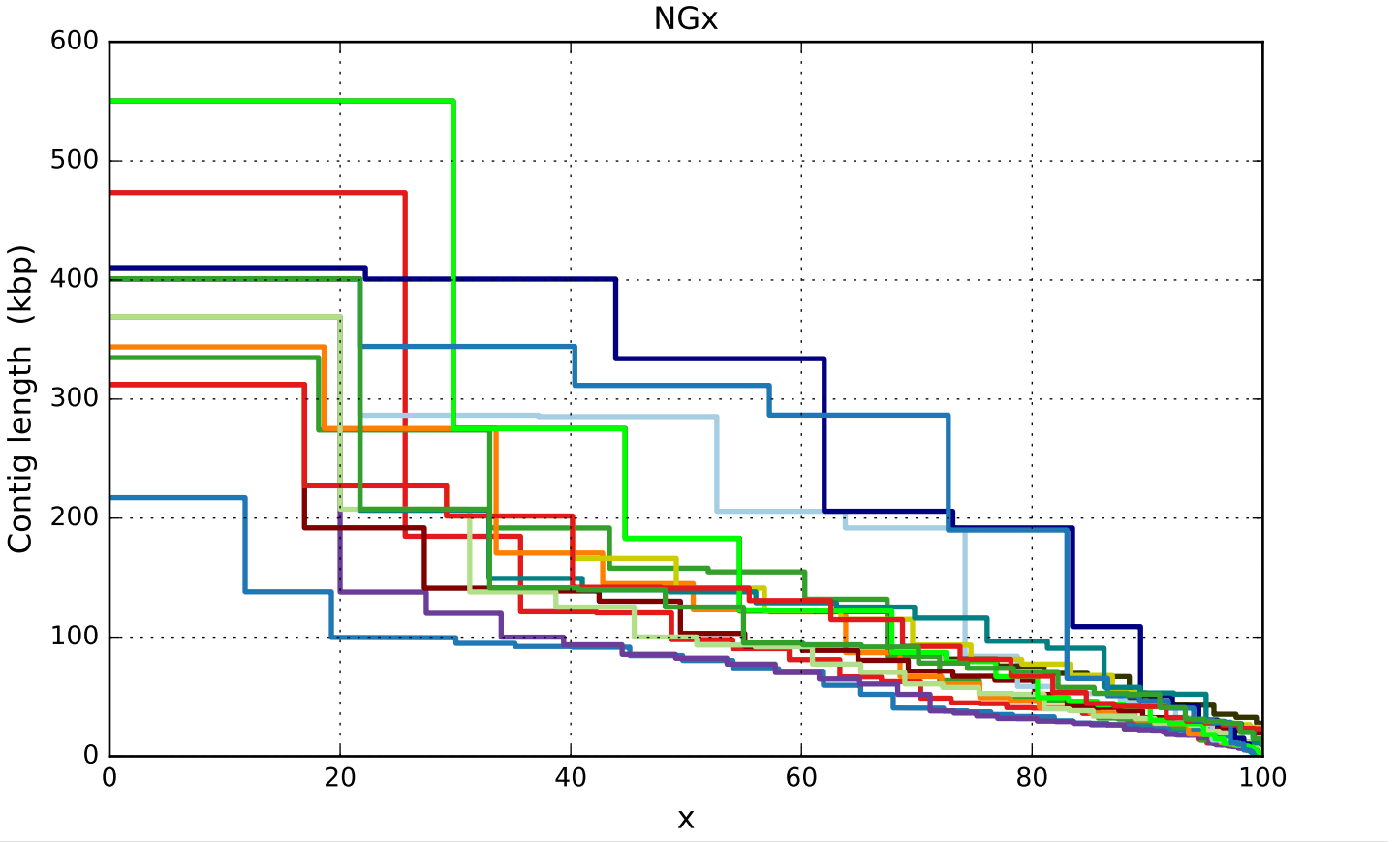
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

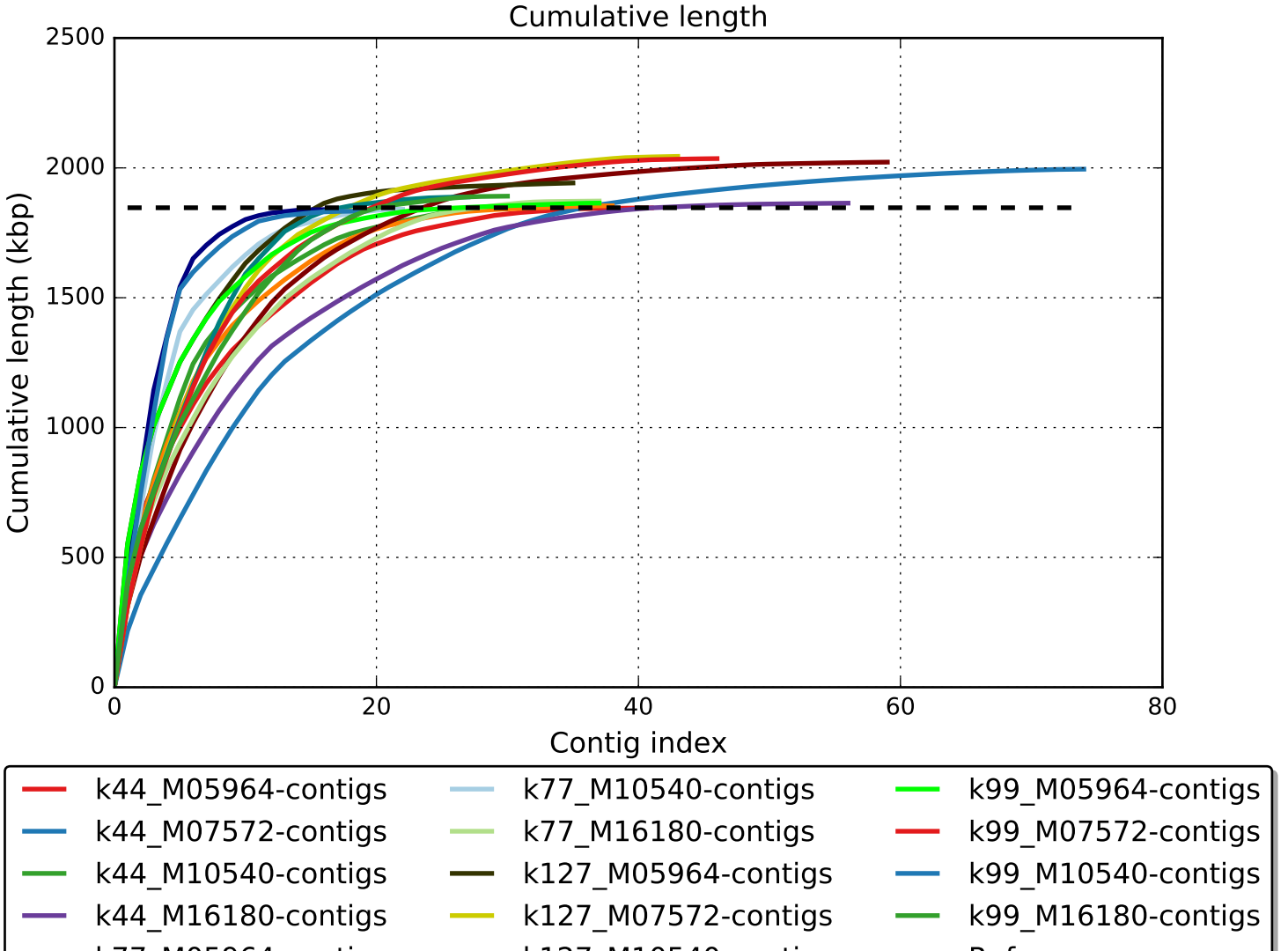
Unaligned report

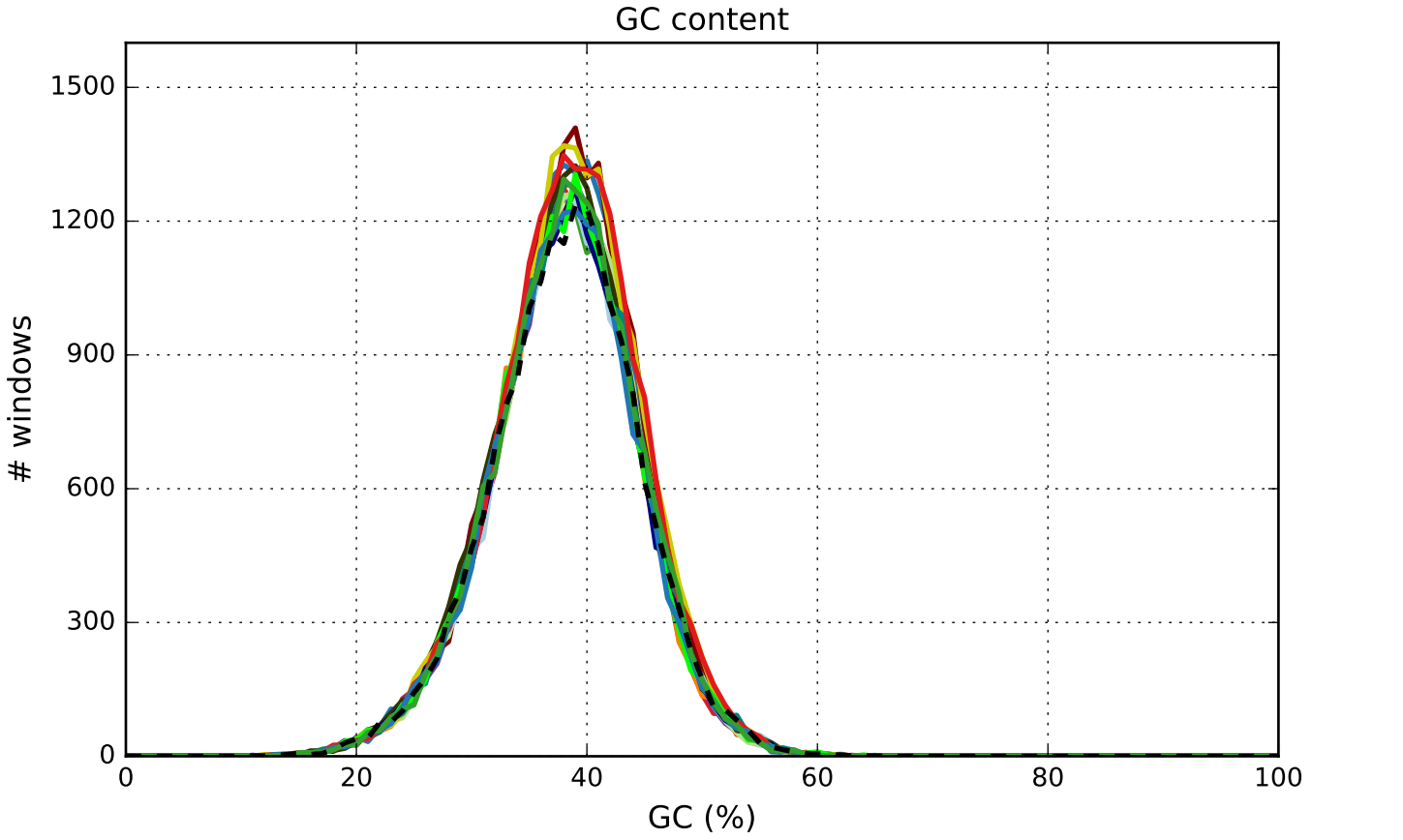
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	3	19	3	13	2	18	2	7	2	11	2	3	3	10	3	3
Fully unaligned length	46945	128513	11615	48512	3416	77715	10649	26978	4647	92289	10749	18430	6028	78103	11513	18318
# partially unaligned contigs	3	14	7	12	4	10	5	4	3	7	0	3	3	8	2	4
# with misassembly	0	1	5	0	0	3	4	1	0	2	0	1	0	2	1	1
# both parts are significant	2	13	7	9	4	7	5	3	3	6	0	3	3	6	2	3
Partially unaligned length	9528	69372	220672	76474	9109	102342	204798	65210	7102	67055	0	33833	8352	98993	28236	39054
# N's	153	166	1	27	22	10	0	15	0	0	0	0	0	0	1	1

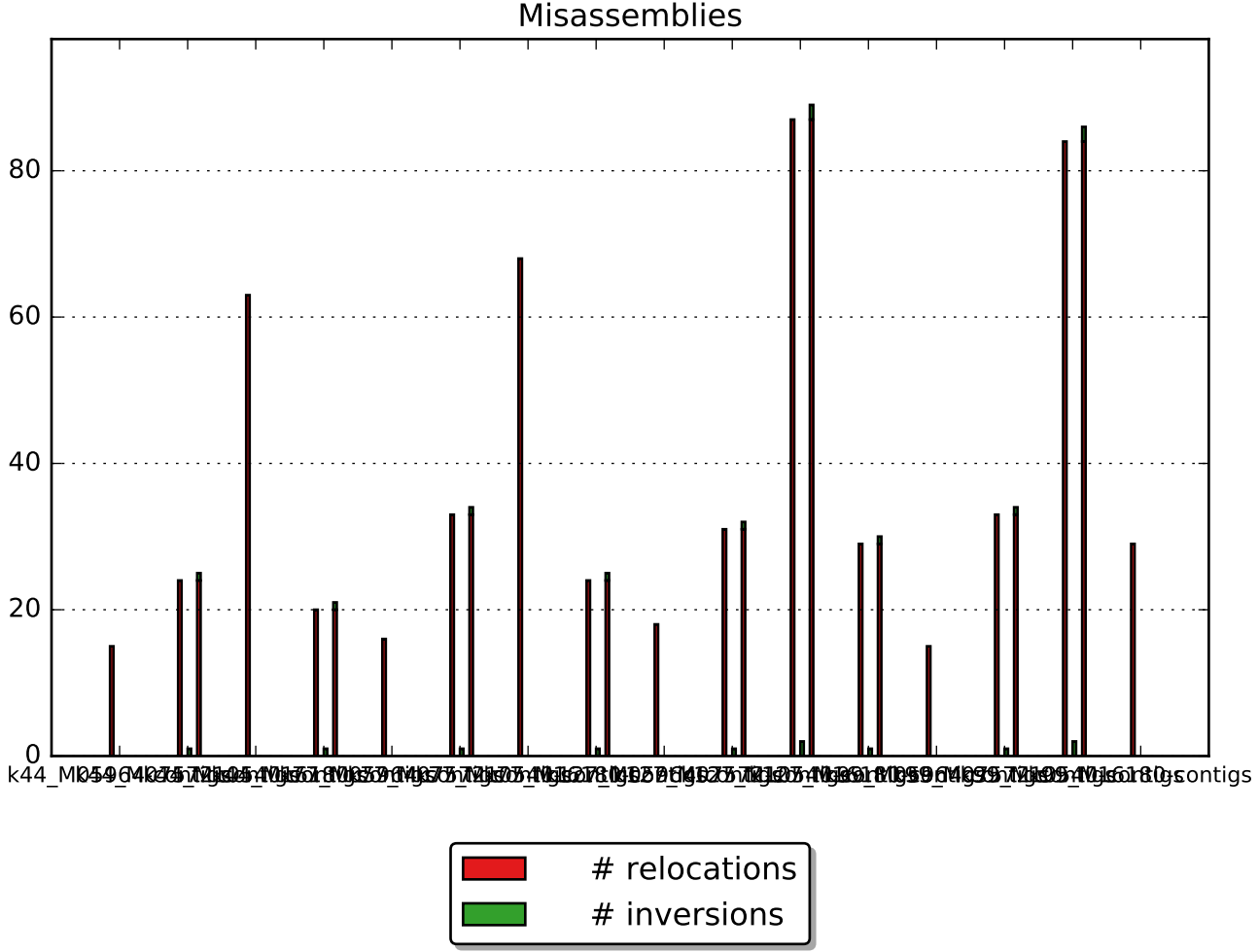
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

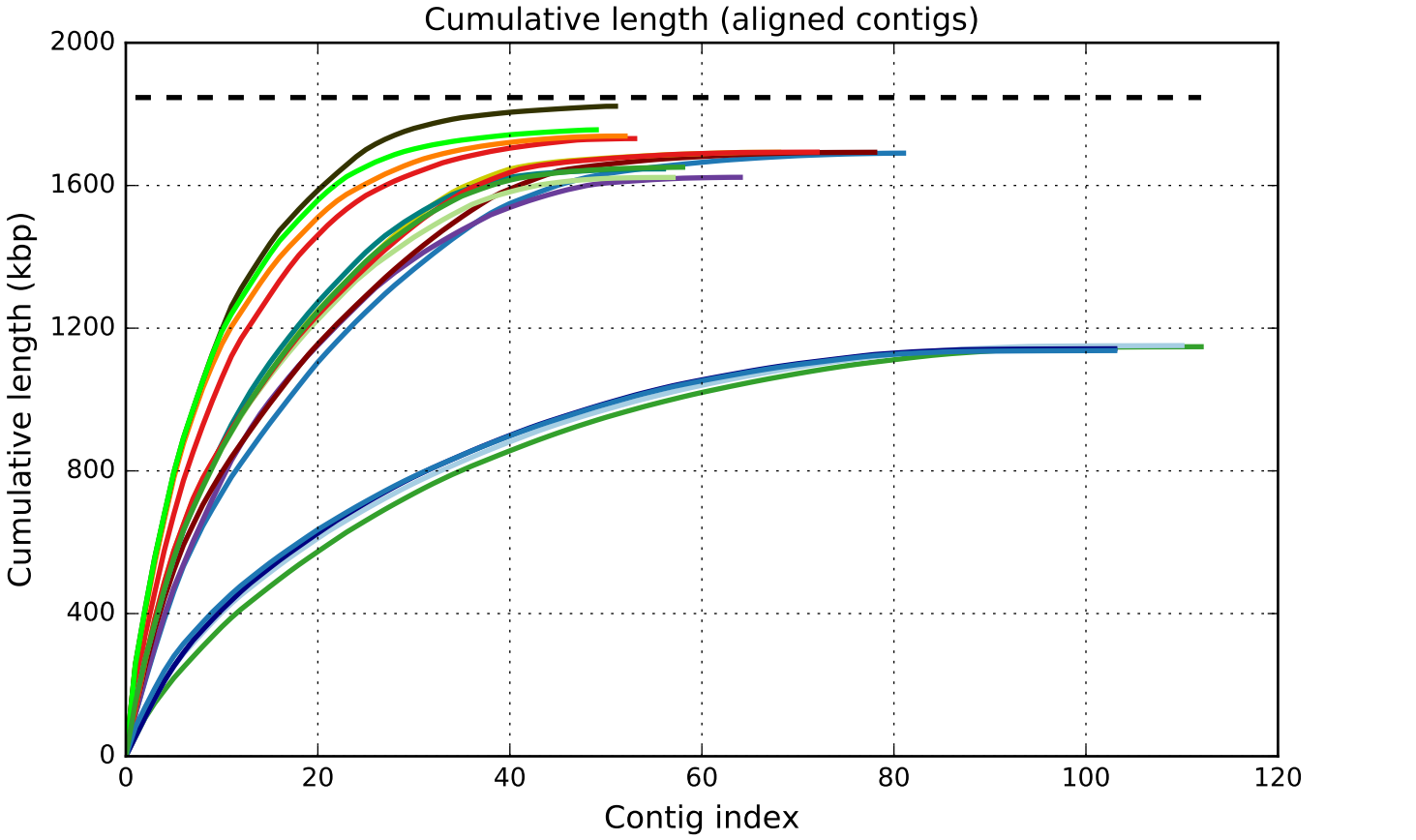

Nx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs

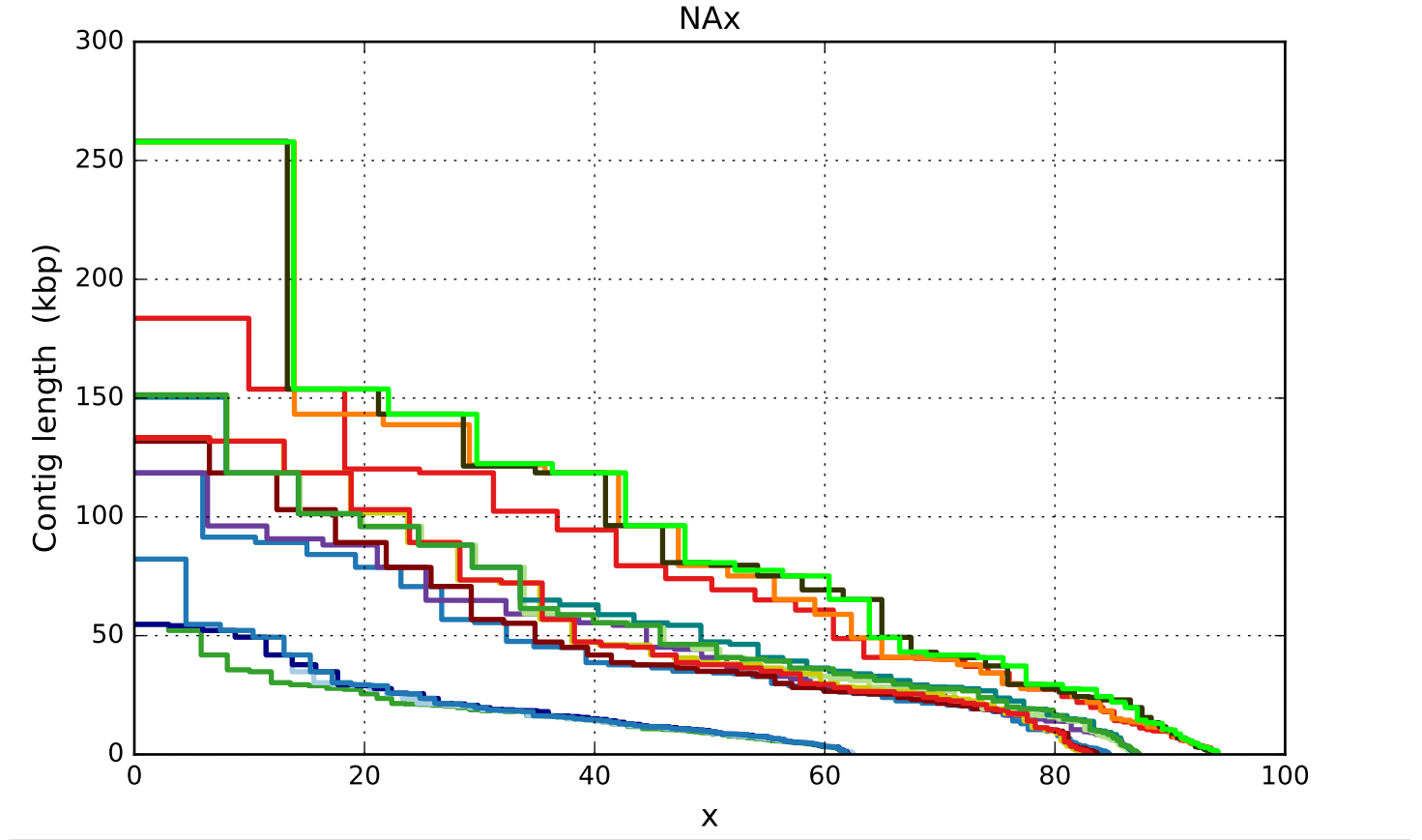

NGx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k127_M16180-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs

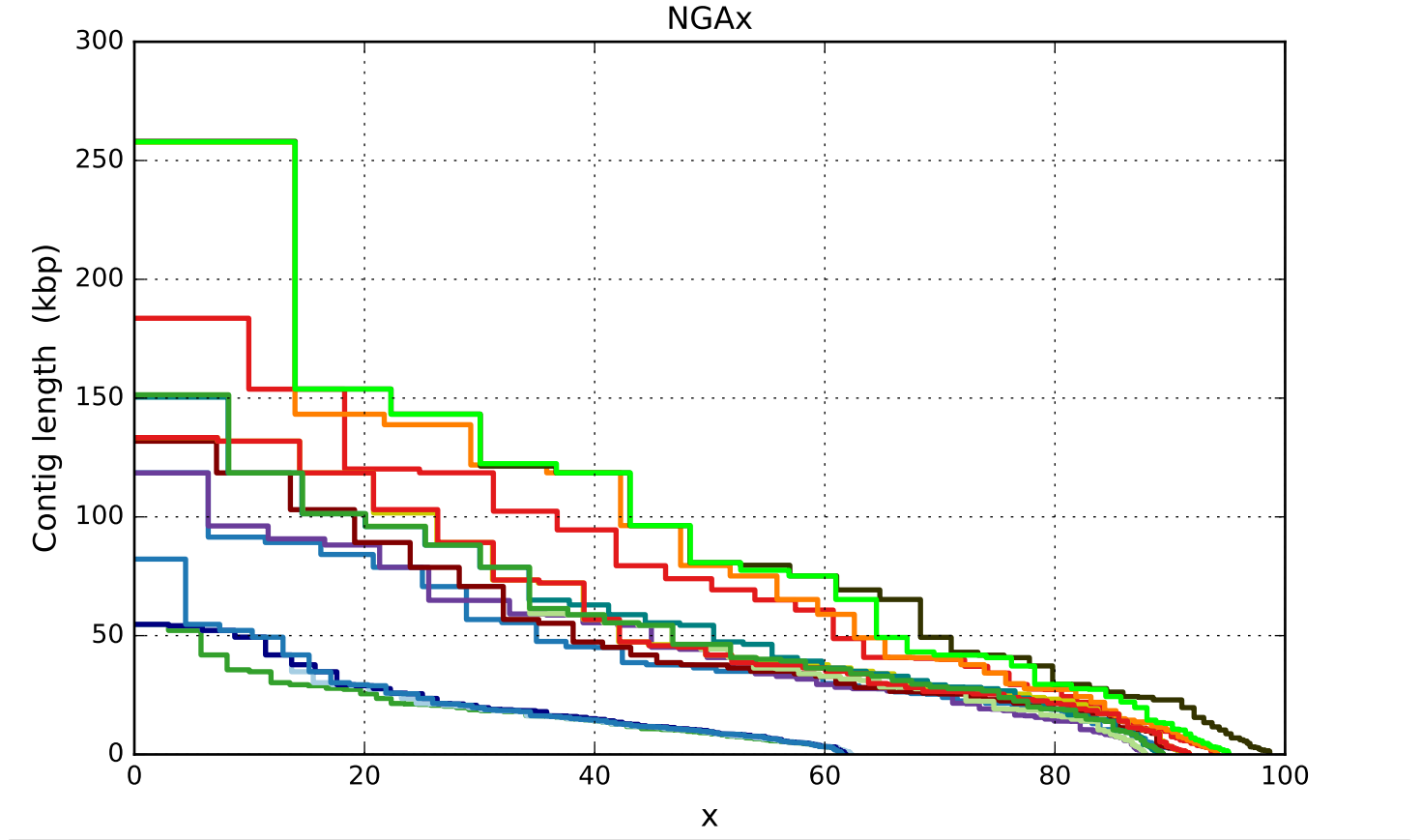

Cumulative length
Cumulative length (kbp)
Contig index
0
500
1000
1500
2000
2500
0
20
40
60
80
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs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

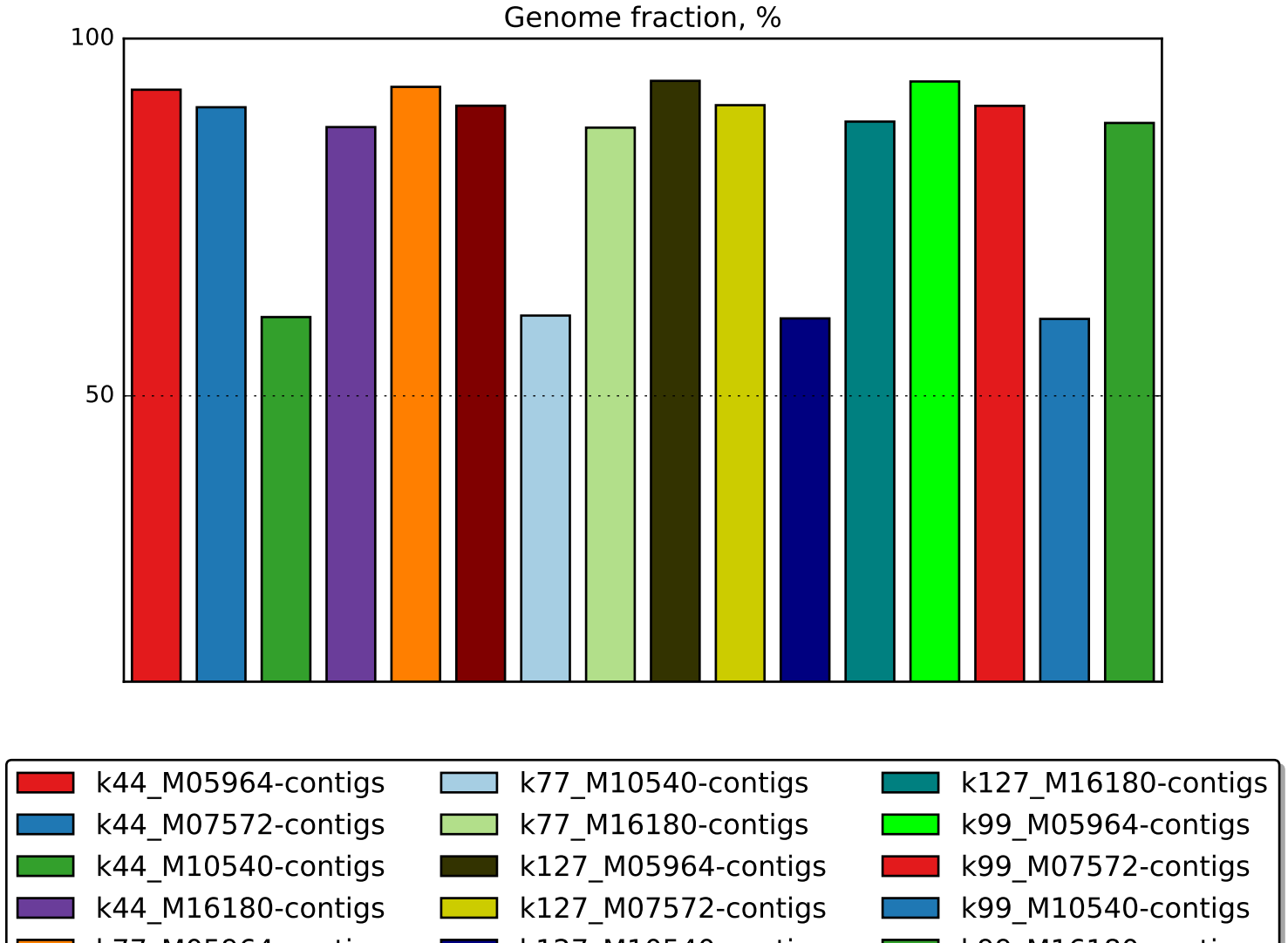

GC content
windows
GC (%)
0
300
600
900
1200
1500
0
20
40
60
80
100
k44_M05964-contigs
k44_M07572-contigs
k44_M10540-contigs
k44_M16180-contigs
k77_M10540-contigs
k77_M16180-contigs
k127_M05964-contigs
k127_M07572-contigs
k99_M05964-contigs
k99_M07572-contigs
k99_M10540-contigs
k99_M16180-contigs


Misassemblies
80
60
40
20
0
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
50
100
150
200
250
300
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)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
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
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