

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	1850897	1850897	1850897	1850897	1850897	1850897	1850897	1850897	1850897	1850897	1850897	1850897	1850897	1850897	1850897	1850897
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	34	8	56	13	40	9	62	17	49	10	84	17	40	10	61	17
# misassembled contigs	14	7	13	8	14	8	12	10	15	10	9	7	11	10	8	8
Misassembled contigs length	1460794	331525	1306962	935765	1521560	623843	1407067	1039687	1692929	919474	1750271	1121560	1524588	773142	1353339	1022861
# local misassemblies	61	15	50	26	64	19	54	32	70	22	57	34	64	23	53	35
# unaligned contigs	4 + 5 part	18 + 10 part	3 + 7 part	5 + 14 part	3 + 5 part	11 + 10 part	2 + 4 part	2 + 7 part	3 + 2 part	4 + 7 part	2 + 2 part	0 + 5 part	3 + 6 part	6 + 6 part	3 + 3 part	0 + 6 part
Unaligned length	84983	137042	286635	80106	33064	116134	257234	77465	12112	93693	55440	44710	33967	110938	268949	46375
Genome fraction (%)	86.581	95.665	61.768	90.324	87.017	96.559	62.068	91.039	87.400	96.851	60.548	91.968	87.318	96.799	61.045	92.259
Duplication ratio	1.099	1.049	1.361	1.067	1.131	1.066	1.378	1.065	1.193	1.088	1.592	1.083	1.133	1.074	1.385	1.080
# 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	2466.85	784.28	3574.33	1742.56	2476.60	796.27	3579.77	1752.90	2466.29	800.78	3571.84	1698.89	2473.81	801.72	3577.83	1696.11
# indels per 100 kbp	60.72	23.61	86.16	46.96	62.90	24.68	88.09	46.71	63.79	25.38	86.29	44.88	64.16	25.40	87.18	45.15
Largest alignment	128087	216748	47680	191527	128120	256031	47680	191540	159838	256047	47680	223389	159838	256043	51516	223389
NA50	38866	73057	9724	42158	38690	83831	10803	55107	40705	114283	10803	89698	40859	113693	10803	58338
NGA50	38866	73523	9721	42158	38690	102175	10424	55107	40859	121740	10803	98123	40859	123191	10283	58338
NA75	14919	26462	-	23796	18403	28331	-	28060	19190	40277	-	33409	19190	39789	-	31629
NGA75	14919	29275	-	26468	18403	44914	-	28060	21333	66987	-	42158	21333	48366	-	33409
LA50	15	10	43	11	15	7	40	10	14	6	40	8	13	6	39	9
LGA50	15	9	44	11	15	6	41	10	13	5	40	7	13	5	40	9
LA75	33	23	-	26	31	17	-	21	31	14	-	16	29	14	-	19
LGA75	33	19	-	25	31	13	-	21	28	10	-	15	28	11	-	18

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

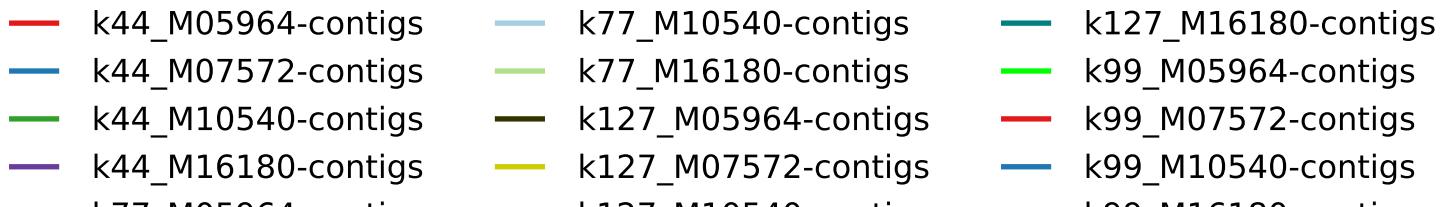
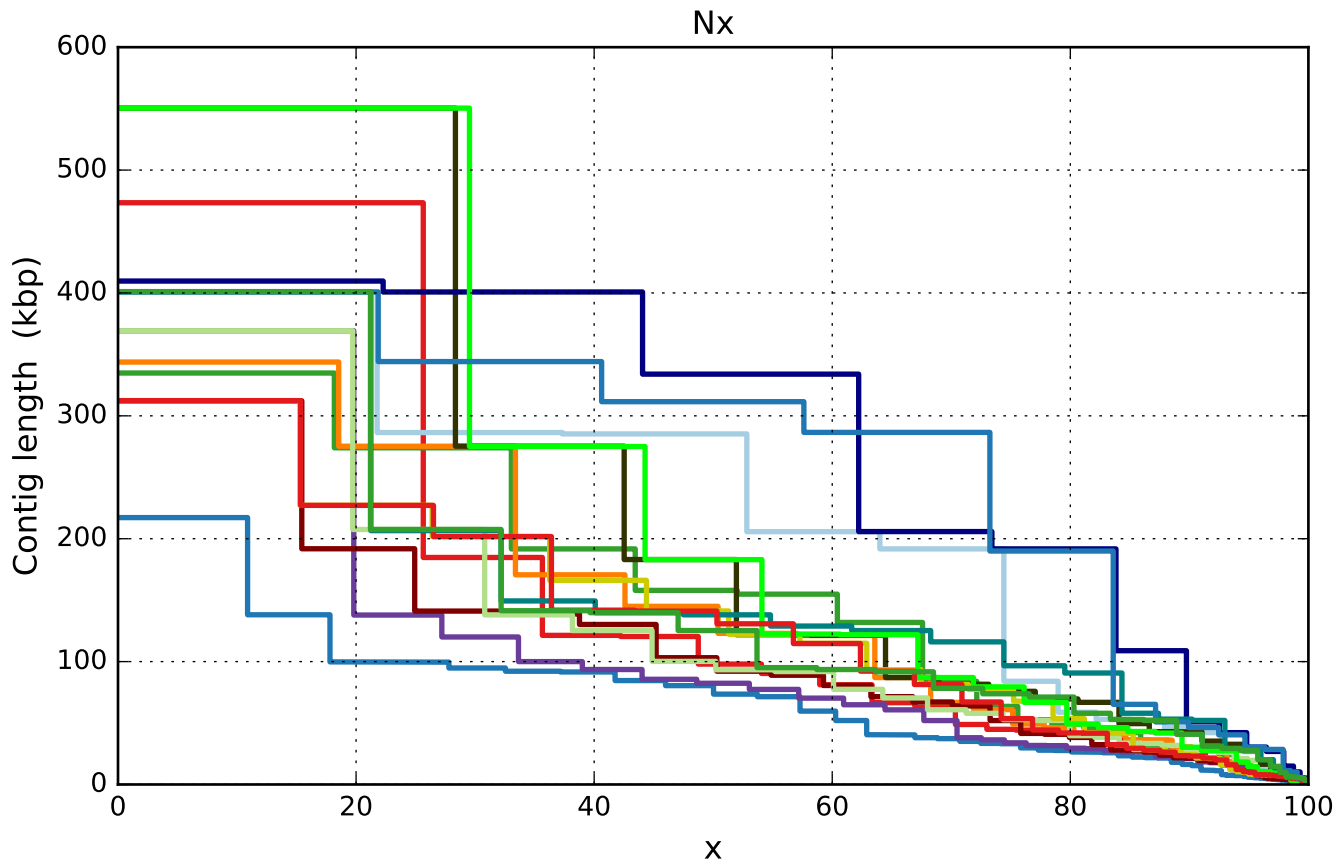
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# misassemblies	34	8	56	13	40	9	62	17	49	10	84	17	40	10	61	17
# relocations	34	8	54	13	39	9	60	17	49	9	84	17	40	9	61	17
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	0	0	2	0	1	0	2	0	0	1	0	0	0	1	0	0
# misassembled contigs	14	7	13	8	14	8	12	10	15	10	9	7	11	10	8	8
Misassembled contigs length	1460794	331525	1306962	935765	1521560	623843	1407067	1039687	1692929	919474	1750271	1121560	1524588	773142	1353339	1022861
# local misassemblies	61	15	50	26	64	19	54	32	70	22	57	34	64	23	53	35
# mismatches	39532	13887	40864	29132	39888	14231	41125	29537	39897	14355	40029	28919	39981	14364	40425	28963
# indels	973	418	985	785	1013	441	1012	787	1032	455	967	764	1037	455	985	771
# short indels	870	346	893	682	901	363	916	679	916	377	878	658	922	379	894	666
# long indels	103	72	92	103	112	78	96	108	116	78	89	106	115	76	91	105
Indels length	2937	1927	2354	2638	3219	2055	2485	2754	3211	2151	2241	2707	3236	2075	2344	2687

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).

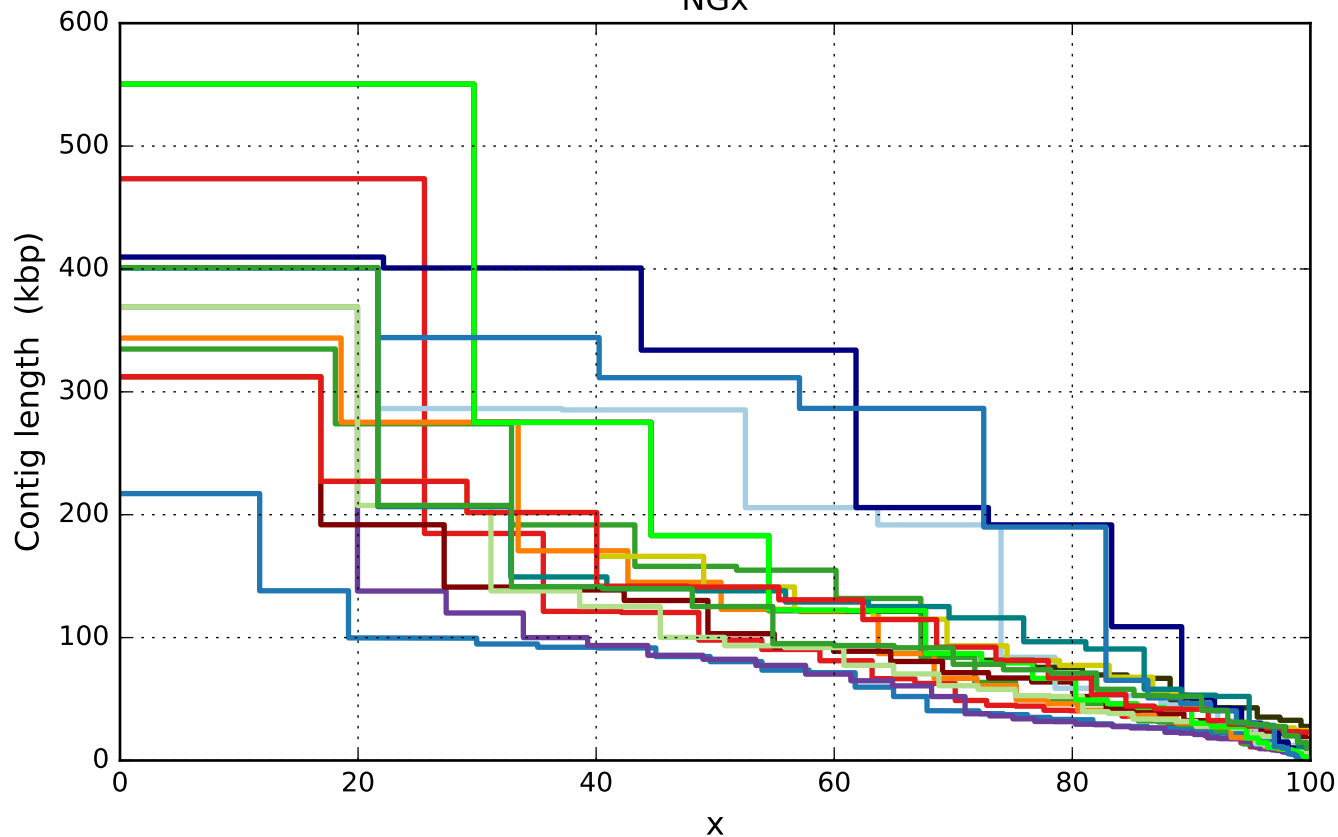
Unaligned report

	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	18	3	5	3	11	2	2	3	4	2	0	3	6	3	0
Fully unaligned length	49931	116432	11615	22408	7192	45758	10649	2215	7857	40704	10749	0	7596	42723	11513	0
# partially unaligned contigs	5	10	7	14	5	10	4	7	2	7	2	5	6	6	3	6
# with misassembly	0	0	5	1	2	3	4	1	0	2	2	1	2	2	3	1
# both parts are significant	4	5	7	7	4	3	4	5	1	5	2	4	3	3	3	5
Partially unaligned length	35052	20610	275020	57698	25872	70376	246585	75250	4255	52989	44691	44710	26371	68215	257436	46375
# 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).



NGx



k44_M05964-contigs

k44_M07572-contigs

k44_M10540-contigs

k44_M16180-contigs

k77_M10540-contigs

k77_M16180-contigs

k127_M05964-contigs

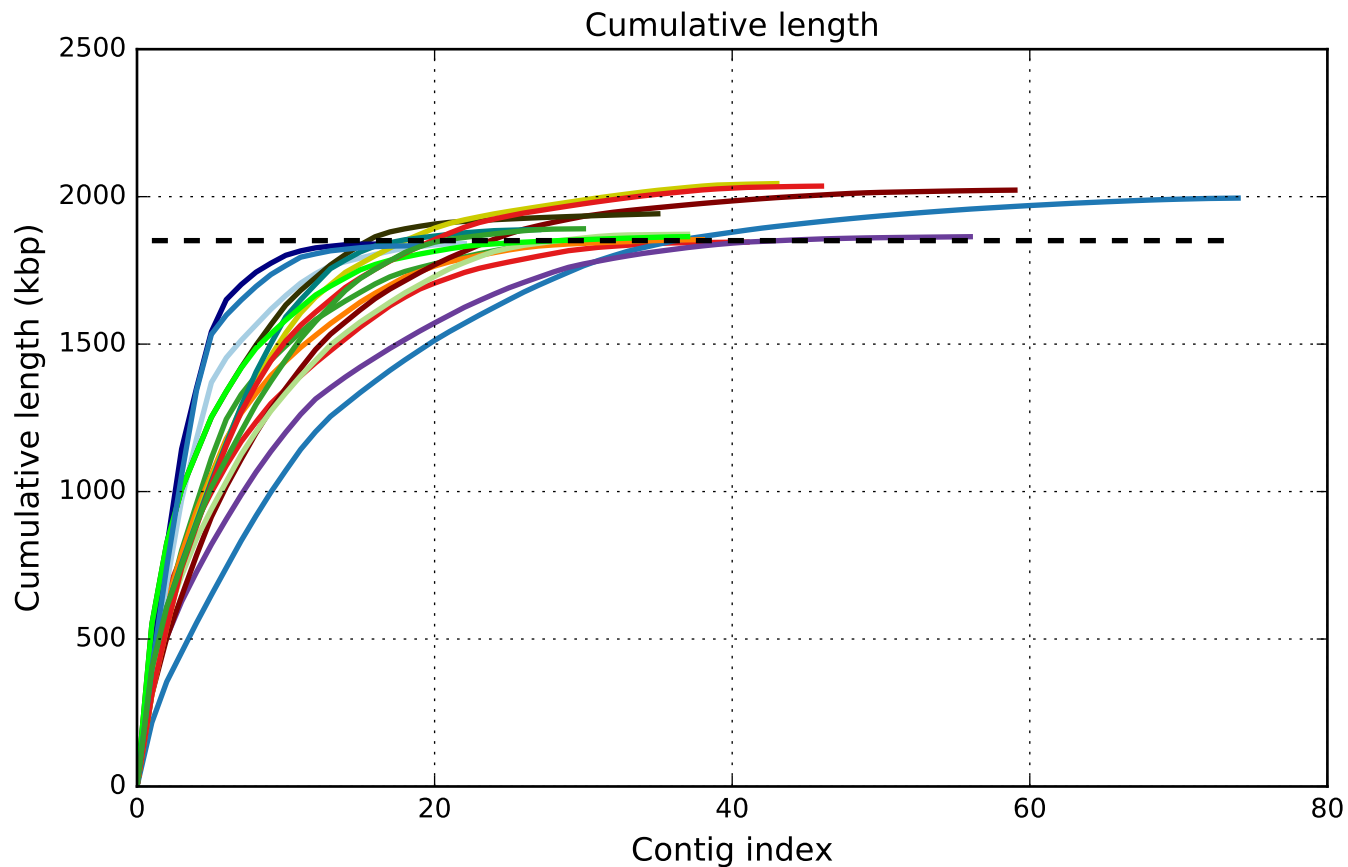
k127_M07572-contigs

k127_M16180-contigs

k99_M05964-contigs

k99_M07572-contigs

k99_M16180-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

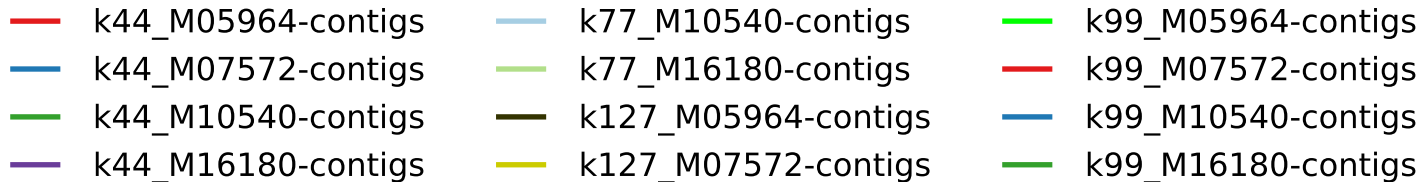
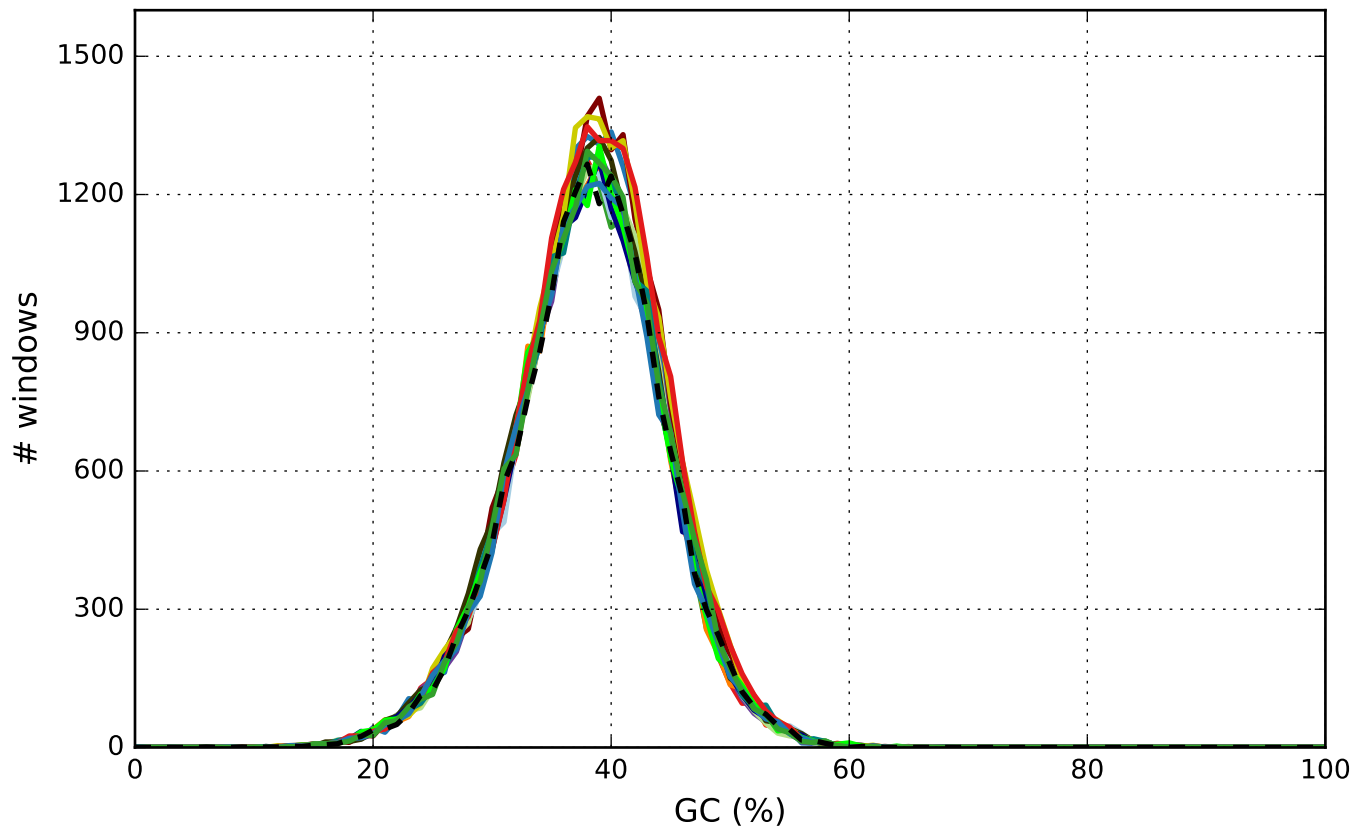
k99_M05964-contigs

k99_M07572-contigs

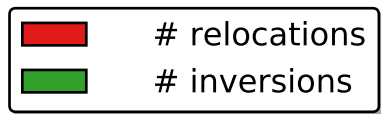
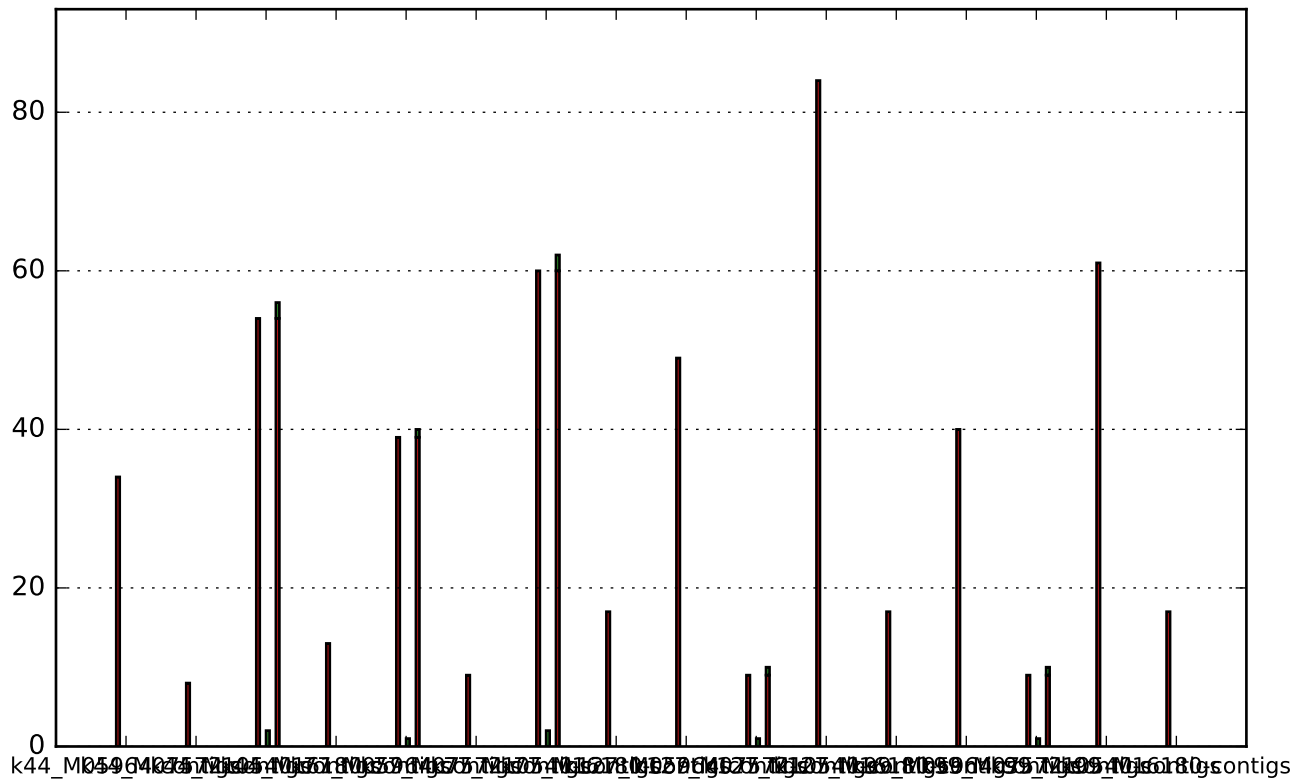
k99_M10540-contigs

k99_M16180-contigs

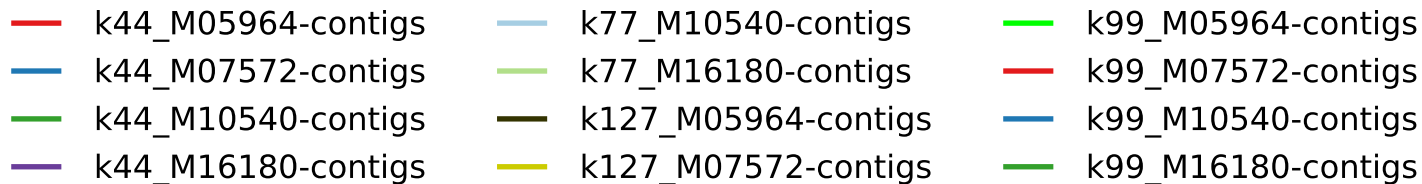
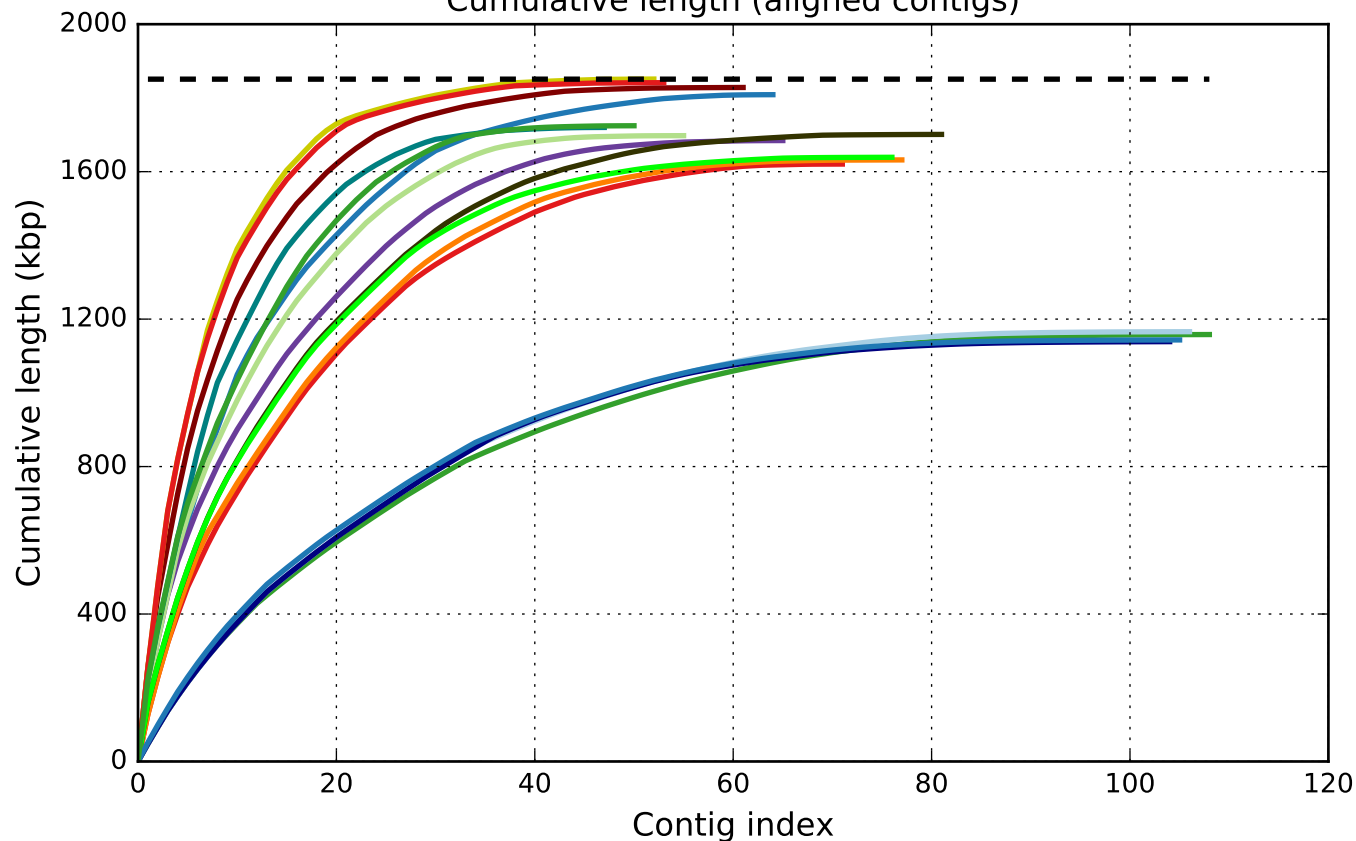
GC content



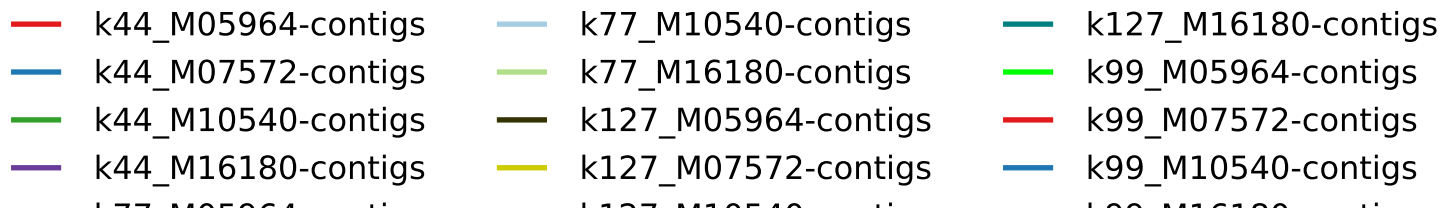
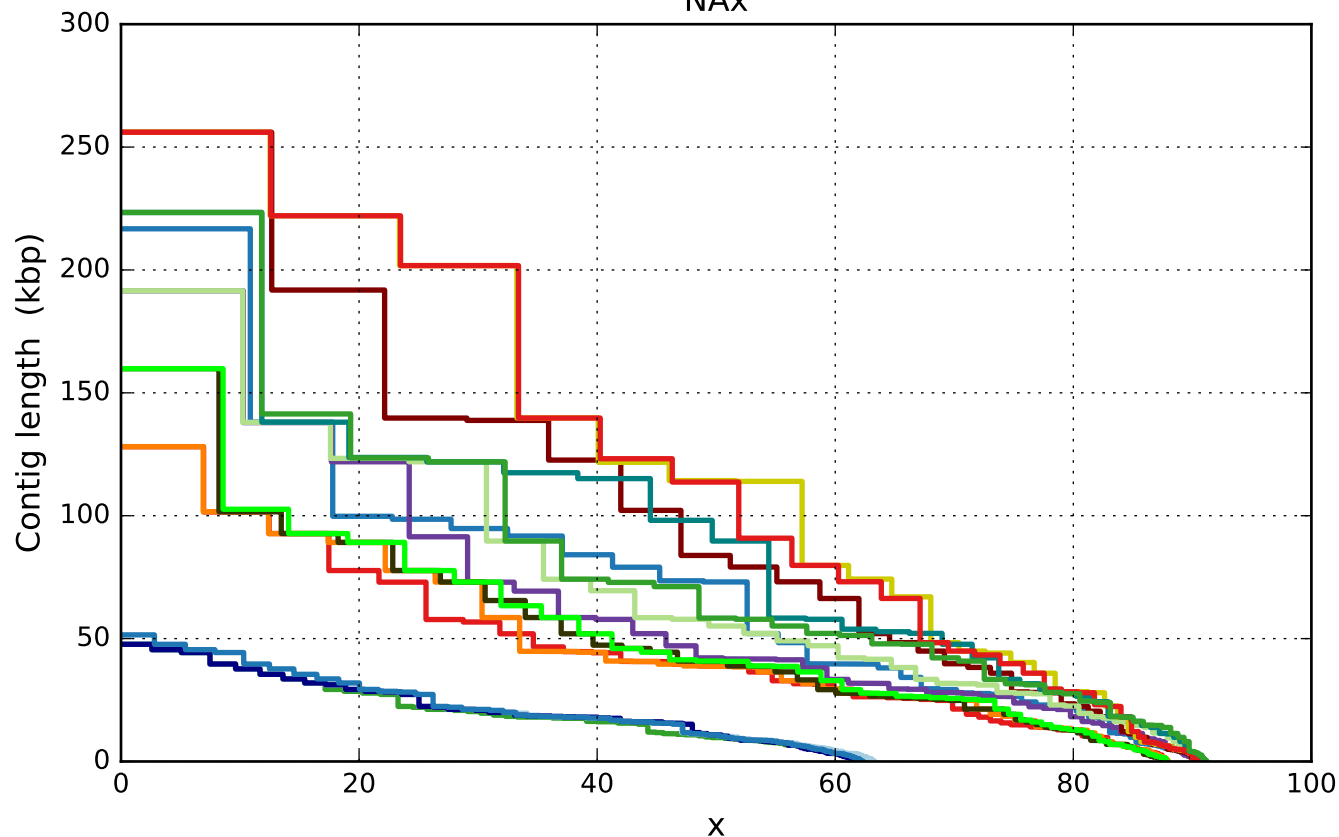
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

