

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	1985832	1985832	1985832	1985832	1985832	1985832	1985832	1985832	1985832	1985832	1985832	1985832	1985832	1985832	1985832	1985832
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 (%)	38.22	38.22	38.22	38.22	38.22	38.22	38.22	38.22	38.22	38.22	38.22	38.22	38.22	38.22	38.22	38.22
N50	97979	80448	157960	82364	144973	103159	285281	100164	183050	141208	333934	138055	182978	141152	311520	125281
NG50	97979	80448	154878	77367	122974	103159	205735	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	40442	33152	49096	29514	40872	52032	58778	52076	75809	77394	191716	96606	49237	67130	189976	71139
L50	5	9	4	7	4	6	3	5	3	5	3	5	3	5	3	5
LG50	5	9	5	8	5	6	4	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	14	20	10	18	12	13	7	13	8	10	5	9	9	10	5	11
# misassemblies	53	57	29	49	61	72	46	63	69	78	24	70	61	70	57	67
# misassembled contigs	17	25	7	19	16	22	7	22	15	17	3	15	14	17	6	17
Misassembled contigs length	1590507	1522404	686957	1505152	1647728	1702430	916348	1758381	1820017	1786859	473373	1803314	1708197	1723198	1098152	1770215
# local misassemblies	52	64	19	61	54	75	24	72	56	78	10	75	54	76	23	76
# unaligned contigs	5 + 3 part	11 + 19 part	3 + 15 part	7 + 13 part	5 + 3 part	7 + 16 part	1 + 10 part	4 + 5 part	3 + 1 part	7 + 11 part	0 + 9 part	3 + 2 part	5 + 2 part	6 + 12 part	1 + 7 part	3 + 5 part
Unaligned length	118814	165517	723881	91633	75475	145859	588005	46195	31813	151934	783930	22938	56816	159130	461391	46266
Genome fraction (%)	74.762	79.241	41.896	77.314	74.861	79.341	42.811	77.390	75.488	79.619	42.811	78.934	74.982	79.538	44.392	78.676
Duplication ratio	1.163	1.163	1.344	1.155	1.196	1.191	1.474	1.188	1.274	1.197	1.241	1.190	1.214	1.188	1.557	1.181
# 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	2694.70	2615.17	3764.06	2515.24	2705.42	2589.79	3785.06	2485.75	2716.14	2553.59	3793.20	2508.40	2705.90	2549.55	3833.44	2498.45
# indels per 100 kbp	72.00	70.60	96.28	66.18	72.04	73.43	95.04	63.90	75.45	73.56	95.39	67.11	74.34	72.87	96.31	65.80
Largest alignment	89978	80803	38880	74294	75077	121607	38880	74294	89989	121623	38880	74294	89989	121619	52175	74294
NA50	26767	23067	-	26504	26781	23216	-	29647	27715	26260	-	30109	27659	24047	-	30802
NGA50	23981	23067	-	25579	23268	23325	-	27759	26878	26550	-	29367	24858	25578	-	29647
NA75	7952	4514	-	9194	7985	3681	-	9654	8003	3579	-	10240	8003	3638	-	10205
NGA75	-	4971	-	3623	1130	5330	-	5330	7460	6151	-	7060	1908	6151	-	6939
LA50	22	25	-	22	21	24	-	20	21	21	-	20	20	22	-	20
LGA50	25	25	-	24	24	23	-	22	22	20	-	22	23	21	-	21
LA75	53	67	-	48	53	65	-	45	53	63	-	42	51	63	-	43
LGA75	-	65	-	62	77	59	-	57	57	53	-	50	71	55	-	52

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

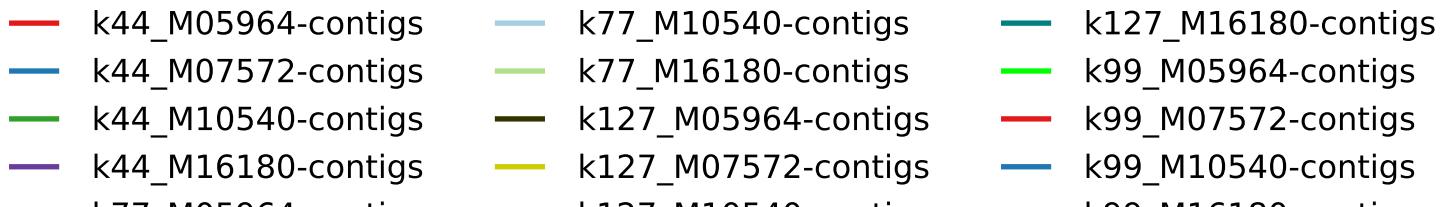
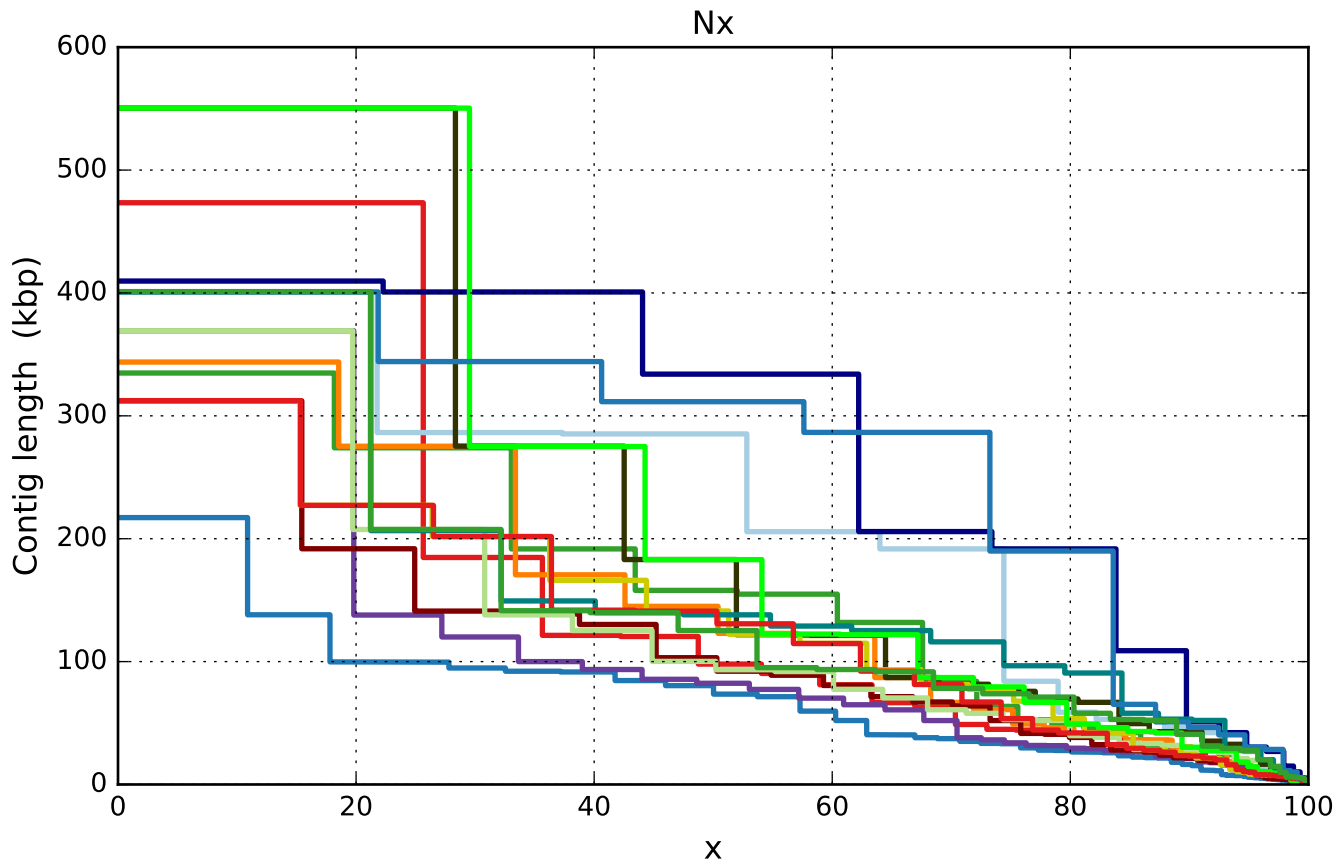
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# misassemblies	53	57	29	49	61	72	46	63	69	78	24	70	61	70	57	67
# relocations	53	56	29	49	61	71	46	63	69	78	24	70	61	69	57	67
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	0	1	0	0	0	1	0	0	0	0	0	0	0	1	0	0
# misassembled contigs	17	25	7	19	16	22	7	22	15	17	3	15	14	17	6	17
Misassembled contigs length	1590507	1522404	686957	1505152	1647728	1702430	916348	1758381	1820017	1786859	473373	1803314	1708197	1723198	1098152	1770215
# local misassemblies	52	64	19	61	54	75	24	72	56	78	10	75	54	76	23	76
# mismatches	40007	41152	31316	38617	40219	40804	32179	38202	40717	40375	32248	39319	40291	40270	33794	39035
# indels	1069	1111	801	1016	1071	1157	808	982	1131	1163	811	1052	1107	1151	849	1028
# short indels	940	996	730	904	945	1035	736	867	997	1038	739	929	976	1028	771	909
# long indels	129	115	71	112	126	122	72	115	134	125	72	123	131	123	78	119
Indels length	3402	3250	1912	3114	3373	3559	1910	3112	3659	3613	1916	3376	3556	3555	2051	3289

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).

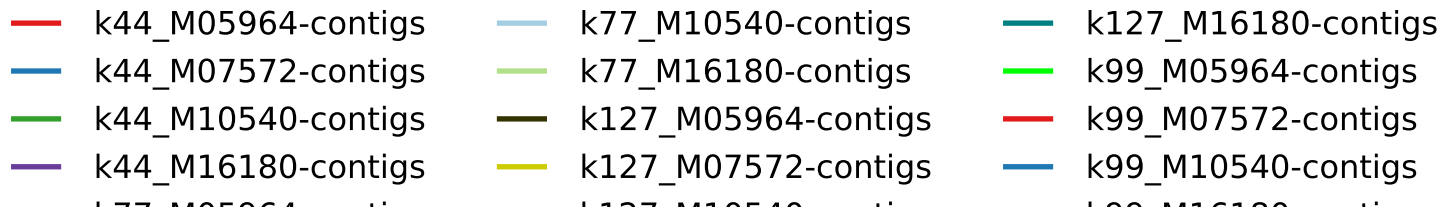
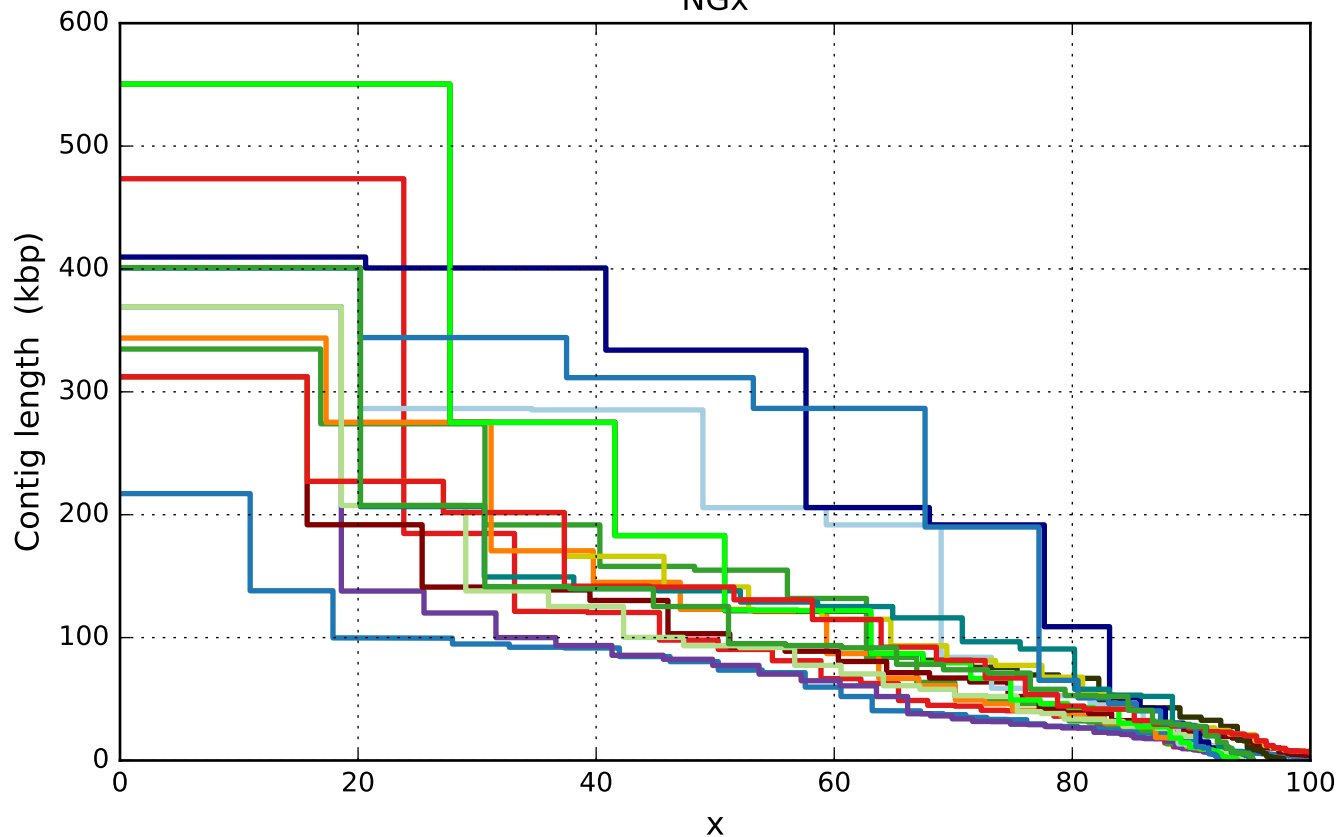
Unaligned report

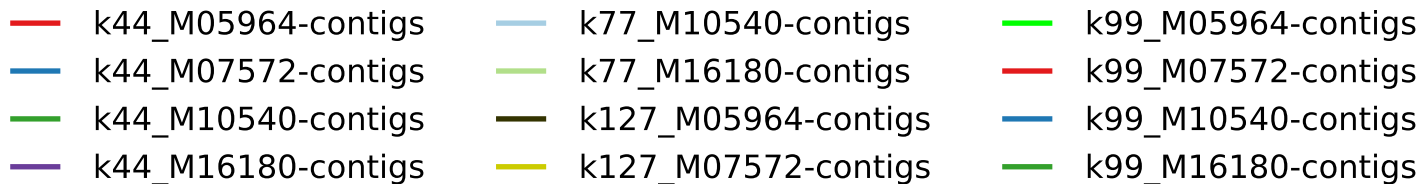
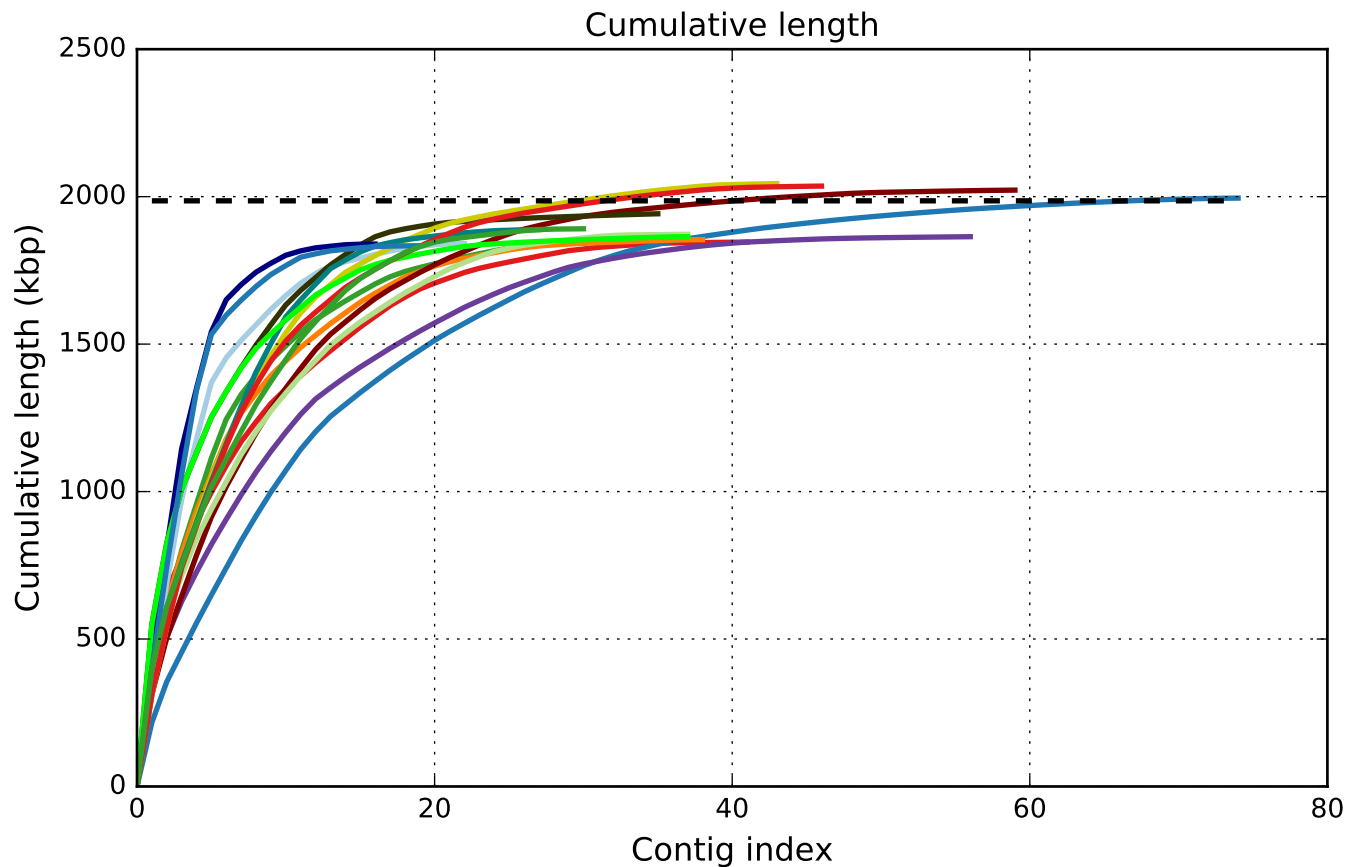
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	5	11	3	7	5	7	1	4	3	7	0	3	5	6	1	3
Fully unaligned length	65316	64779	23521	25712	22076	27669	10113	19081	12276	54488	0	17772	22862	40158	10157	17707
# partially unaligned contigs	3	19	15	13	3	16	10	5	1	11	9	2	2	12	7	5
# with misassembly	0	5	11	3	3	5	9	2	1	9	8	0	2	9	5	2
# both parts are significant	3	14	13	8	3	7	9	3	1	9	8	1	2	8	6	3
Partially unaligned length	53498	100738	700360	65921	53399	118190	577892	27114	19537	97446	783930	5166	33954	118972	451234	28559
# 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).

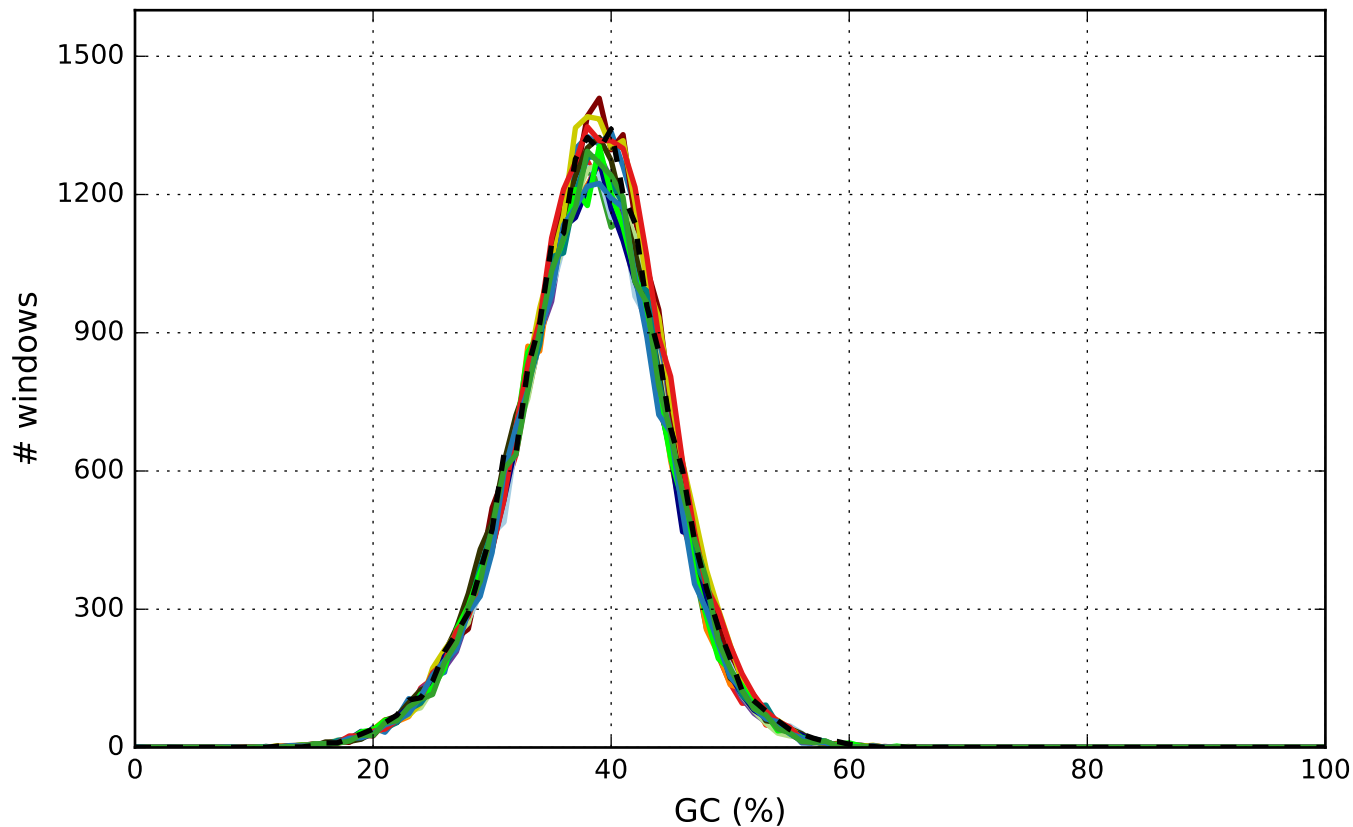


NGx



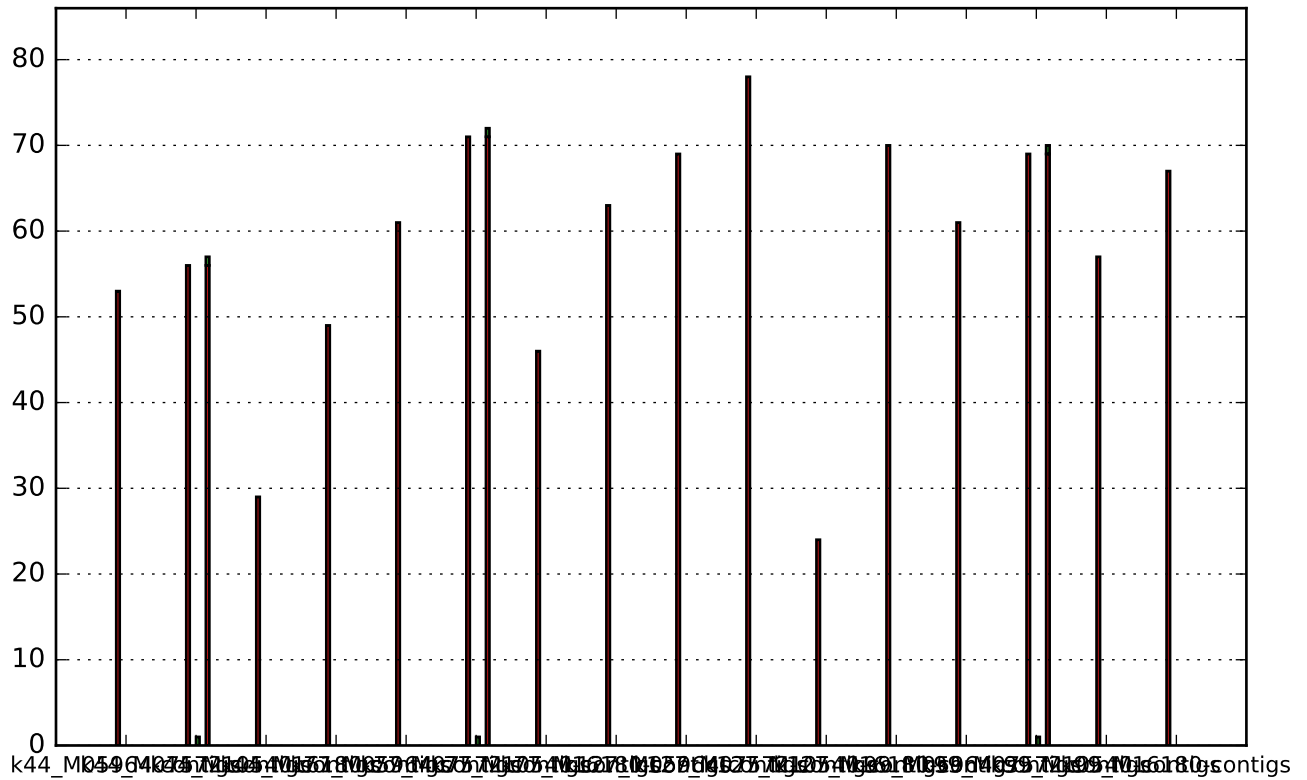


GC content

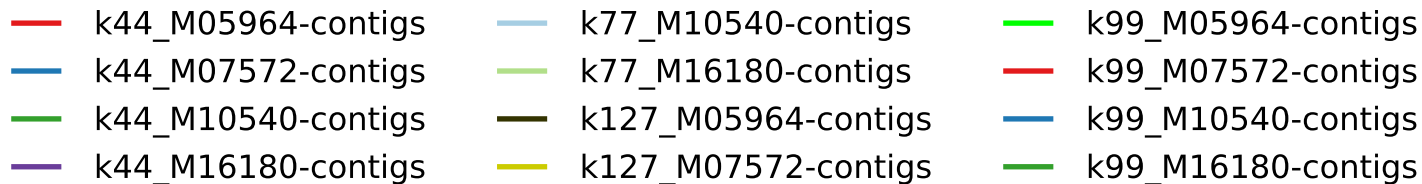
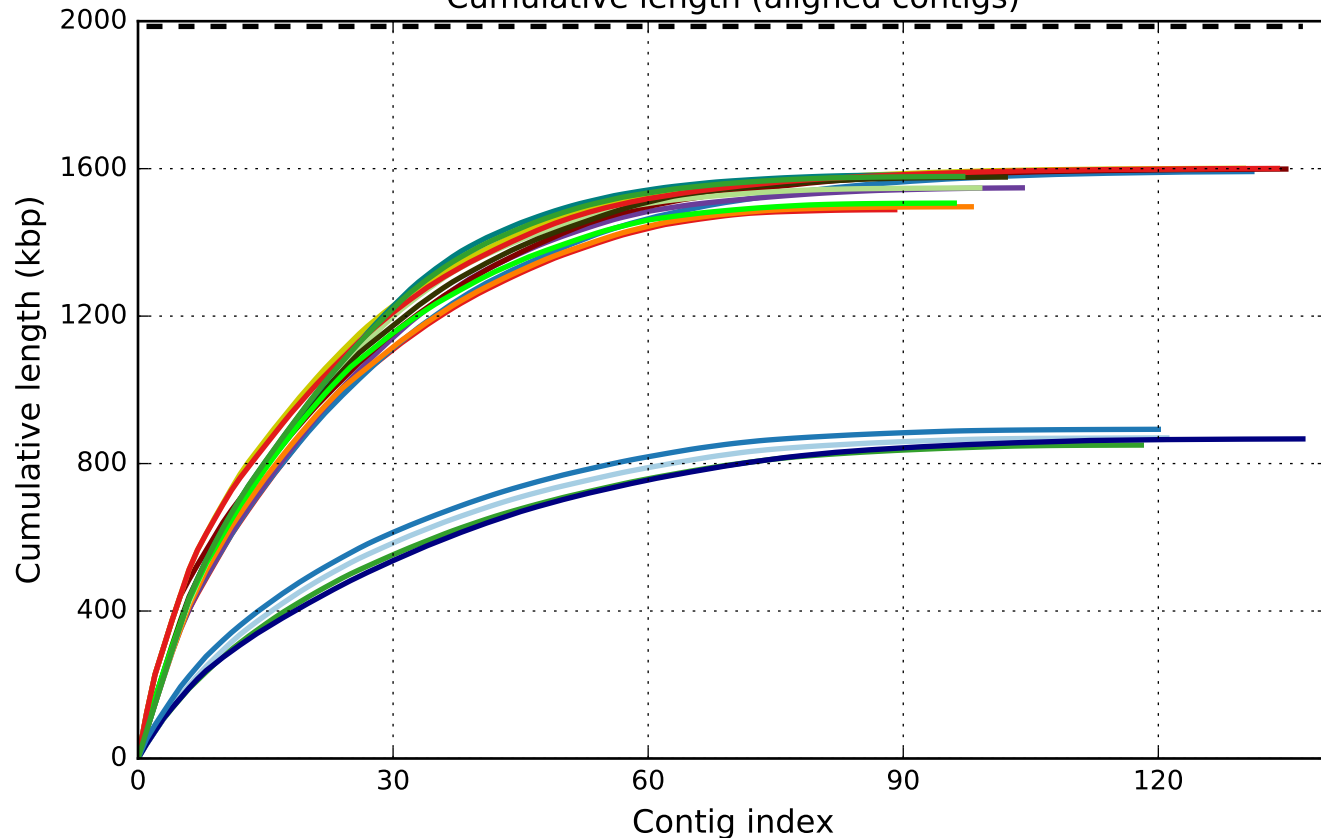


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|--------------------|---------------------|--------------------|
| k44_M05964-contigs | k77_M10540-contigs | k99_M05964-contigs |
| k44_M07572-contigs | k77_M16180-contigs | k99_M07572-contigs |
| k44_M10540-contigs | k127_M05964-contigs | k99_M10540-contigs |
| k44_M16180-contigs | k127_M07572-contigs | k99_M16180-contigs |

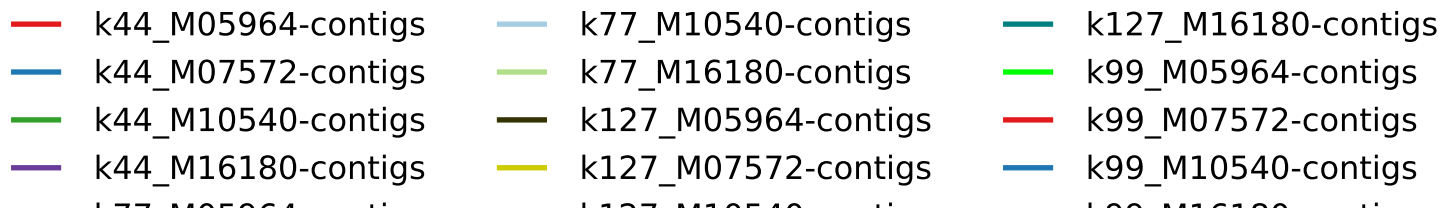
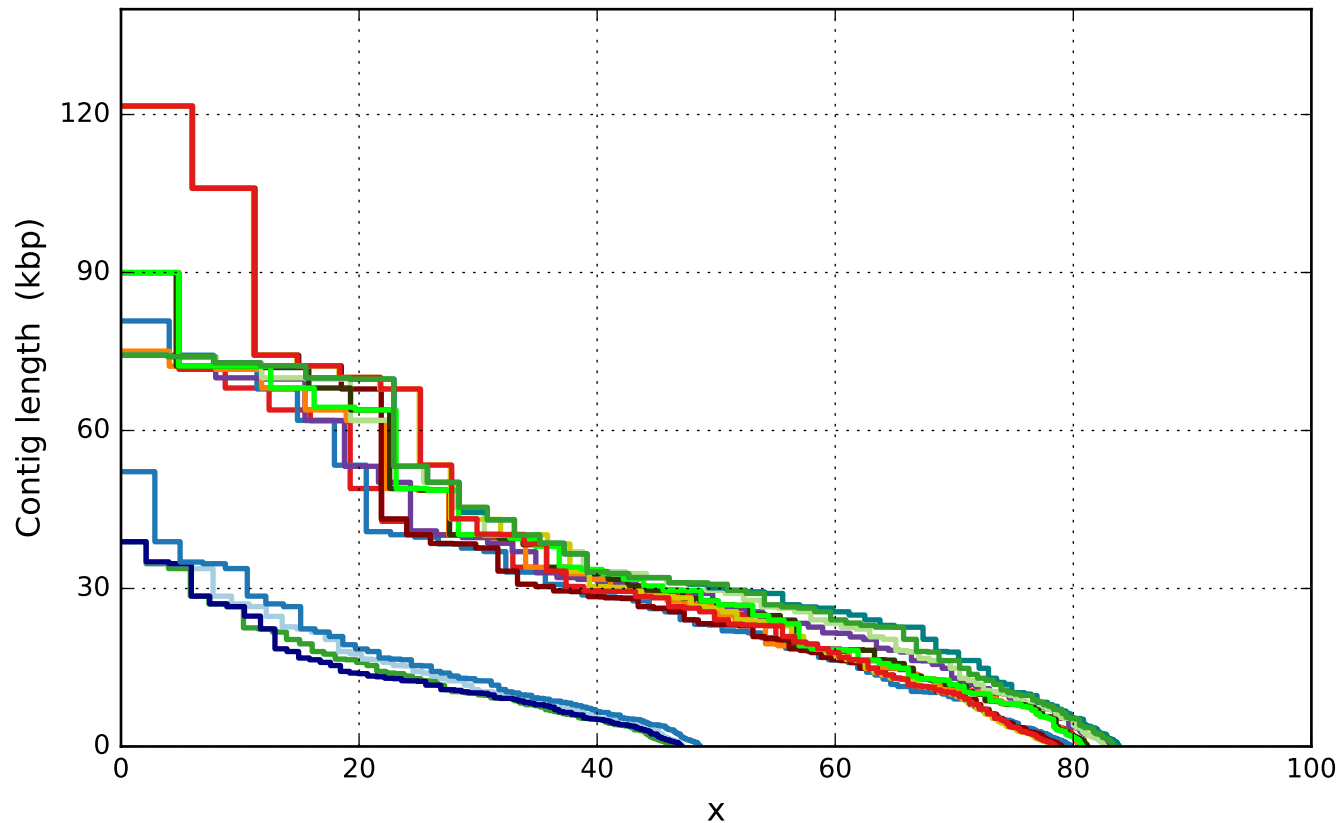
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

