

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	1981535	1981535	1981535	1981535	1981535	1981535	1981535	1981535	1981535	1981535	1981535	1981535	1981535	1981535	1981535	1981535
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 (%)	38.14	38.14	38.14	38.14	38.14	38.14	38.14	38.14	38.14	38.14	38.14	38.14	38.14	38.14	38.14	38.14
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	46134	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	11	13	7	13	8	10	5	9	9	10	5	11
# misassemblies	44	40	52	37	44	53	50	48	63	56	45	50	52	53	43	50
# misassembled contigs	15	20	11	13	16	18	9	17	17	18	6	11	17	18	6	13
Misassembled contigs length	1505595	1386000	1232764	1291399	1557512	1659553	1112764	1563813	1846313	1811835	1005722	1650389	1724877	1760278	956393	1617398
# local misassemblies	61	50	46	54	62	54	43	61	63	57	32	62	65	55	35	64
# unaligned contigs	5 + 3 part	24 + 11 part	2 + 10 part	11 + 12 part	5 + 2 part	15 + 13 part	1 + 7 part	5 + 7 part	3 + 1 part	10 + 4 part	0 + 5 part	4 + 4 part	5 + 0 part	12 + 5 part	1 + 6 part	5 + 5 part
Unaligned length	28507	197673	373358	120686	54401	163432	431761	96164	15177	136411	429882	58835	22862	153687	475965	64147
Genome fraction (%)	81.265	81.439	51.763	79.815	81.869	81.830	51.429	80.020	81.639	81.943	51.049	80.580	82.062	81.902	51.490	80.619
Duplication ratio	1.129	1.114	1.432	1.102	1.109	1.146	1.383	1.120	1.191	1.175	1.393	1.146	1.132	1.160	1.331	1.144
# 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	2413.89	2338.17	3721.62	2306.40	2425.43	2348.90	3716.18	2275.95	2416.46	2347.81	3717.24	2272.98	2424.11	2343.51	3719.55	2274.07
# indels per 100 kbp	64.03	63.95	87.65	60.19	65.09	65.19	88.51	59.72	65.22	64.85	87.59	60.19	65.49	64.64	87.82	60.47
Largest alignment	122175	111163	67998	111001	122175	111239	67998	128690	122175	111187	67998	127705	122175	111187	67998	128690
NA50	35062	25941	6068	28264	39547	28875	6063	29558	37549	29563	5740	36363	41426	29469	6063	36363
NGA50	31854	26503	4602	27440	35879	28875	3304	27762	35879	30722	2554	30733	37549	29563	3303	31181
NA75	13678	7870	-	13841	13877	8825	-	13841	10718	8825	-	13841	13556	8825	-	13841
NGA75	9714	7910	-	8628	9732	9729	-	9443	10432	9829	-	9853	10042	9859	-	9731
LA50	15	21	53	19	13	19	53	17	15	18	56	16	13	19	55	16
LGA50	17	20	66	21	15	19	68	19	16	17	73	18	15	18	70	18
LA75	35	51	-	41	31	49	-	39	37	48	-	37	31	48	-	37
LGA75	44	50	-	49	40	46	-	46	40	43	-	43	38	44	-	43

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	44	40	52	37	44	53	50	48	63	56	45	50	52	53	43	50
# relocations	43	40	49	37	42	53	47	48	61	56	45	50	49	53	42	50
# translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# inversions	1	0	3	0	2	0	3	0	2	0	0	0	3	0	1	0
# misassembled contigs	15	20	11	13	16	18	9	17	17	18	6	11	17	18	6	13
Misassembled contigs length	1505595	1386000	1232764	1291399	1557512	1659553	1112764	1563813	1846313	1811835	1005722	1650389	1724877	1760278	956393	1617398
# local misassemblies	61	50	46	54	62	54	43	61	63	57	32	62	65	55	35	64
# mismatches	38871	37732	38173	36477	39347	38087	37871	36088	39091	38122	37602	36293	39418	38033	37950	36328
# indels	1031	1032	899	952	1056	1057	902	947	1055	1053	886	961	1065	1049	896	966
# short indels	908	913	830	844	925	932	833	840	926	928	817	854	935	925	826	858
# long indels	123	119	69	108	131	125	69	107	129	125	69	107	130	124	70	108
Indels length	3321	3207	2126	3138	3581	3458	2070	3057	3407	3438	2058	3085	3493	3425	2128	3102

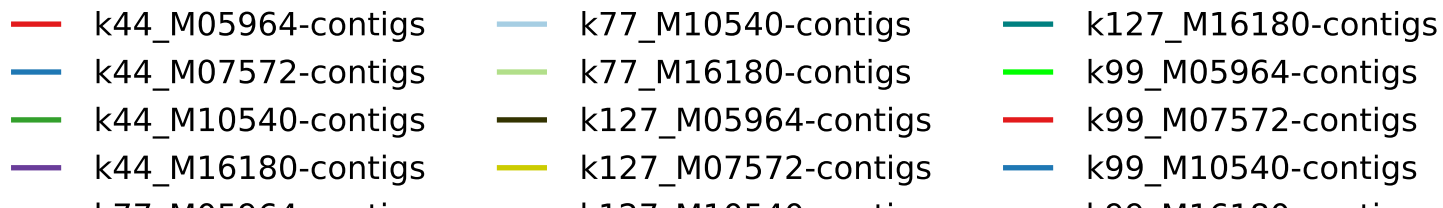
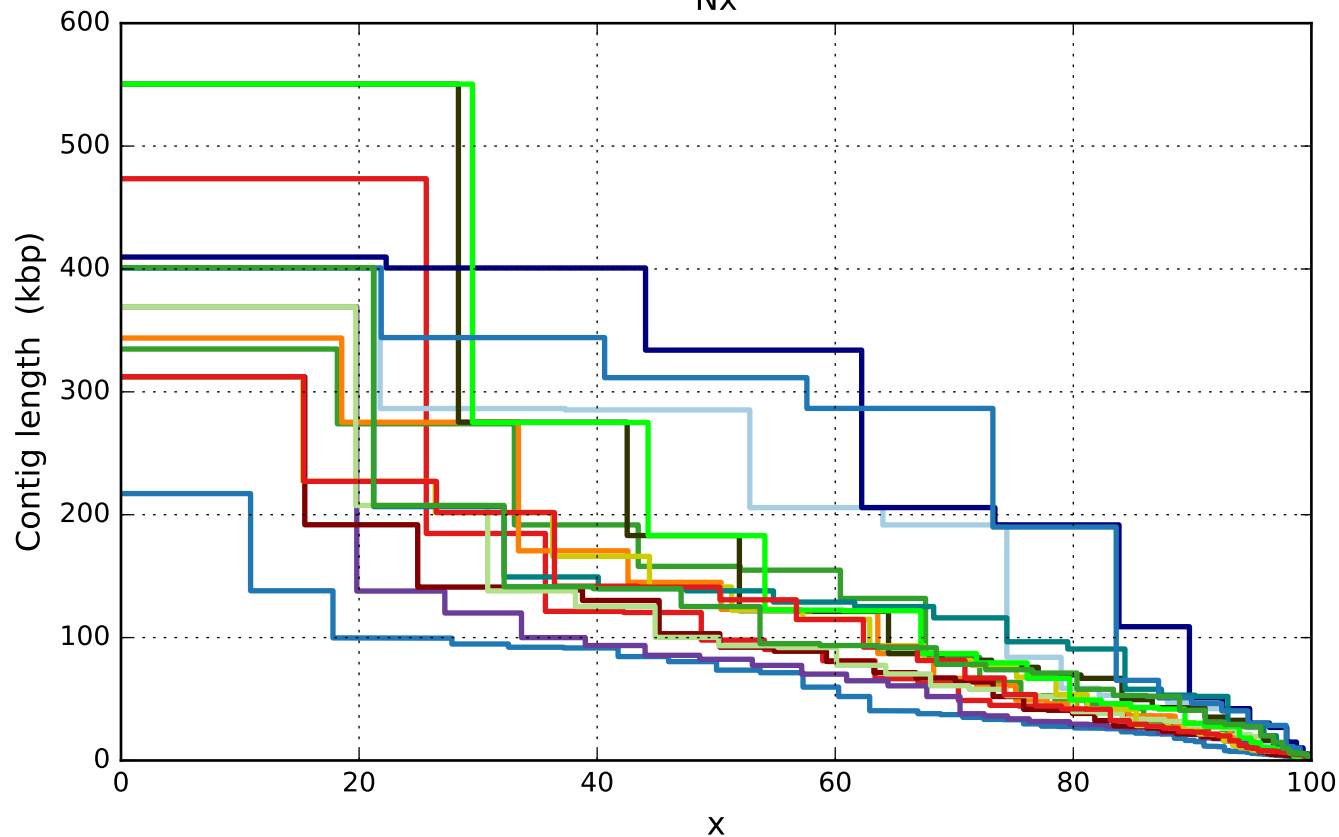
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

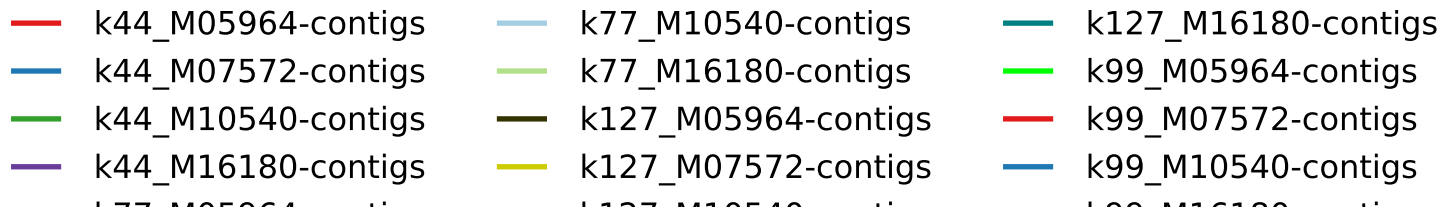
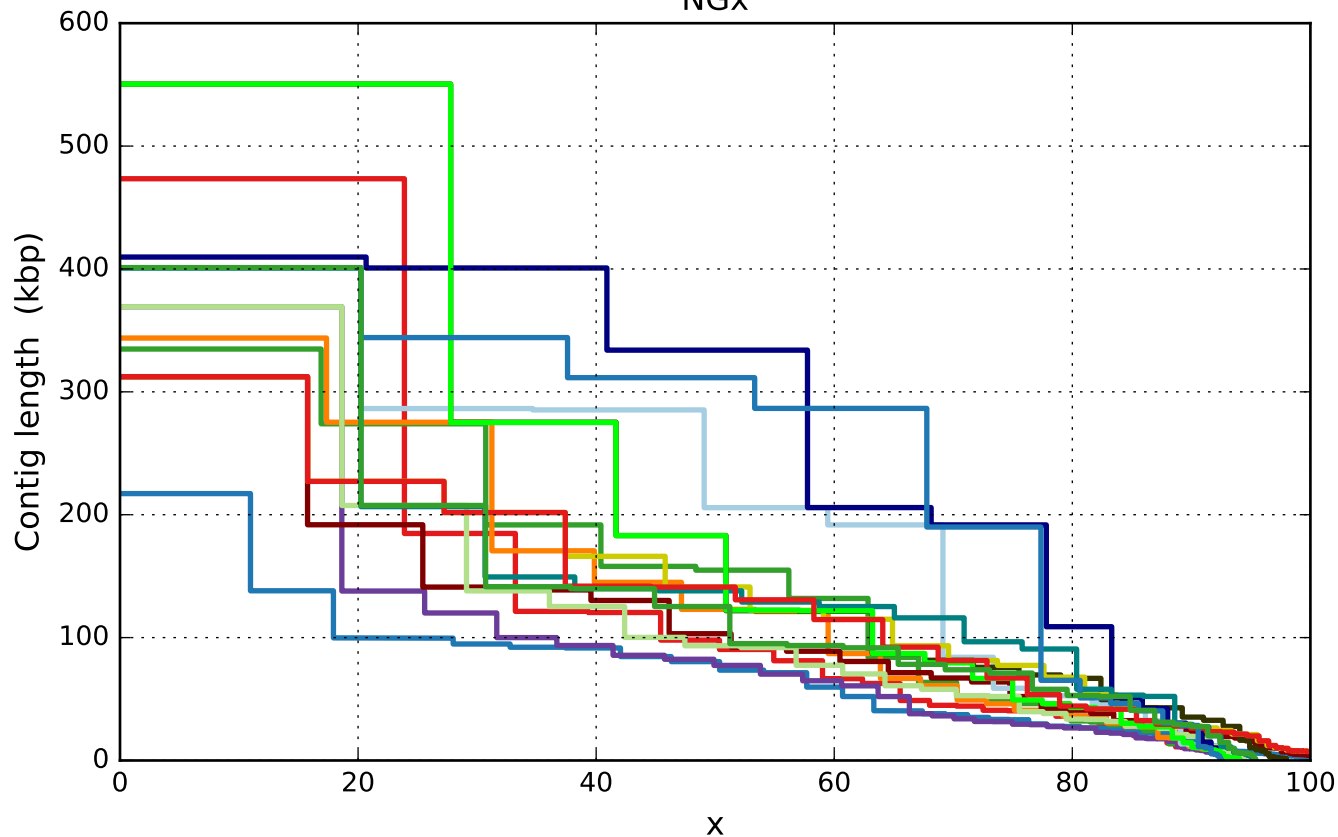
	k44_M05964-contigs	k44_M07572-contigs	k44_M10540-contigs	k44_M16180-contigs	k77_M05964-contigs	k77_M07572-contigs	k77_M10540-contigs	k77_M16180-contigs	k127_M05964-contigs	k127_M07572-contigs	k127_M10540-contigs	k127_M16180-contigs	k99_M05964-contigs	k99_M07572-contigs	k99_M10540-contigs	k99_M16180-contigs
# fully unaligned contigs	5	24	2	11	5	15	1	5	3	10	0	4	5	12	1	5
Fully unaligned length	21066	139260	46841	47430	22076	71388	46337	20711	12276	96974	0	18287	22862	83716	46381	18791
# partially unaligned contigs	3	11	10	12	2	13	7	7	1	4	5	4	0	5	6	5
# with misassembly	0	3	5	3	1	5	6	3	0	4	5	2	0	5	4	2
# both parts are significant	2	9	7	8	2	7	7	5	1	4	5	4	0	5	5	4
Partially unaligned length	7441	58413	326517	73256	32325	92044	385424	75453	2901	39437	429882	40548	0	69971	429584	45356
# N's	153	166	1	27	22	10	0	15	0	0	0	0	0	0	1	1

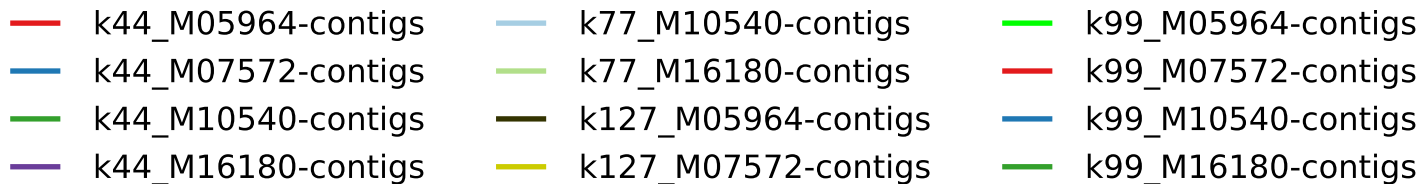
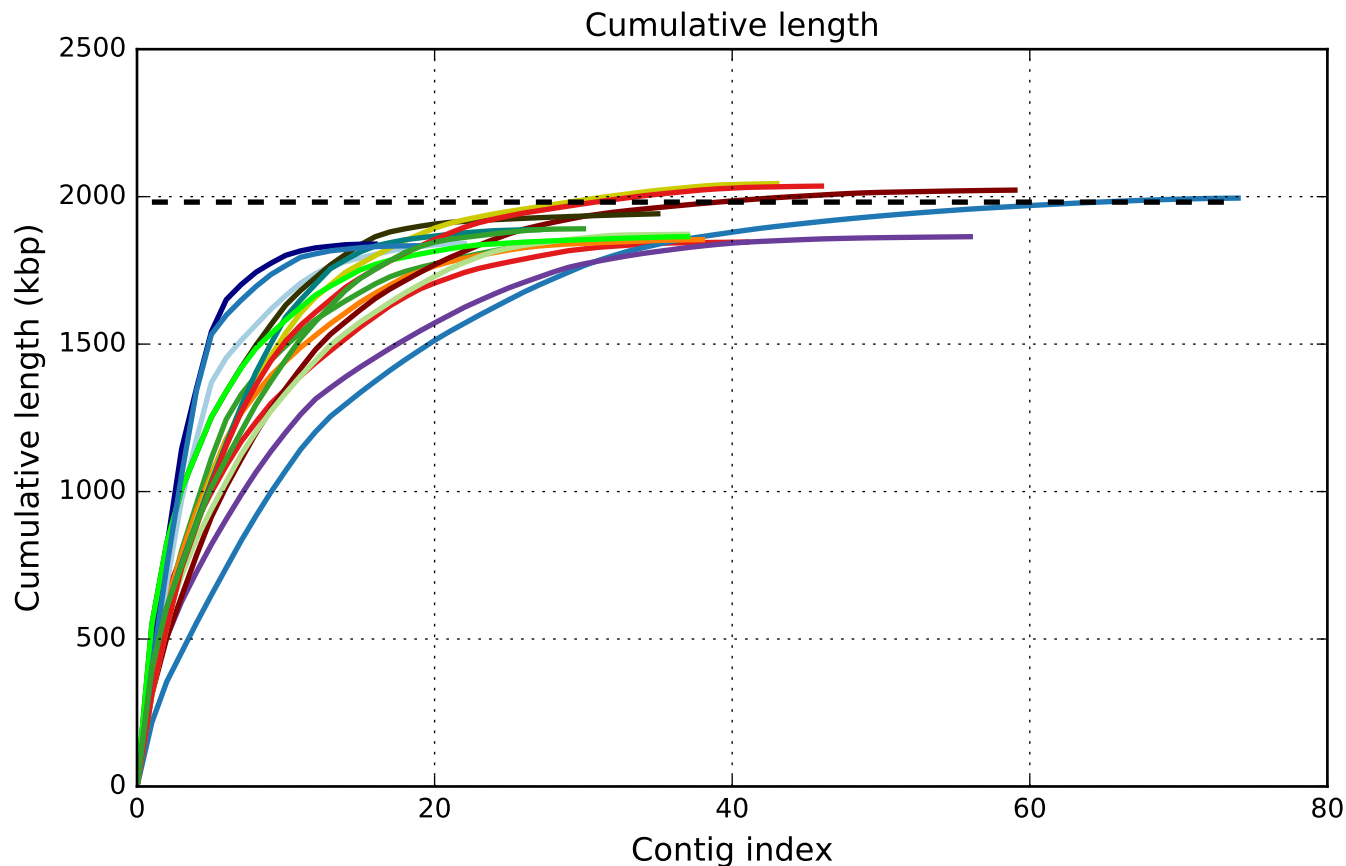
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

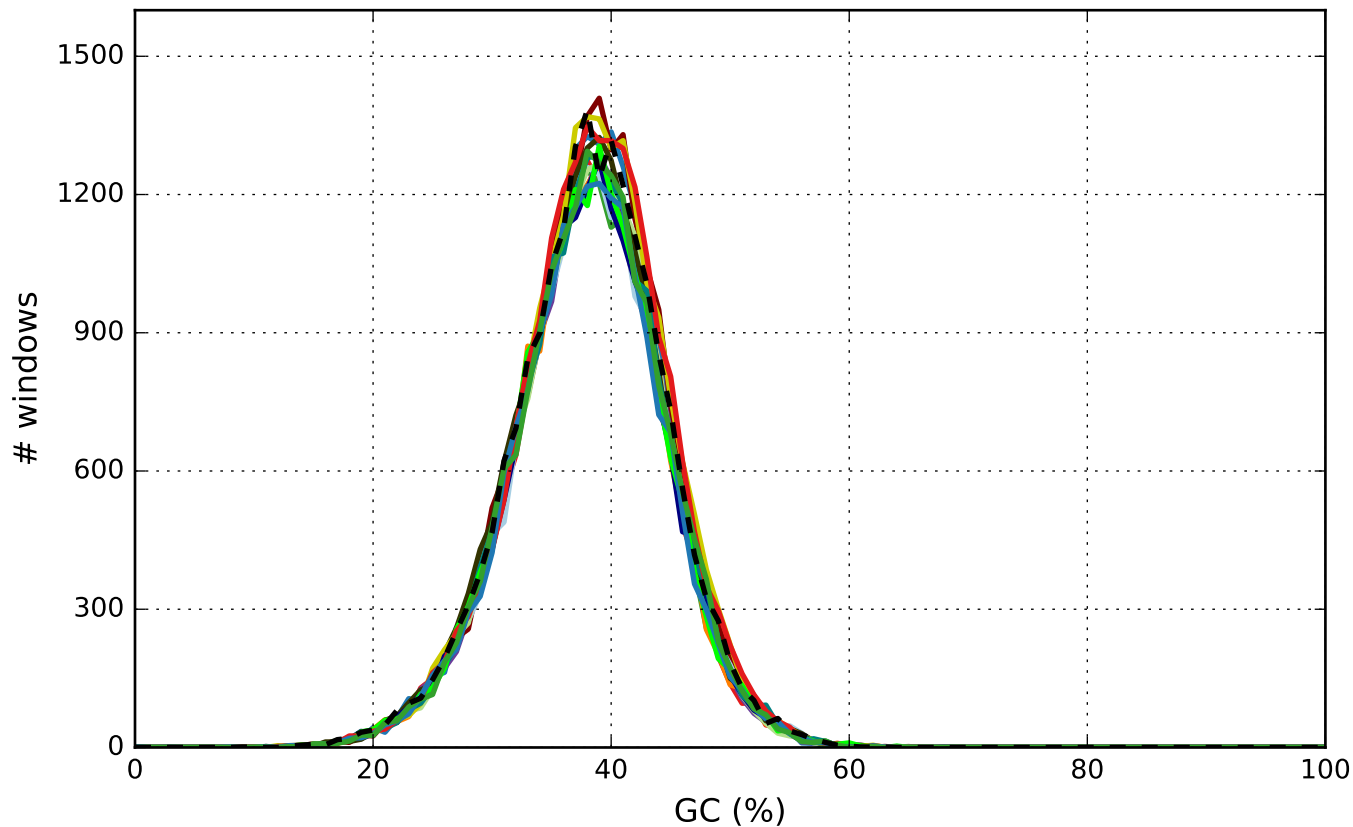


NGx



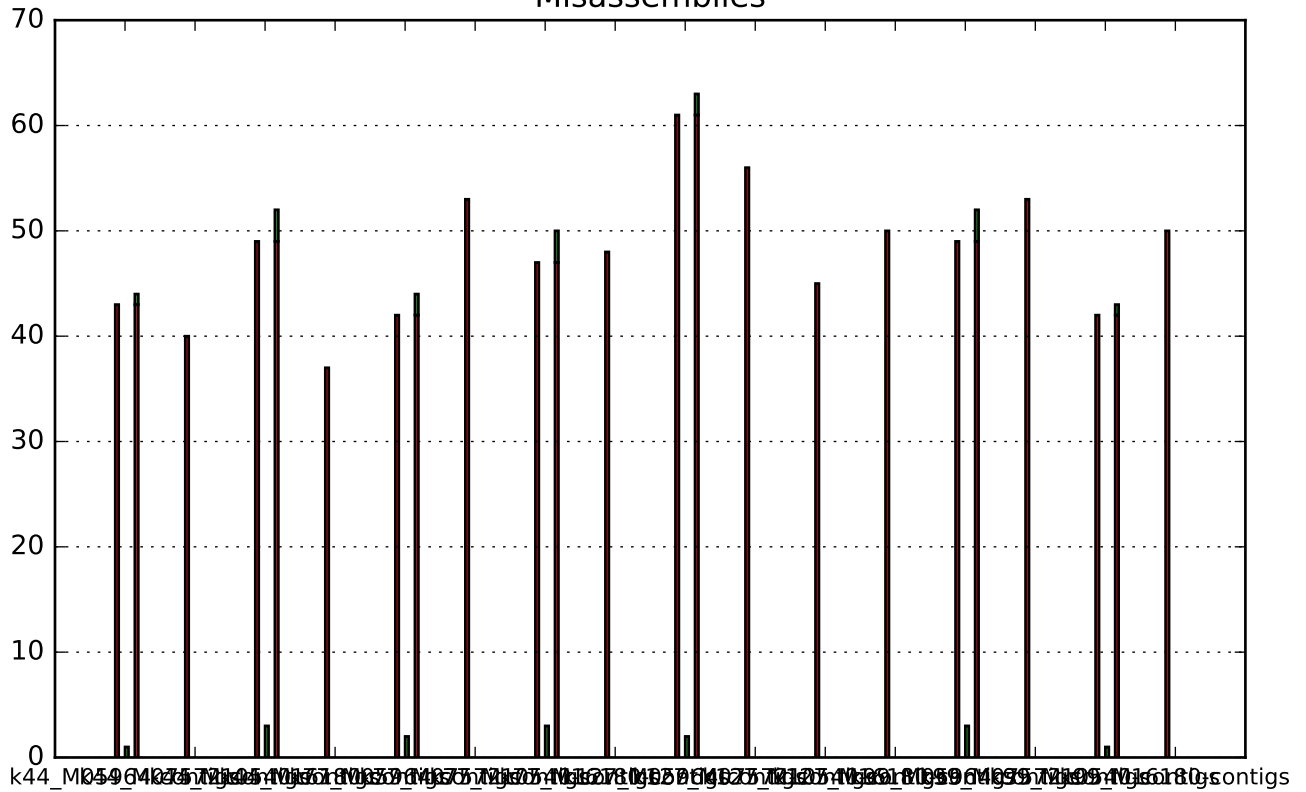


GC content



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



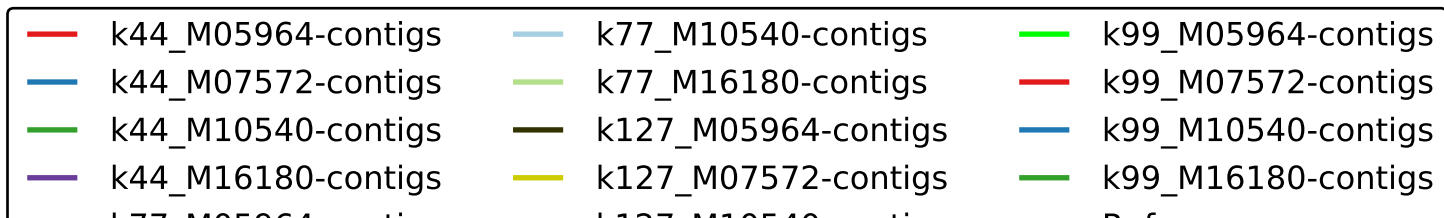
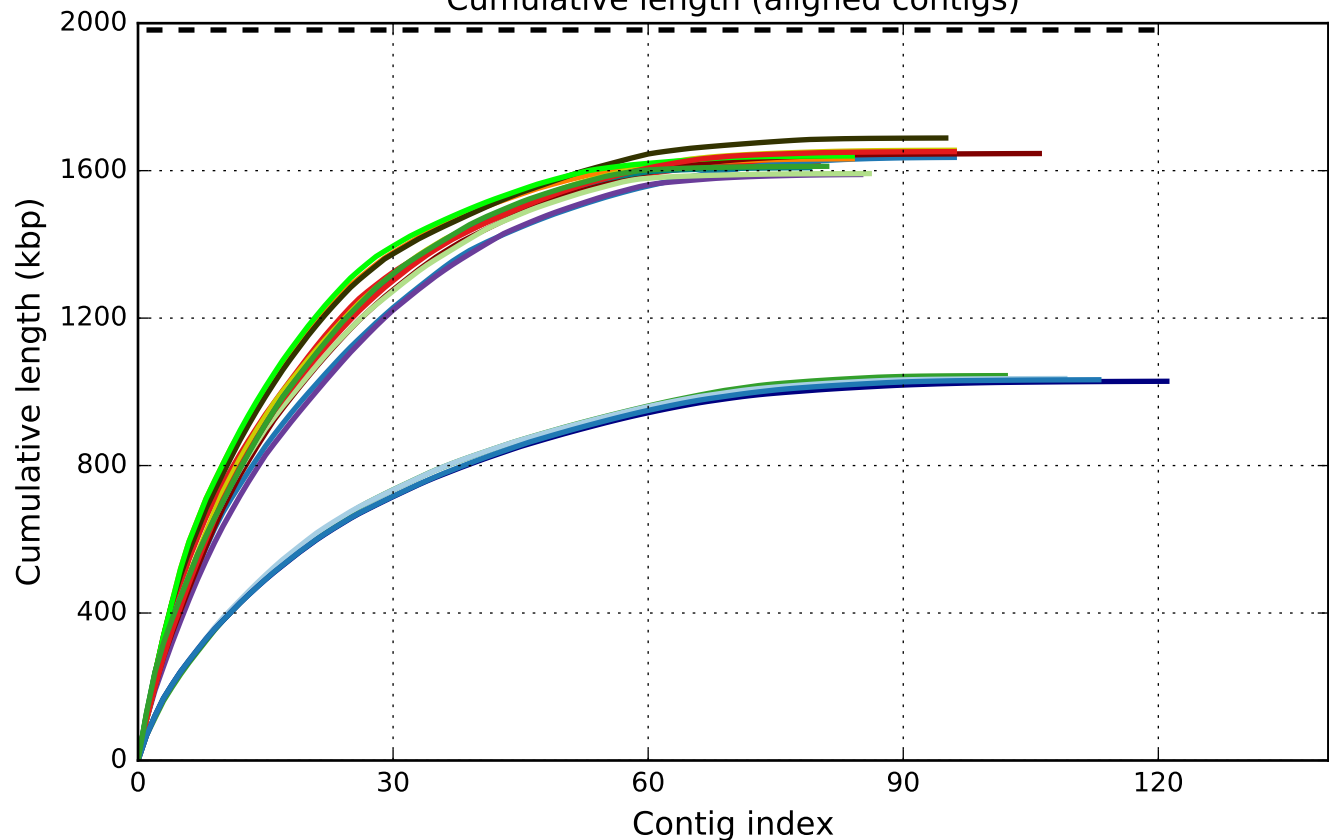
# relocations



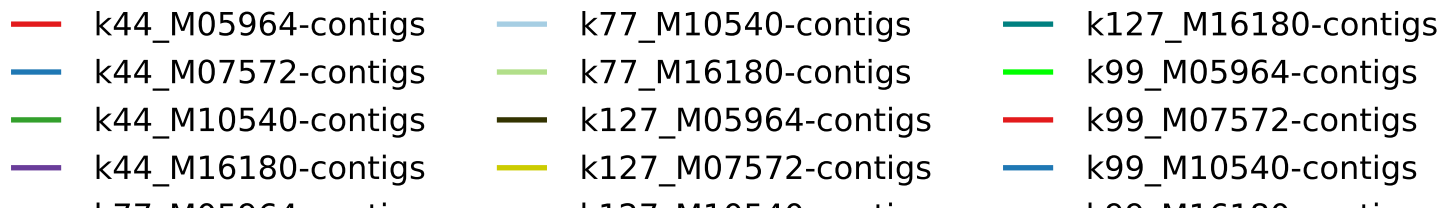
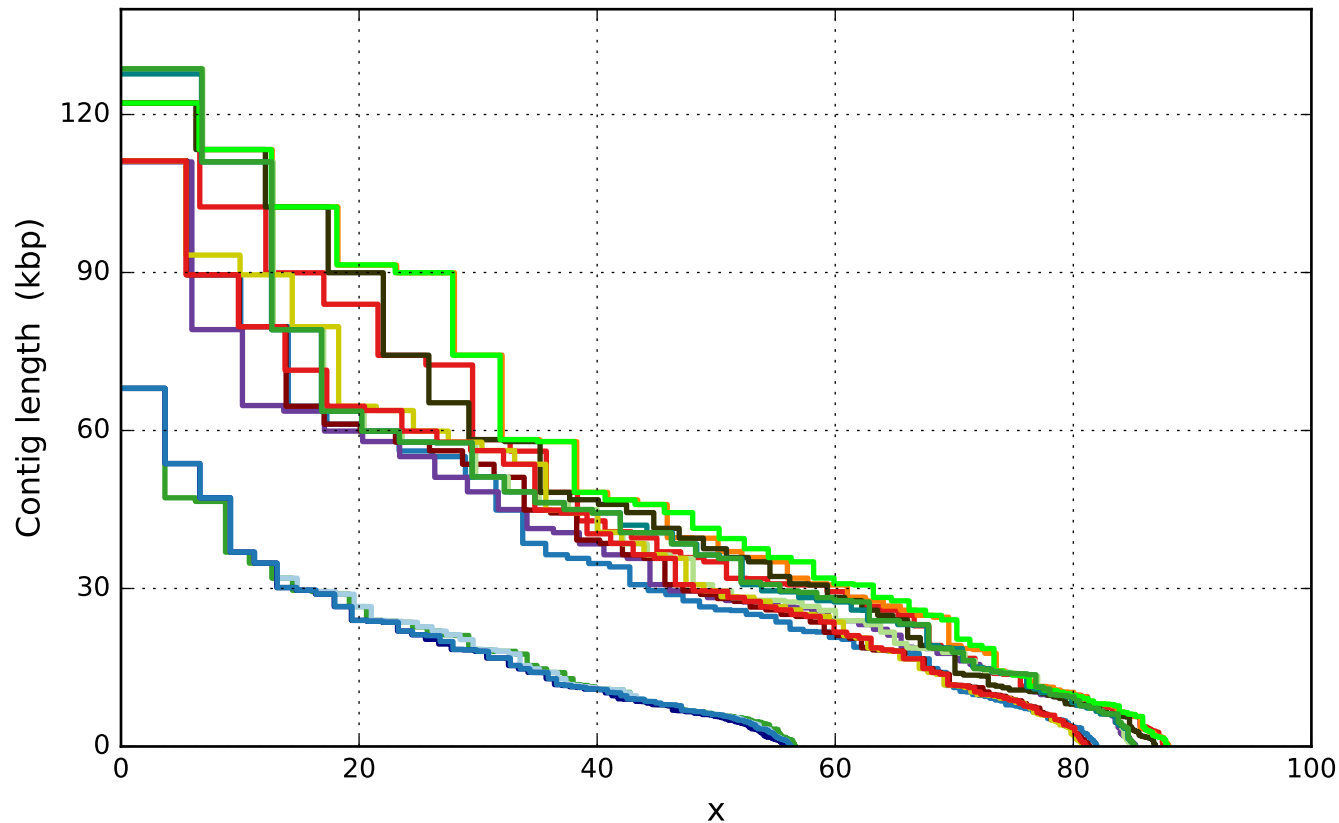
# inversions



Cumulative length (aligned contigs)



NAx



# NGAx

