Report

	canu_6hr	canu_9hr	canu_12hr	canu_all	canu_pass	miniasm_6hr	miniasm_9hr	miniasm_12hr	miniasm_all	miniasm_pass	miniasm_pass_nanopolish	PBcR_pass	SPAdes3.6_pass_and_Illumina
# contigs (>= 0 bp)	75	16	17	9	15	88	18	17	16	16	16	21	13
# contigs (>= 1000 bp)	75	16	17	9	15	88	18	17	16	16	16	21	13
# contigs (>= 5000 bp)	71	14	15	9	13	88	17	16	14	15	15	21	4
# contigs (>= 10000 bp)	59	12	11	7	11	84	16	15	12	14	13	15	3
# contigs (>= 25000 bp)	43	8	7	6	7	57	14	12	9	11	11	11	3
# contigs (>= 50000 bp)	30	7	6	6	7	36	13	12	9	10	10	11	3
Total length (>= 0 bp)	5379433	5525206	5538411	5567521	5542520	5525400	5770365	5795329	5872081	5843777	5673354	5490929	5576147
Total length (>= 1000 bp)	5379433	5525206	5538411	5567521	5542520	5525400	5770365	5795329	5872081	5843777	5673354	5490929	5576147
Total length (>= 5000 bp)	5365383	5517199	5530314	5567521	5534416	5525400	5765481	5790450	5862577	5838884	5668667	5490929	5552253
Total length (>= 10000 bp)	5275286	5499726	5497751	5553231	5519816	5499076	5758694	5783663	5850507	5832188	5652255	5440718	5545574
Total length (>= 25000 bp)	5011507	5446178	5431803	5540180	5453465	5002119	5736118	5744002	5812019	5793702	5624647	5387165	5545574
Total length (>= 50000 bp)	4527726	5398428	5382437	5540180	5453465	4289992	5686774	5744002	5812019	5768109	5599544	5387165	5545574
# contigs	75	16	17	9	15	88	18	17	16	16	16	21	13
Largest contig	675208	2791286	2779987	2714767	2782732	286427	768302	1573329	1835694	1548218	1504104	1615977	5303011
Total length	5379433	5525206	5538411	5567521	5542520	5525400	5770365	5795329	5872081	5843777	5673354	5490929	5576147
Reference length	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413
GC (%)	54.18	54.34	54.36	54.34	54.39	52.94	52.96	52.93	52.99	52.99	54.18	54.30	54.37
Reference GC (%)	54.31	54.31	54.31	54.31	54.31	54.31	54.31	54.31	54.31	54.31	54.31	54.31	54.31
N50	149559	2791286	2779987	1470967	2782732	100863	519558	586887	1542074	661959	641515	1197808	5303011
NG50	149559	1457839	1460618	1470967	1462764	98442	519558	586887	1542074	1289590	641515	1197808	5303011
N75	83603	1457839	1460618	1470967	1462764	59570	440722	441017	658193	561033	544397	401155	5303011
NG75	81954	1457839	1460618	484996	1462764	58986	440722	441017	658193	561033	544397	365932	5303011
L50	11	1	1	2	1	16	5	3	2	3	3	2	1
LG50	11	2	2	2	2	17	5	3	2	2	3	2	1
L75	23	2	2	2	2	34	8	6	4	5	5	5	1
LG75	25	2	2	3	2	35	8	6	4	5	5	6	1
# misassemblies	4	4	4	5	2	0	0	0	0	0	3	5	5
# misassembled contigs	4	4	3	1	1	0	0	0	0	0	2	3	2
Misassembled contigs length	1003837	2834370	40371	2714767	20317	0	0	0	0	0	1513926	2026976	5305242
# local misassemblies	5	23	8	7	0	0	0	0	0	0	139	37	0
# unaligned contigs	4 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	85 + 3 part	14 + 4 part	13 + 4 part	14 + 2 part	12 + 4 part	0 + 2 part	1 + 4 part	3 + 0 part
Unaligned length	33268	0	0	0	0	5524774	5769556	5794574	5871897	5843019	10848	14614	5479
Genome fraction (%)	95.922	98.973	99.088	99.549	99.255	0.011	0.015	0.013	0.003	0.013	96.930	98.510	99.352
Duplication ratio	0.998	0.999	1.001	1.001	1.000	0.994	0.998	1.008	1.005	1.009	1.046	0.995	1.004
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05
# mismatches per 100 kbp	180.87	64.12	49.17	31.09	35.35	1428.57	1356.35	801.07	1092.90	665.78	548.02	100.38	3.71
# indels per 100 kbp	1397.19	933.56	859.21	755.71	777.65	2222.22	1849.57	2136.18	546.45	1864.18	898.50	1216.68	3.60
Largest alignment	550317	2777588	2779984	1468923	2782728	305	305	305	114	305	1276039	1197735	2125655
NA50	129306	2777588	2779984	1161166	2782728	-	-	-	-	-	629654	522609	1476211
NGA50	124783	1456360	1460599	1161166	1462758	-	-	-	-	-	629654	522609	1476211
NA75	82700	1456360	1460599	484996	1462758	-	-	-	-	-	536933	365932	1002852
NGA75	76142	1456360	1460599	484996	1462758	-	-	-	-	-	536933	365932	1002852
LA50	12	1	1	3	1	-	-	-	-	-	3	3	2
LGA50	13	2	2	3	2	-	-	-	-	-	3	3	2
LA75	25	2	2	4	2	-	-	-	-	-	5	7	3
LGA75	27	2	2	4	2	-	-	-	-	-	5	7	3

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).

Gage report

	canu_6hr	canu_9hr	canu_12hr	canu_all	canu_pass	miniasm_6hr	miniasm_9hr	miniasm_12hr	miniasm_all	miniasm_pass	miniasm_pass_nanopolish	PBcR_pass	SPAdes3.6_pass_and_Illumina
Contigs #	75	16	17	9	15	88	18	17	16	16	16	21	13
Min contig	2632	3878	3960	6594	3955	5263	4884	4879	4611	4893	4687	5205	1053
Max contig	675208	2791286	2779987	2714767	2782732	286427	768302	1573329	1835694	1548218	1504104	1615977	5303011
N50	149559 COUNT: 11	1457839 COUNT: 2	1460618 COUNT: 2	1470967 COUNT: 2	1462764 COUNT: 2	98442 COUNT: 17	519558 COUNT: 5	586887 COUNT: 3	1542074 COUNT: 2	1289590 COUNT: 2	641515 COUNT: 3	1197808 COUNT: 2	5303011 COUNT: 1
Genome size	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413	5586413
Assembly size	5379433	5525206	5538411	5567521	5542520	5525400	5770365	5795329	5872081	5843777	5673354	5490929	5576147
Chaff bases	0	0	0	0	0	0	0	0	0	0	0	0	0
Missing reference bases	322789(5.78%)	85822(1.54%)	60348(1.08%)	21908(0.39%)	47924(0.86%)	5568137(99.67%)	5562907(99.58%)	5557505(99.48%)	5554417(99.43%)	5551914(99.38%)	246681(4.42%)	126260(2.26%)	165(0.00%)
Missing assembly bases	119382(2.22%)	27994(0.51%)	10090(0.18%)	3545(0.06%)	2820(0.05%)	5507563(99.68%)	5747607(99.61%)	5770194(99.57%)	5845497(99.55%)	5817178(99.54%)	262241(4.62%)	66842(1.22%)	5520(0.10%)
Missing assembly contigs	0(0.00%)	0(0.00%)	0(0.00%)	0(0.00%)	0(0.00%)	30(34.09%)	2(11.11%)	3(17.65%)	5(31.25%)	3(18.75%)	0(0.00%)	0(0.00%)	2(15.38%)
Duplicated reference bases	111582	76955	49391	72536	53225	0	0	0	0	0	86161	90739	2863
Compressed reference bases	67065	38599	23308	46529	17736	586	930	3990	6682	8965	105264	74368	14662
Bad trim	61364	1385	3426	288	495	2822889	1031583	848989	758644	711573	42160	31853	1545
Avg idy	98.07	98.68	98.80	98.92	98.92	96.48	96.38	96.37	96.45	96.36	98.41	98.35	99.99
SNPs	8162	3364	2646	1906	1952	172	211	207	224	222	20164	4737	257
Indels < 5bp	92630	68783	63229	57472	57236	462	622	715	730	757	64601	84152	273
Indels >= 5	1739	1175	890	697	663	90	150	165	170	176	1969	1777	5
Inversions	2	0	0	3	0	1	0	4	6	7	1	2	1
Relocation	9	8	3	7	7	2	5	11	7	9	22	11	9
Translocation	0	1	1	2	0	0	4	0	0	1	3	3	2
Corrected contig #	1512	1047	822	666	637	1	1	0	2	1	1453	1502	24
Corrected assembly size	5162853	5462371	5515012	5550473	5535281	613	582	0	1255	736	5167882	5345010	5591555
Min correct contig	501	505	504	504	503	613	582	2147483647	601	736	501	503	812
Max correct contig	26191	40963	53169	60723	82730	613	582	-2147483648	654	736	34047	42293	2125219
Corrected N50	4778 COUNT: 325	8556 COUNT: 193	11330 COUNT: 154	14358 COUNT: 132	14730 COUNT: 114	0 COUNT: 0	0 COUNT: 0	422 COUNT: 1	0 COUNT: 0	0 COUNT: 0	5208 COUNT: 303	5243 COUNT: 321	1284313 COUNT: 2

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).
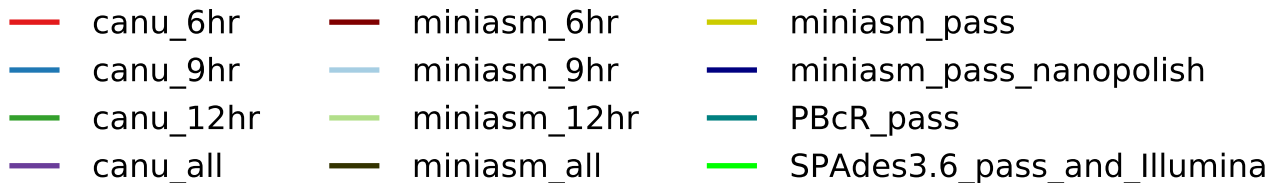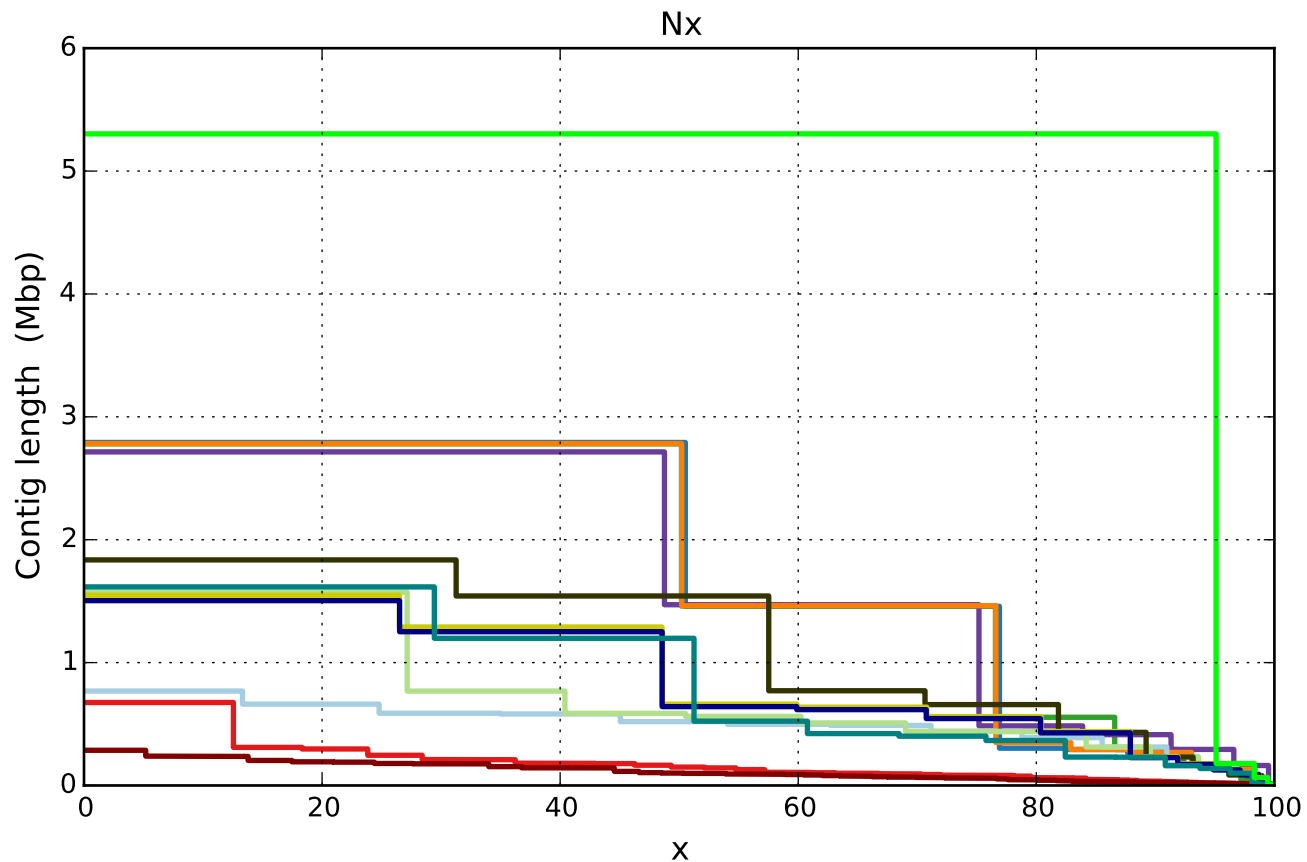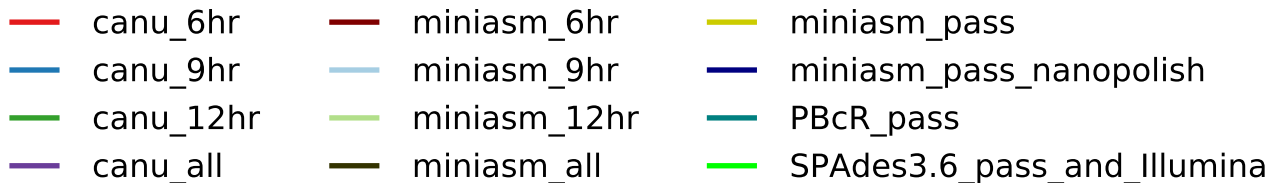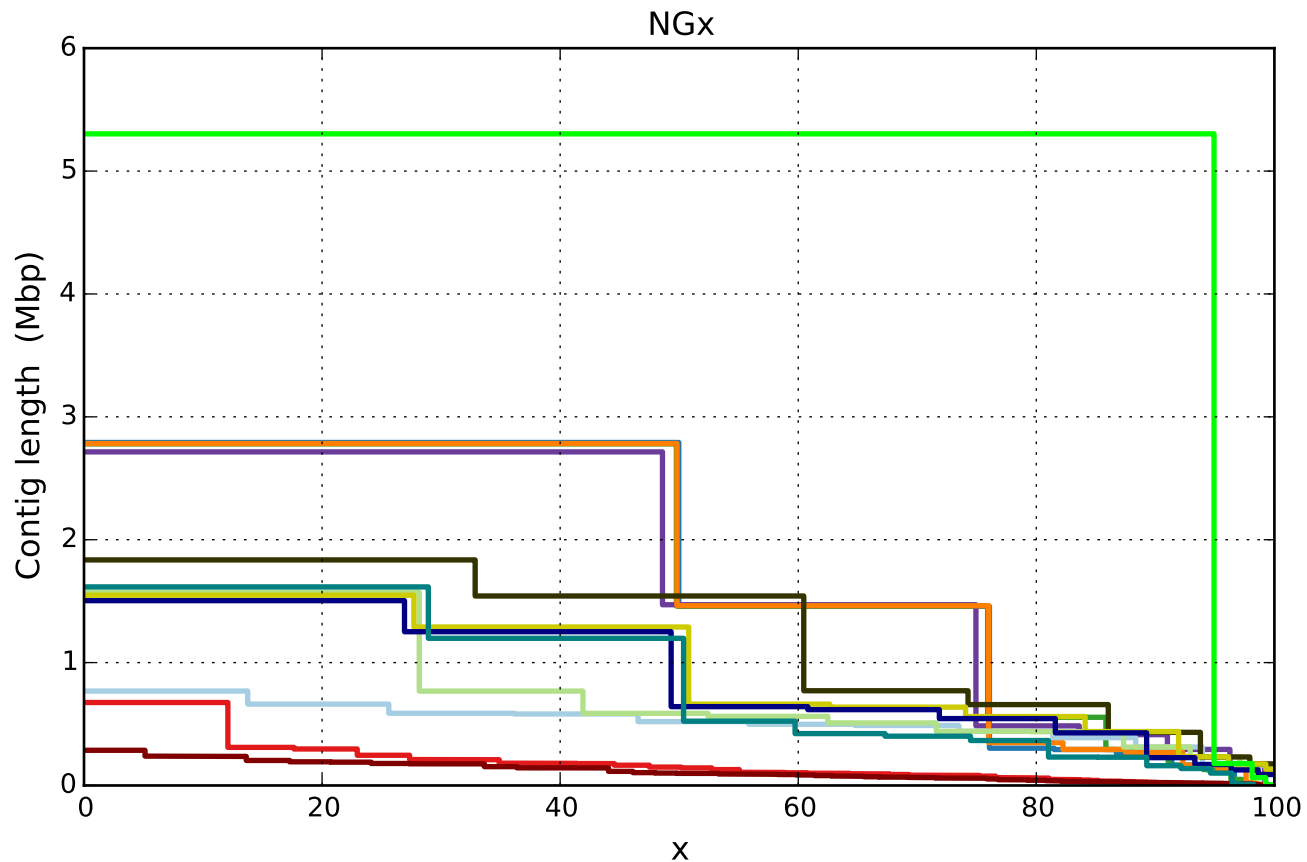
Misassemblies report

	canu_6hr	canu_9hr	canu_12hr	canu_all	canu_pass	miniasm_6hr	miniasm_9hr	miniasm_12hr	miniasm_all	miniasm_pass	miniasm_pass_nanopolish	PBcR_pass	SPAdes3.6_pass_and_Illumina
# misassemblies	4	4	4	5	2	0	0	0	0	0	3	5	5
# relocations	4	2	3	4	2	0	0	0	0	0	2	1	2
# translocations	0	2	1	1	0	0	0	0	0	0	1	4	3
# inversions	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	4	4	3	1	1	0	0	0	0	0	2	3	2
Misassembled contigs length	1003837	2834370	40371	2714767	20317	0	0	0	0	0	1513926	2026976	5305242
# local misassemblies	5	23	8	7	0	0	0	0	0	0	139	37	0
# mismatches	9692	3545	2722	1729	1960	9	11	6	2	5	29675	5524	206
# indels	74870	51617	47561	42027	43119	14	15	16	1	14	48653	66956	200
# short indels	73791	50786	46995	41570	42696	14	15	16	1	14	47801	65383	194
# long indels	1079	831	566	457	423	0	0	0	0	0	852	1573	6
Indels length	115946	80427	70369	61693	62263	20	22	24	1	23	91119	111805	482

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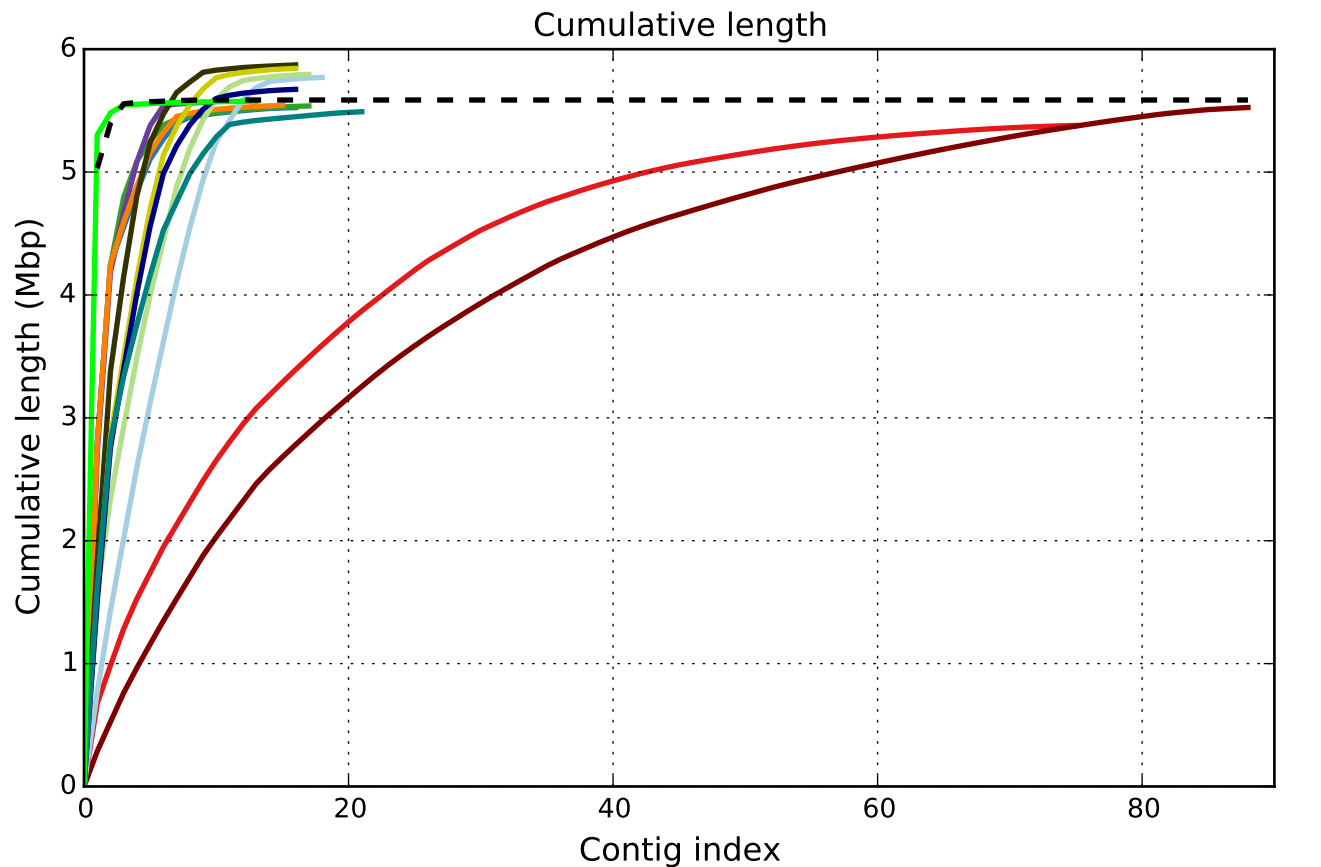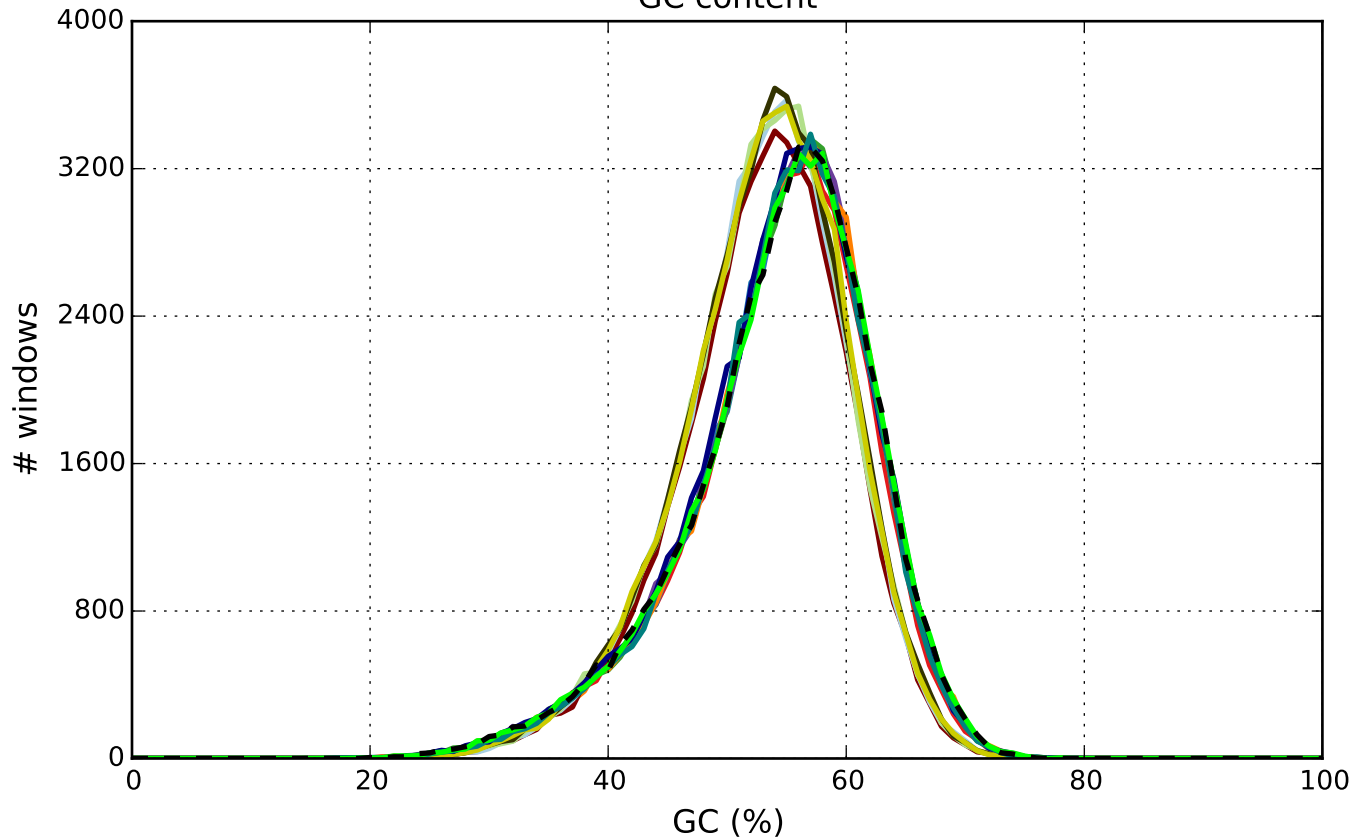(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	canu_6hr	canu_9hr	canu_12hr	canu_all	canu_pass	miniasm_6hr	miniasm_9hr	miniasm_12hr	miniasm_all	miniasm_pass	miniasm_pass_nanopolish	PBcR_pass	SPAdes3.6_pass_and_Illumina
# fully unaligned contigs	4	0	0	0	0	85	14	13	14	12	0	1	3
Fully unaligned length	33268	0	0	0	0	5346123	3584646	3436982	4781539	2892359	0	5205	5479
# partially unaligned contigs	0	0	0	0	0	3	4	4	2	4	2	4	0
# with misassembly	0	0	0	0	0	0	0	0	0	1	0	0	0
# both parts are significant	0	0	0	0	0	0	0	0	0	0	2	3	0
Partially unaligned length	0	0	0	0	0	178651	2184910	2357592	1090358	2950660	10848	9409	0
# N's	0	0	0	0	0	0	0	0	0	0	0	0	3

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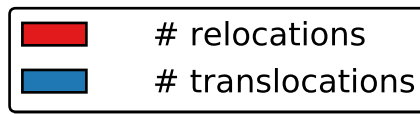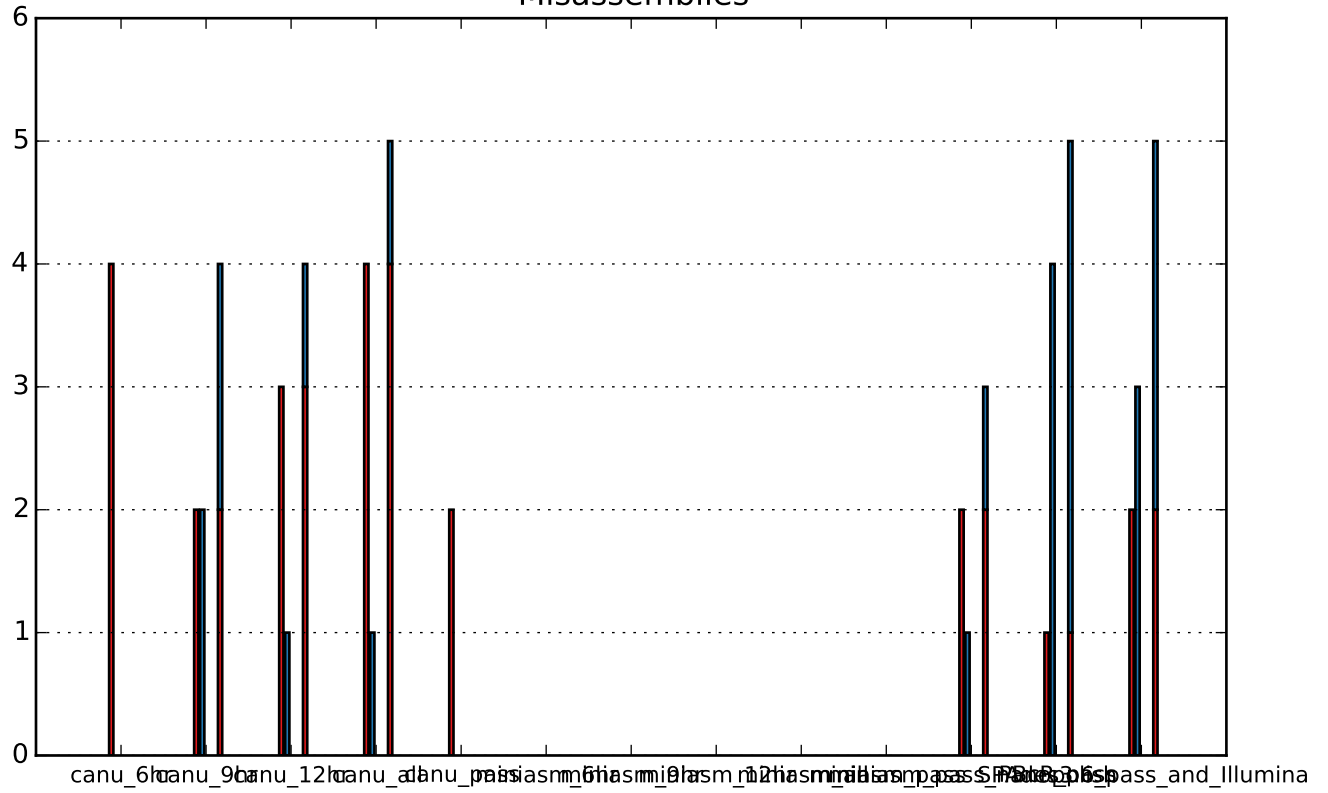(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
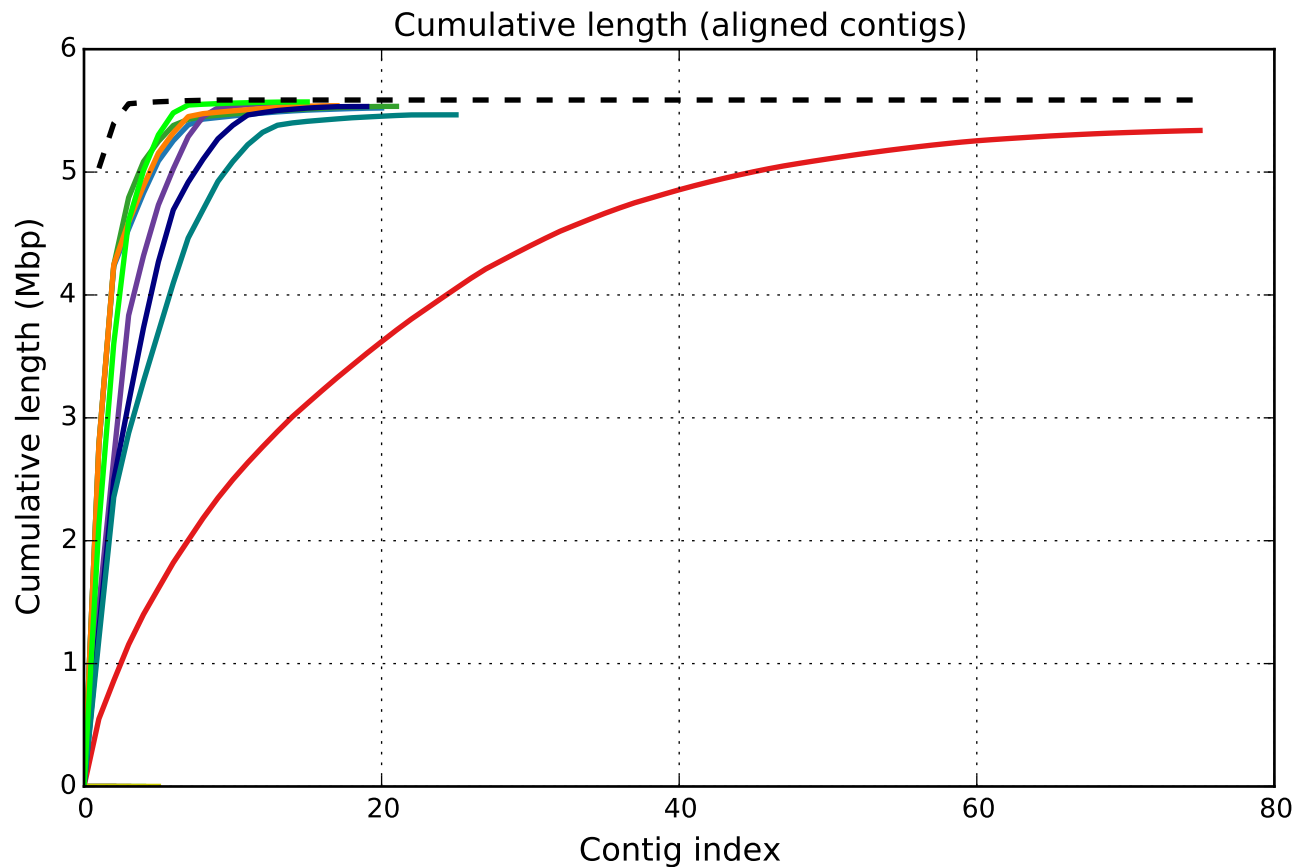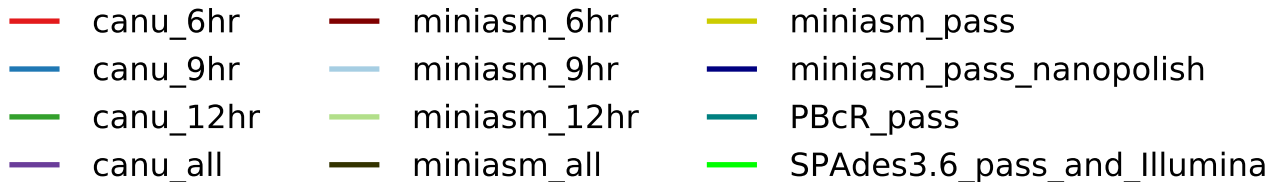
Nx

Legend:
- canu_6hr
- canu_9hr
- canu_12hr
- canu_all
- miniasm_6hr
- miniasm_9hr
- miniasm_12hr
- miniasm_all
- miniasm_pass
- miniasm_pass_nanopolish
- PBcR_pass
- SPAdes3.6_pass_and_Illumina

Cumulative length

Cumulative length (Mbp) vs Contig index

Legend:
- canu_6hr
- canu_9hr
- canu_12hr
- canu_all
- miniasm_6hr
- miniasm_9hr
- miniasm_12hr
- miniasm_all
- miniasm_pass_nanopolish
- PBcR_pass
- SPAdes3.6_pass_and_Illumina
- Reference

GC content

canu_6hr	miniasm_6hr	miniasm_pass_nanopolish
canu_9hr	miniasm_9hr	PBcR_pass
canu_12hr	miniasm_12hr	SPAdes3.6_pass_and_Illumina
canu_all	miniasm_all	Reference

Misassemblies

Legend:
- # relocations
- # translocations

x-axis labels: canu_6h, canu_9h, canu_12h, canu_all, canu_pass, miniasm_6h, miniasm_9h, miniasm_12h, miniasm_all, miniasm_pass, SMARTdenovo, PBcR, Falcon, smis_fish, pass_and_Illumina

Cumulative length (aligned contigs)

canu_6hr	miniasm_6hr	miniasm_pass_nanopolish
canu_9hr	miniasm_9hr	PBcR_pass
canu_12hr	miniasm_12hr	SPAdes3.6_pass_and_Illumina
canu_all	miniasm_all	Reference

Genome fraction, %

Legend:
- canu_6hr
- canu_9hr
- canu_12hr
- canu_all
- miniasm_6hr
- miniasm_9hr
- miniasm_12hr
- miniasm_all
- miniasm_pass
- miniasm_pass_nanopolish
- PBcR_pass
- SPAdes3.6_pass_and_Illumina