

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	1846259	1846259	1846259	1846259	1846259	1846259	1846259	1846259	1846259	1846259	1846259	1846259	1846259	1846259	1846259	1846259
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	27	13	48	8	38	15	57	15	43	16	51	13	39	14	55	14
# misassembled contigs	10	12	13	4	14	12	13	9	16	11	10	7	15	10	9	8
Misassembled contigs length	1201381	798302	1149337	649012	1420303	946392	1273682	1055177	1630554	1150083	1220192	1098674	1503531	1086367	1219662	1100330
# local misassemblies	55	35	28	28	61	43	32	30	67	44	32	32	60	43	34	32
# unaligned contigs	4 + 4 part	21 + 14 part	3 + 10 part	4 + 8 part	2 + 3 part	13 + 12 part	2 + 5 part	5 + 2 part	2 + 1 part	8 + 10 part	2 + 2 part	2 + 2 part	2 + 3 part	9 + 11 part	3 + 4 part	2 + 2 part
Unaligned length	67212	188850	421755	62103	13921	168961	364665	53995	7655	155640	331180	19567	14699	172094	361917	19502
Genome fraction (%)	85.168	91.821	57.748	94.155	85.786	92.994	58.268	94.656	86.730	93.350	57.816	95.393	86.785	93.188	57.895	95.102
Duplication ratio	1.131	1.065	1.332	1.037	1.162	1.079	1.372	1.041	1.208	1.096	1.413	1.061	1.154	1.083	1.377	1.066
# 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	2538.69	1757.03	3571.75	1500.80	2545.17	1787.51	3577.81	1479.92	2552.94	1780.17	3592.36	1454.75	2555.60	1790.19	3511.22	1455.89
# indels per 100 kbp	64.93	51.32	91.26	39.46	66.99	54.46	91.56	39.83	68.38	53.61	93.31	39.86	68.71	53.65	89.63	39.75
Largest alignment	101207	138099	68317	204039	101952	190168	68317	204054	109376	221974	68317	235862	109376	221946	69003	235862
NA50	39556	52150	8526	57293	39589	63597	8671	70436	46339	109006	8632	116180	46311	90855	8671	92843
NGA50	39556	56786	8236	57293	39589	83739	8671	70436	47325	114001	8632	116180	46311	91176	8632	92843
NA75	18024	21960	-	27779	18403	25583	-	31760	19190	28434	-	51639	19190	28353	-	40836
NGA75	18024	27271	-	27779	18403	37081	-	32497	21339	44108	-	51639	21339	39078	-	46707
LA50	15	12	45	9	14	9	43	8	13	7	45	7	12	8	42	7
LGA50	15	11	46	9	14	8	43	8	12	6	45	7	12	7	43	7
LA75	30	28	-	22	30	21	-	18	29	17	-	13	27	18	-	15
LGA75	30	23	-	22	30	16	-	17	26	13	-	13	26	14	-	14

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	27	13	48	8	38	15	57	15	43	16	51	13	39	14	55	14
# relocations	26	13	48	8	38	15	57	15	42	16	49	13	38	14	53	14
# 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	2	0
# misassembled contigs	10	12	13	4	14	12	13	9	16	11	10	7	15	10	9	8
Misassembled contigs length	1201381	798302	1149337	649012	1420303	946392	1273682	1055177	1630554	1150083	1220192	1098674	1503531	1086367	1219662	1100330
# local misassemblies	55	35	28	28	61	43	32	30	67	44	32	32	60	43	34	32
# mismatches	39919	29786	38081	26089	40311	30690	38489	25863	40879	30681	38346	25621	40948	30800	37531	25563
# indels	1021	870	973	686	1061	935	985	696	1095	924	996	702	1101	923	958	698
# short indels	906	774	879	610	940	820	886	618	970	815	892	622	973	816	859	618
# long indels	115	96	94	76	121	115	99	78	125	109	104	80	128	107	99	80
Indels length	3061	2479	2458	1967	3231	3125	2521	2147	3376	2991	2634	2175	3364	2956	2507	2170

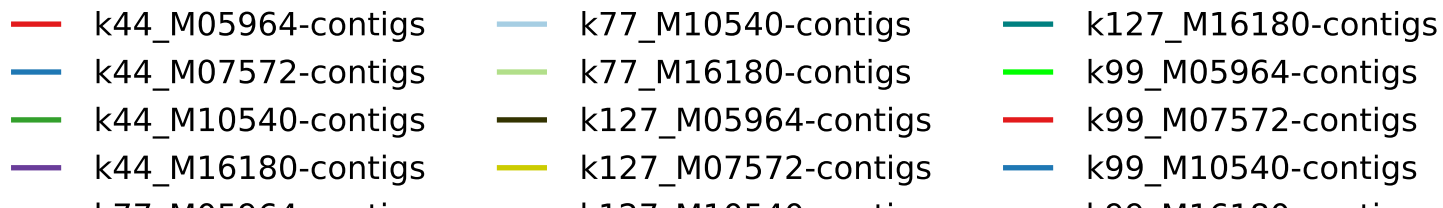
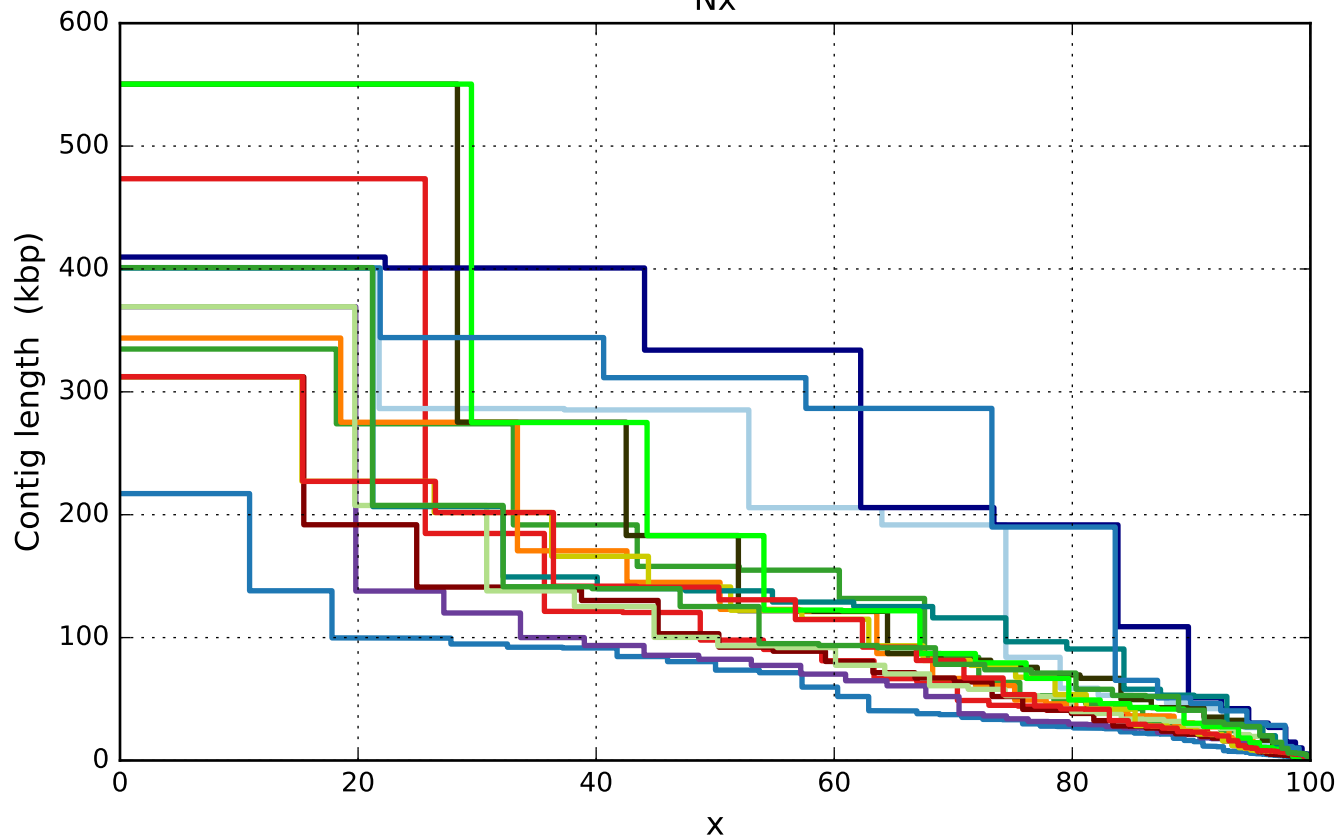
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

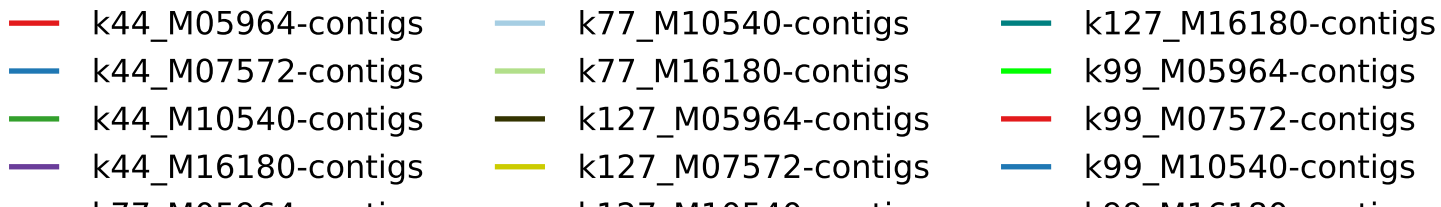
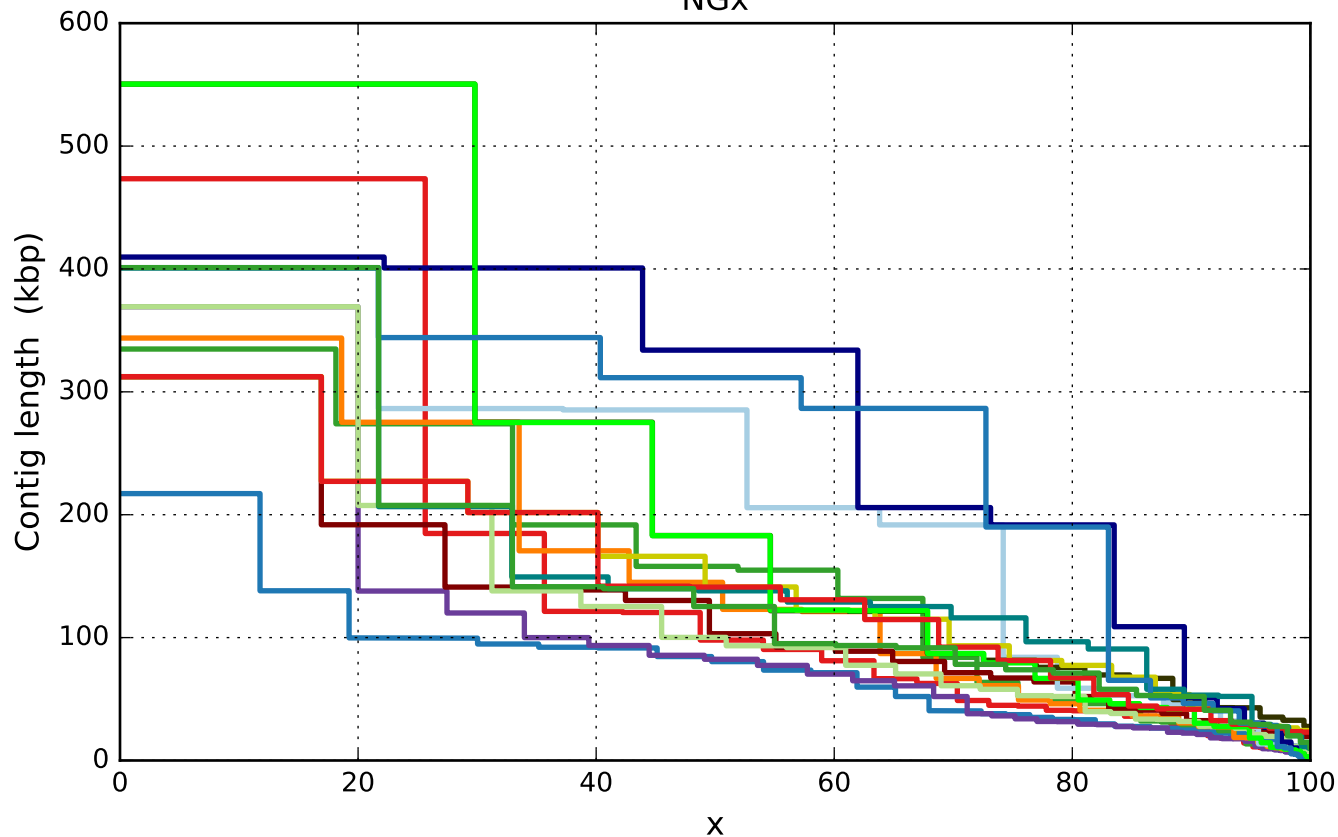
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	4	21	3	4	2	13	2	5	2	8	2	2	2	9	3	2
Fully unaligned length	47624	143454	11615	20741	3632	87495	10649	20746	4647	93173	10749	12653	4414	86673	11513	12597
# partially unaligned contigs	4	14	10	8	3	12	5	2	1	10	2	2	3	11	4	2
# with misassembly	2	0	6	0	1	2	4	0	0	3	2	0	1	6	3	0
# both parts are significant	4	6	9	5	2	5	4	2	1	8	2	2	2	9	3	2
Partially unaligned length	19588	45396	410140	41362	10289	81466	354016	33249	3008	62467	320431	6914	10285	85421	350404	6905
# N's	153	166	1	27	22	10	0	15	0	0	0	0	0	0	1	1

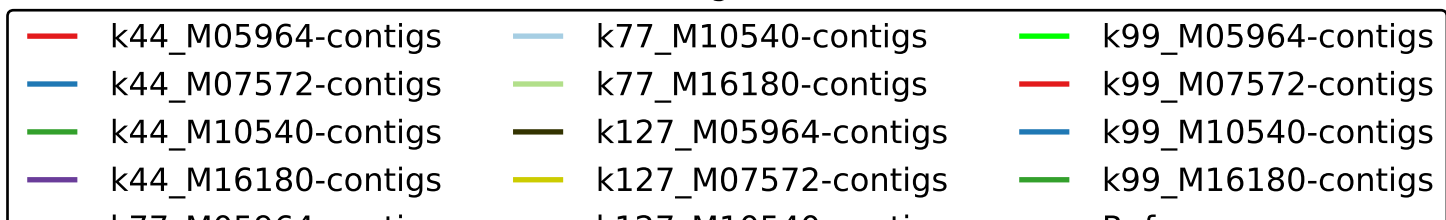
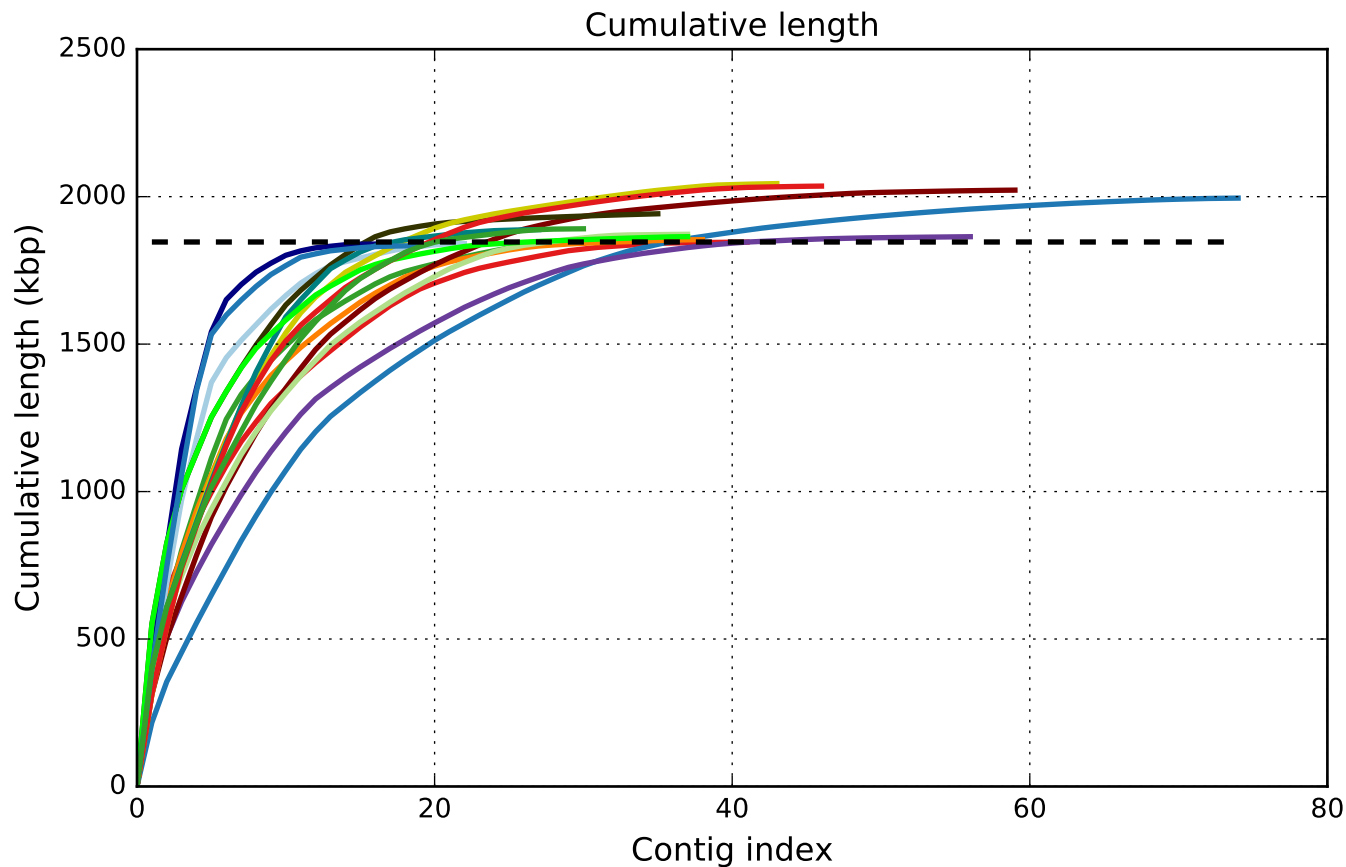
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

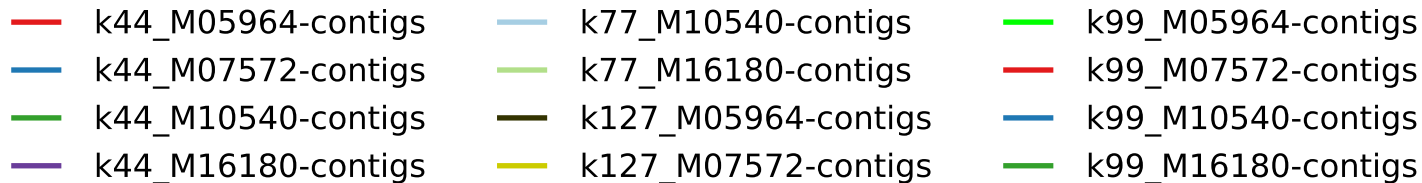
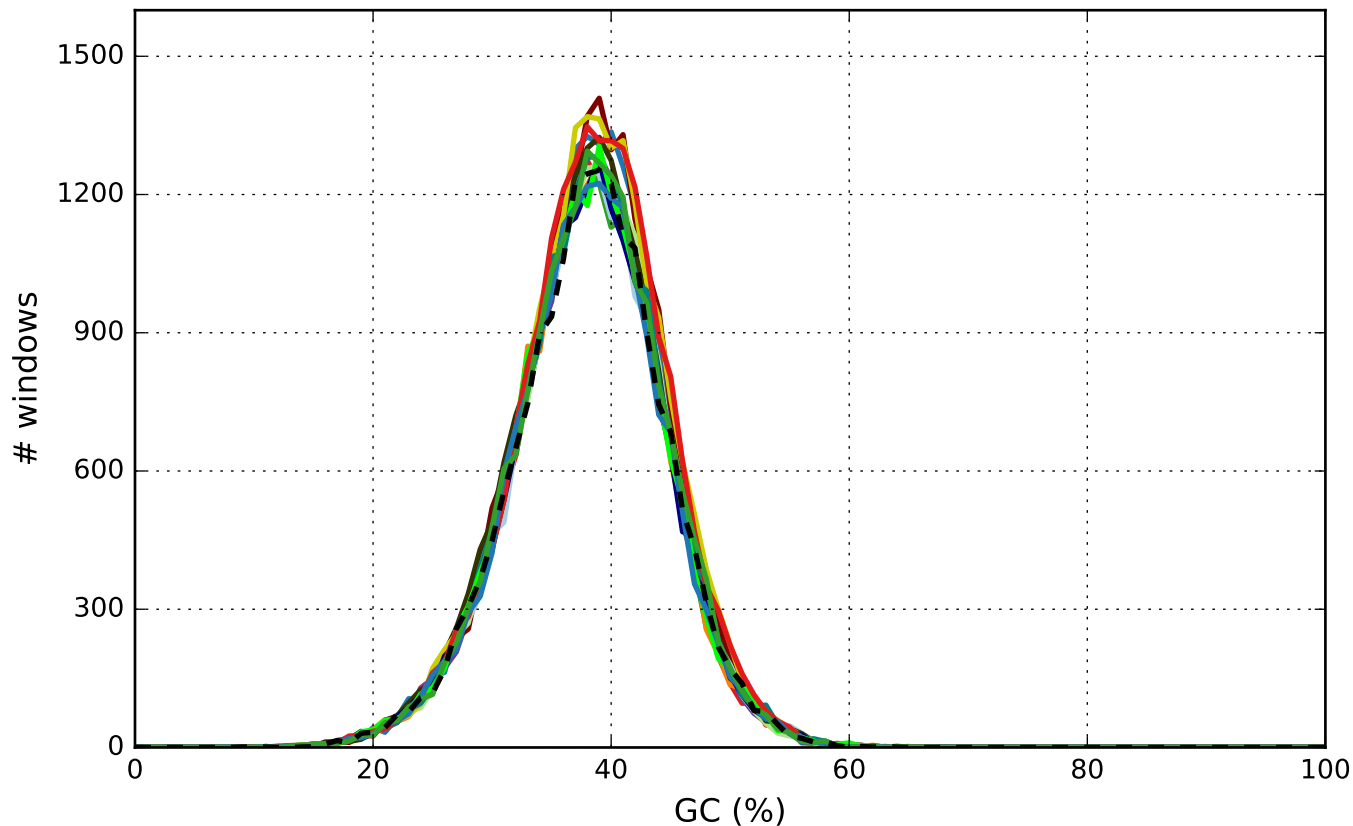


NGx

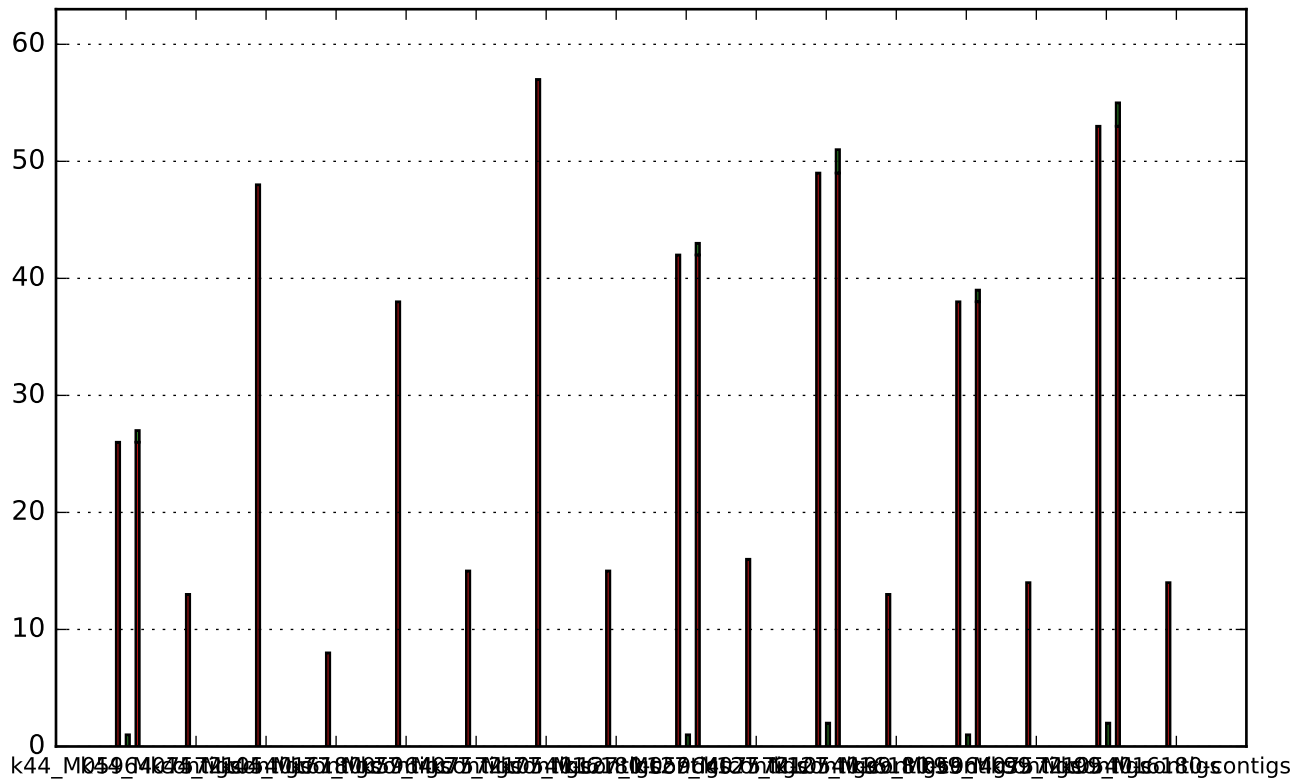




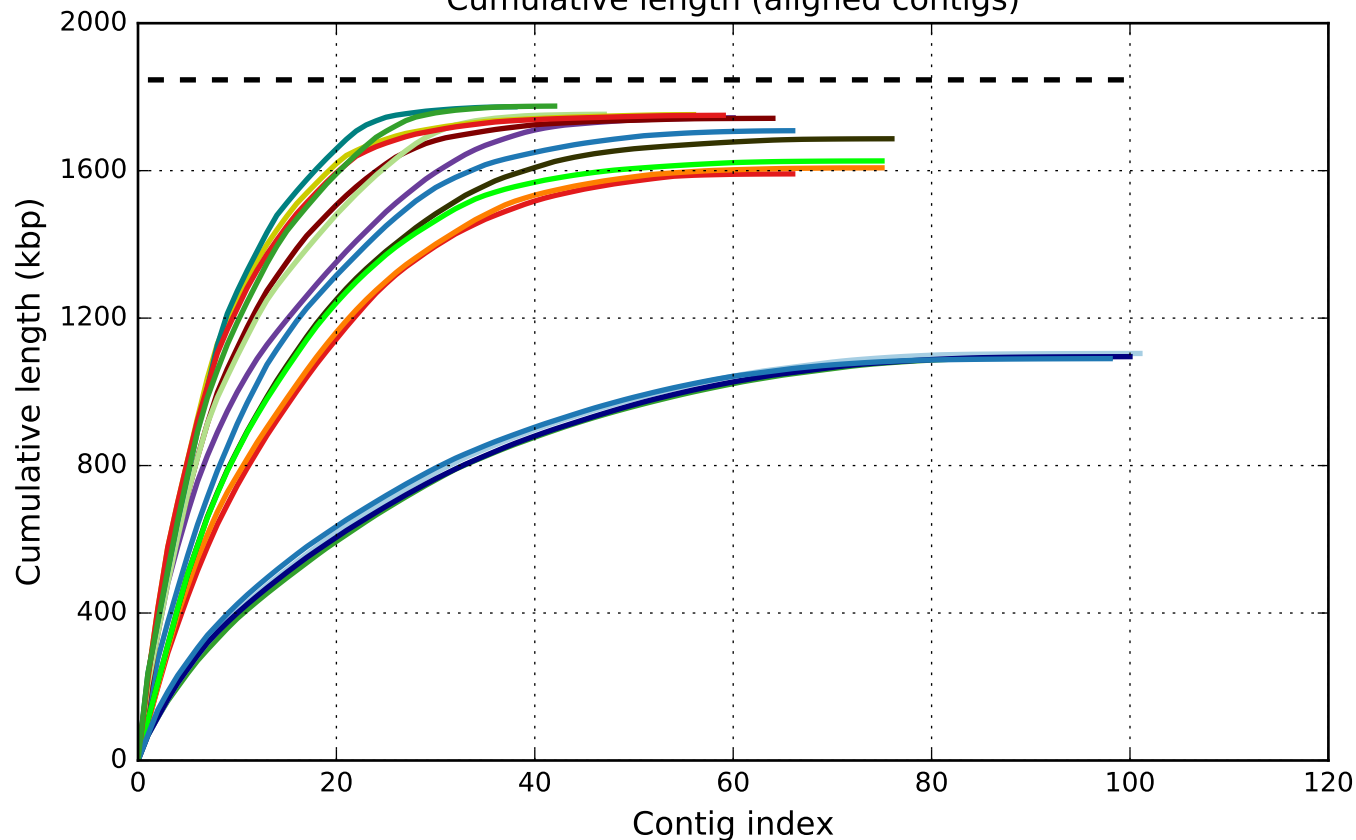
GC content



Misassemblies



Cumulative length (aligned contigs)



k44_M05964-contigs

k44_M07572-contigs

k44_M10540-contigs

k44_M16180-contigs

k77_M10540-contigs

k77_M16180-contigs

k127_M05964-contigs

k127_M07572-contigs

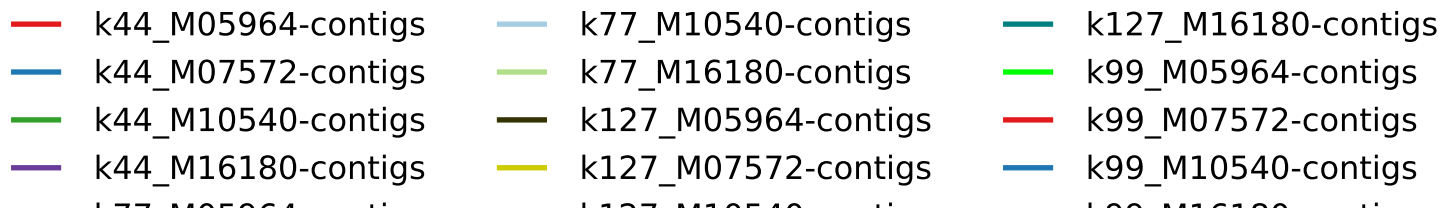
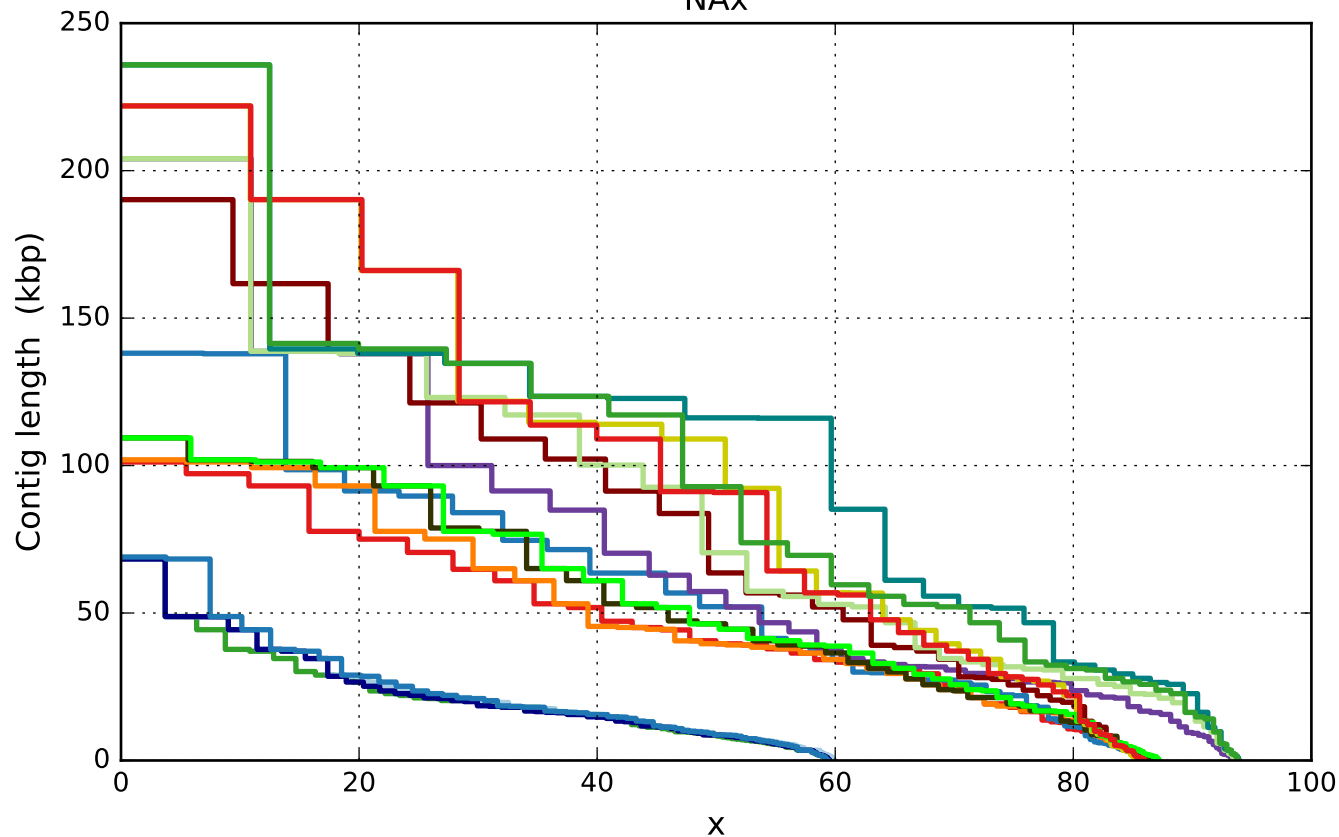
k99_M05964-contigs

k99_M07572-contigs

k99_M10540-contigs

k99_M16180-contigs

NAx



NGAx

