

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	illumina_only
# contigs (>= 0 bp)	75	16	17	9	15	88	18	17	16	16	16	21	13	90
# contigs (>= 1000 bp)	75	16	17	9	15	88	18	17	16	16	16	21	13	83
# contigs (>= 5000 bp)	71	14	15	9	13	88	17	16	14	15	15	21	4	63
# contigs (>= 10000 bp)	59	12	11	7	11	84	16	15	12	14	13	15	3	52
# contigs (>= 25000 bp)	43	8	7	6	7	57	14	12	9	11	11	11	3	43
# contigs (>= 50000 bp)	30	7	6	6	7	36	13	12	9	10	10	11	3	35
Total length (>= 0 bp)	5379433	5525206	5538411	5567521	5542520	5525400	5770365	5795329	5872081	5843777	5673354	5490929	5576147	5454767
Total length (>= 1000 bp)	5379433	5525206	5538411	5567521	5542520	5525400	5770365	5795329	5872081	5843777	5673354	5490929	5576147	5450142
Total length (>= 5000 bp)	5365383	5517199	5530314	5567521	5534416	5525400	5765481	5790450	5862577	5838884	5668667	5490929	5552253	5397674
Total length (>= 10000 bp)	5275286	5499726	5497751	5553231	5519816	5499076	5758694	5783663	5850507	5832188	5652255	5440718	5545574	5322905
Total length (>= 25000 bp)	5011507	5446178	5431803	5540180	5453465	5002119	5736118	5744002	5812019	5793702	5624647	5387165	5545574	5183775
Total length (>= 50000 bp)	4527726	5398428	5382437	5540180	5453465	4289992	5686774	5744002	5812019	5768109	5599544	5387165	5545574	4893423
# contigs	75	16	17	9	15	88	18	17	16	16	16	21	13	87
Largest contig	675208	2791286	2779987	2714767	2782732	286427	768302	1573329	1835694	1548218	1504104	1615977	5303011	686305
Total length	5379433	5525206	5538411	5567521	5542520	5525400	5770365	5795329	5872081	5843777	5673354	5490929	5576147	5453647
Reference length	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045
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	54.40
Reference GC (%)	54.30	54.30	54.30	54.30	54.30	54.30	54.30	54.30	54.30	54.30	54.30	54.30	54.30	54.30
N50	149559	2791286	2779987	1470967	2782732	100863	519558	586887	1542074	661959	641515	1197808	5303011	153115
NG50	149559	1457839	1460618	1470967	1462764	98442	519558	586887	1542074	1289590	641515	1197808	5303011	153115
N75	83603	1457839	1460618	1470967	1462764	59570	440722	441017	658193	561033	544397	401155	5303011	79102
NG75	81954	1457839	1460618	484996	1462764	58986	440722	441017	658193	561033	544397	365932	5303011	72689
L50	11	1	1	2	1	16	5	3	2	3	3	2	1	10
LG50	11	2	2	2	2	17	5	3	2	2	3	2	1	10
L75	23	2	2	2	2	34	8	6	4	5	5	5	1	23
LG75	25	2	2	3	2	35	8	6	4	5	5	6	1	24
# misassemblies	4	4	4	4	2	0	0	0	0	0	3	5	5	6
# misassembled contigs	4	4	3	1	1	0	0	0	0	0	2	3	2	6
Misassembled contigs length	1003837	2834370	40371	2714767	20317	0	0	0	0	0	1513926	2026976	5305242	1260503
# local misassemblies	5	23	8	7	0	0	0	0	0	0	139	37	0	10
# 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	0 + 0 part
Unaligned length	33268	0	0	0	0	5524774	5769556	5794574	5871897	5843019	13909	14614	5479	0
Genome fraction (%)	95.942	98.879	99.077	99.550	99.236	0.011	0.015	0.013	0.003	0.013	96.861	98.446	99.288	97.370
Duplication ratio	0.997	1.000	1.000	1.000	0.999	0.994	0.998	1.008	1.005	1.009	1.045	0.995	1.004	1.002
# 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	134.42
# mismatches per 100 kbp	179.15	64.01	48.61	30.76	34.94	1428.57	1356.35	801.07	1092.90	665.78	548.43	100.38	3.71	3.55
# indels per 100 kbp	1393.43	931.47	858.23	757.00	776.90	2222.22	1849.57	2136.18	546.45	1864.18	898.70	1216.68	3.53	3.22
Largest alignment	550317	2777588	2779984	1468923	2782728	305	305	305	114	305	1276039	1197735	2125655	372132
NA50	129306	2777588	2779984	1161166	2782728	-	-	-	-	-	629654	522609	1476211	152838
NGA50	124783	1456360	1460599	1161166	1462758	-	-	-	-	-	629654	522609	1476211	131571
NA75	82700	1456360	1460599	484996	1462758	-	-	-	-	-	536933	365932	1002852	72670
NGA75	76142	1456360	1460599	484996	1462758	-	-	-	-	-	536933	365932	1002852	65092
LA50	12	1	1	3	1	-	-	-	-	-	3	3	2	11
LGA50	13	2	2	3	2	-	-	-	-	-	3	3	2	12
LA75	25	2	2	4	2	-	-	-	-	-	5	7	3	25
LGA75	27	2	2	4	2	-	-	-	-	-	5	7	3	27

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	Illumina_only
Contigs #	75	16	17	9	15	88	18	17	16	16	16	21	13	87
Min contig	2632	3878	3960	6594	3955	5263	4884	4879	4611	4893	4687	5205	1053	759
Max contig	675208	2791286	2779987	2714767	2782732	286427	768302	1573329	1835694	1548218	1504104	1615977	5303011	686305
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	153115 COUNT: 10
Genome size	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045	5590045
Assembly size	5379433	5525206	5538411	5567521	5542520	5525400	5770365	5795329	5872081	5843777	5673354	5490929	5576147	5453647
Chaff bases	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Missing reference bases	322789(5.77%)	85838(1.54%)	60348(1.08%)	21916(0.39%)	47940(0.86%)	5571447(99.67%)	5566418(99.58%)	5561016(99.48%)	5557886(99.42%)	5555425(99.38%)	246681(4.41%)	126280(2.26%)	165(0.00%)	20958(0.37%)
Missing assembly bases	119382(2.22%)	27994(0.51%)	10093(0.18%)	3529(0.06%)	2820(0.05%)	5507231(99.67%)	5747484(99.60%)	5770071(99.56%)	5845278(99.54%)	5817055(99.54%)	262394(4.63%)	66624(1.21%)	5520(0.10%)	7432(0.14%)
Missing assembly contigs	0(0.00%)	0(0.00%)	0(0.00%)	0(0.00%)	0(0.00%)	29(32.95%)	2(11.11%)	3(17.65%)	5(31.25%)	3(18.75%)	0(0.00%)	0(0.00%)	2(15.38%)	0(0.00%)
Duplicated reference bases	116033	76955	48641	72046	50315	0	0	0	0	0	86008	93451	2863	1025
Compressed reference bases	63488	31257	33484	53566	19133	586	930	3990	6631	9303	110428	78346	25390	129989
Bad trim	61367	1385	3429	279	483	2857689	1022656	840062	724628	702631	42313	31663	1545	0
Avg idy	98.07	98.68	98.80	98.92	98.92	96.46	96.38	96.37	96.46	96.36	98.41	98.35	99.99	99.99
SNPs	8151	3364	2656	1915	1950	174	214	210	225	225	20164	4748	254	142
Indels < 5bp	92483	68853	63307	57616	57224	476	624	717	735	760	64601	84174	263	197
Indels >= 5	1739	1175	890	697	663	91	149	165	167	175	1969	1777	5	31
Inversions	2	0	0	3	0	1	0	4	8	7	1	3	1	2
Relocation	10	9	4	9	8	2	6	12	8	10	23	12	11	19
Translocation	2	1	1	1	1	0	5	1	1	2	3	3	2	2
Corrected contig #	1514	1048	823	667	640	1	1	0	2	1	1454	1503	26	137
Corrected assembly size	5171157	5462316	5515352	5547559	5538224	613	582	0	1255	736	5167882	5345064	5595517	5454719
Min correct contig	501	505	504	504	503	613	582	2147483647	601	736	501	503	812	505
Max correct contig	26191	40963	48830	60723	82730	613	582	-2147483648	654	736	34047	42293	2125219	316649
Corrected N50	4799 COUNT: 324	8540 COUNT: 194	11330 COUNT: 155	14358 COUNT: 132	14730 COUNT: 115	0 COUNT: 0	0 COUNT: 0	422 COUNT: 1	0 COUNT: 0	0 COUNT: 0	5201 COUNT: 304	5243 COUNT: 321	1284313 COUNT: 2	90683 COUNT: 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

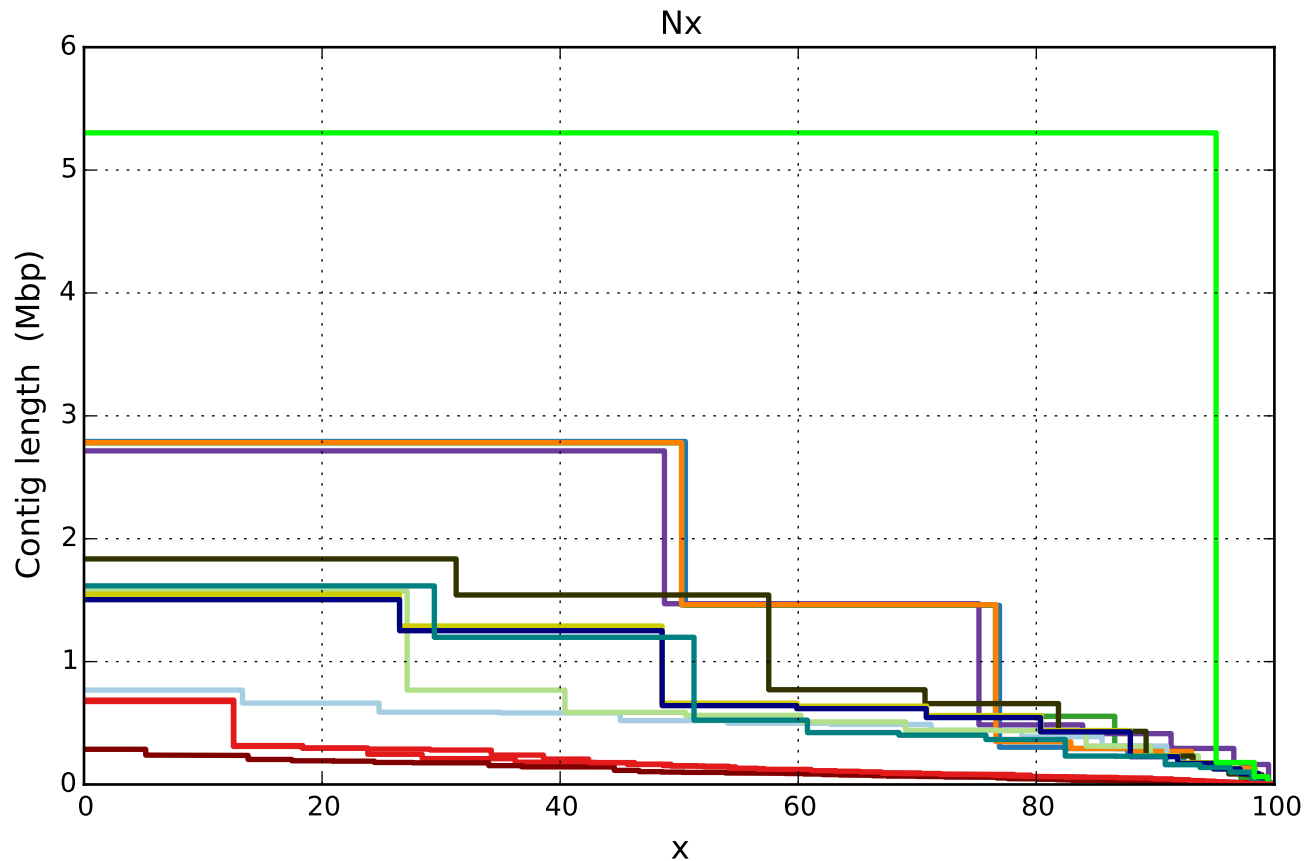
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# misassemblies	4	4	4	4	2	0	0	0	0	0	3	5	5	6
# relocations	4	2	3	3	2	0	0	0	0	0	2	1	2	4
# translocations	0	2	1	1	0	0	0	0	0	0	1	4	3	2
# inversions	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	4	4	3	1	1	0	0	0	0	0	2	3	2	6
Misassembled contigs length	1003837	2834370	40371	2714767	20317	0	0	0	0	0	1513926	2026976	5305242	1260503
# local misassemblies	5	23	8	7	0	0	0	0	0	0	139	37	0	10
# mismatches	9608	3538	2692	1712	1938	9	11	6	2	5	29695	5524	206	193
# indels	74732	51486	47533	42126	43097	14	15	16	1	14	48661	66956	196	175
# short indels	73651	50655	46965	41669	42673	14	15	16	1	14	47808	65383	190	145
# long indels	1081	831	568	457	424	0	0	0	0	0	853	1573	6	30
Indels length	115810	80253	70368	61844	62262	20	22	24	1	23	91120	111805	477	1047

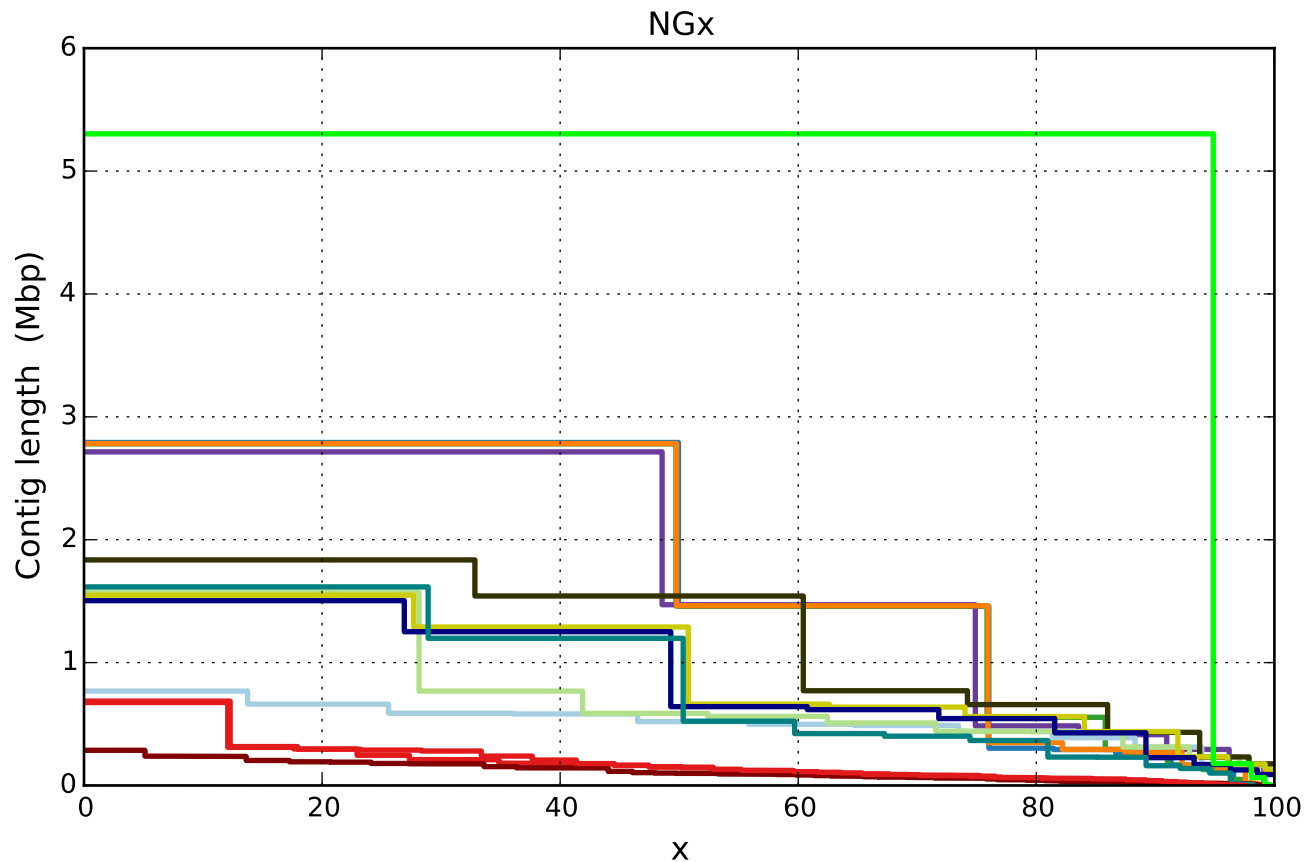
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

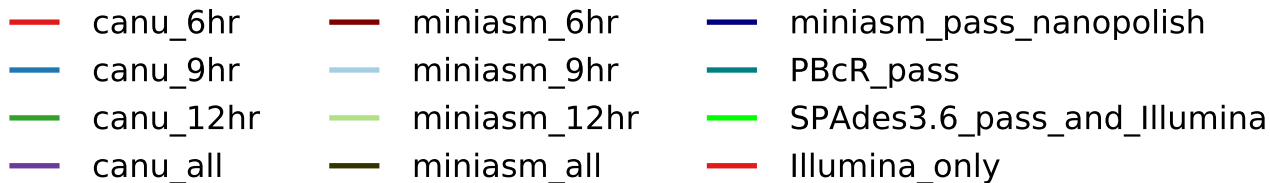
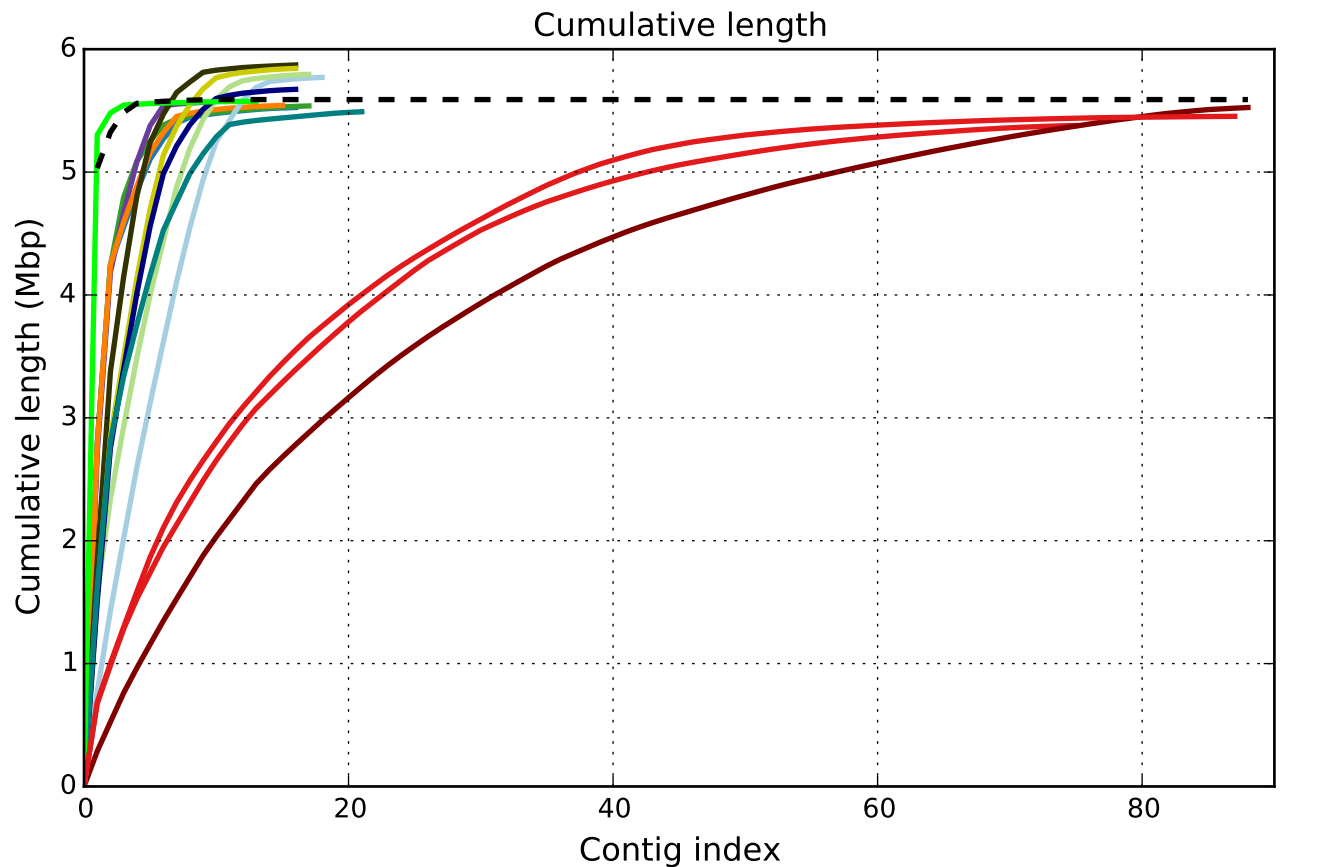
Unaligned report

	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	Illumina_only
# fully unaligned contigs	4	0	0	0	0	85	14	13	14	12	0	1	3	0
Fully unaligned length	33268	0	0	0	0	5346123	3584646	3436982	4781539	2892359	0	5205	5479	0
# partially unaligned contigs	0	0	0	0	0	3	4	4	2	4	2	4	0	0
# with misassembly	0	0	0	0	0	0	0	0	0	1	0	0	0	0
# both parts are significant	0	0	0	0	0	0	0	0	0	0	2	3	0	0
Partially unaligned length	0	0	0	0	0	178651	2184910	2357592	1090358	2950660	13909	9409	0	0
# N's	0	0	0	0	0	0	0	0	0	0	0	0	3	7331

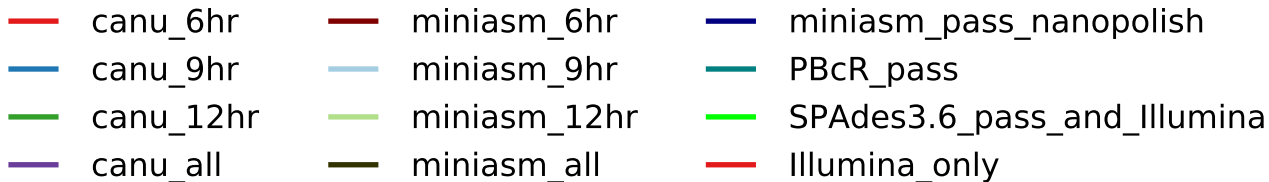
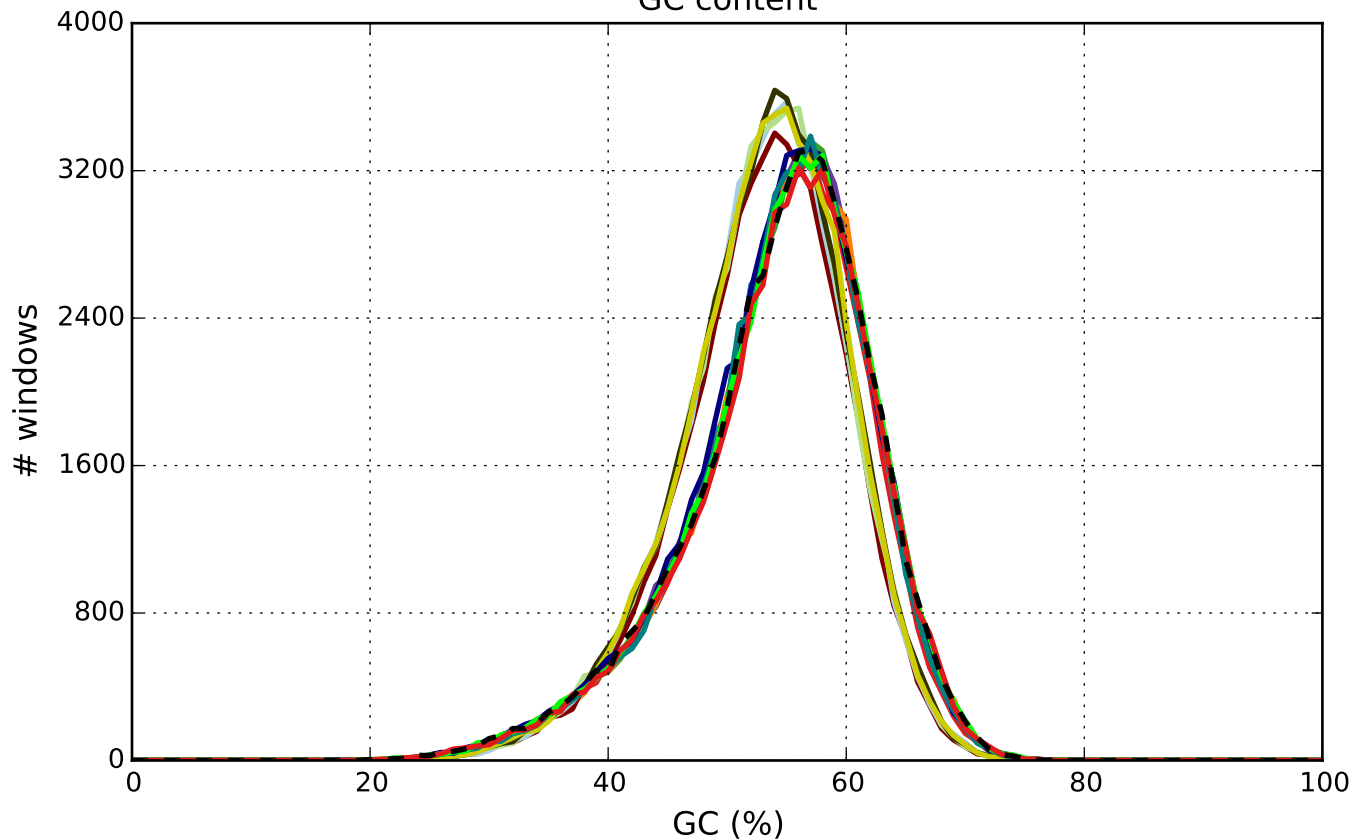
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



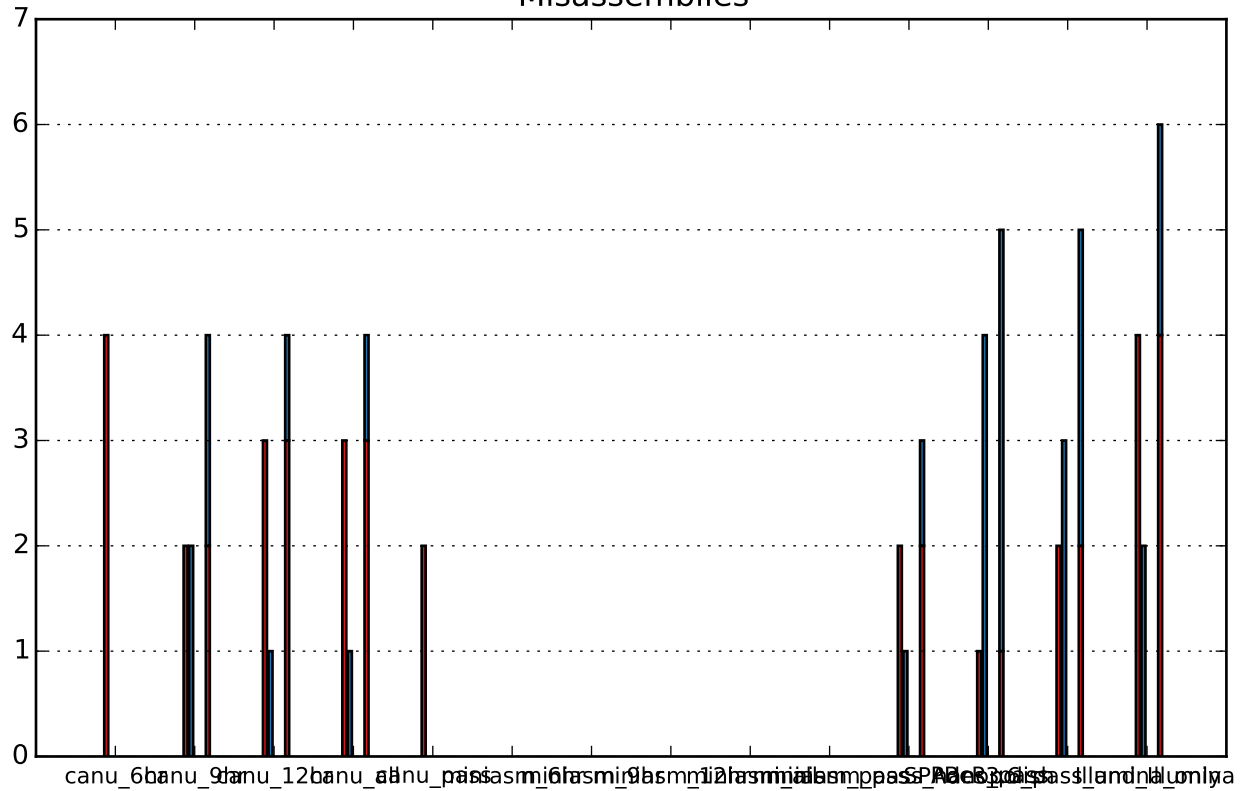


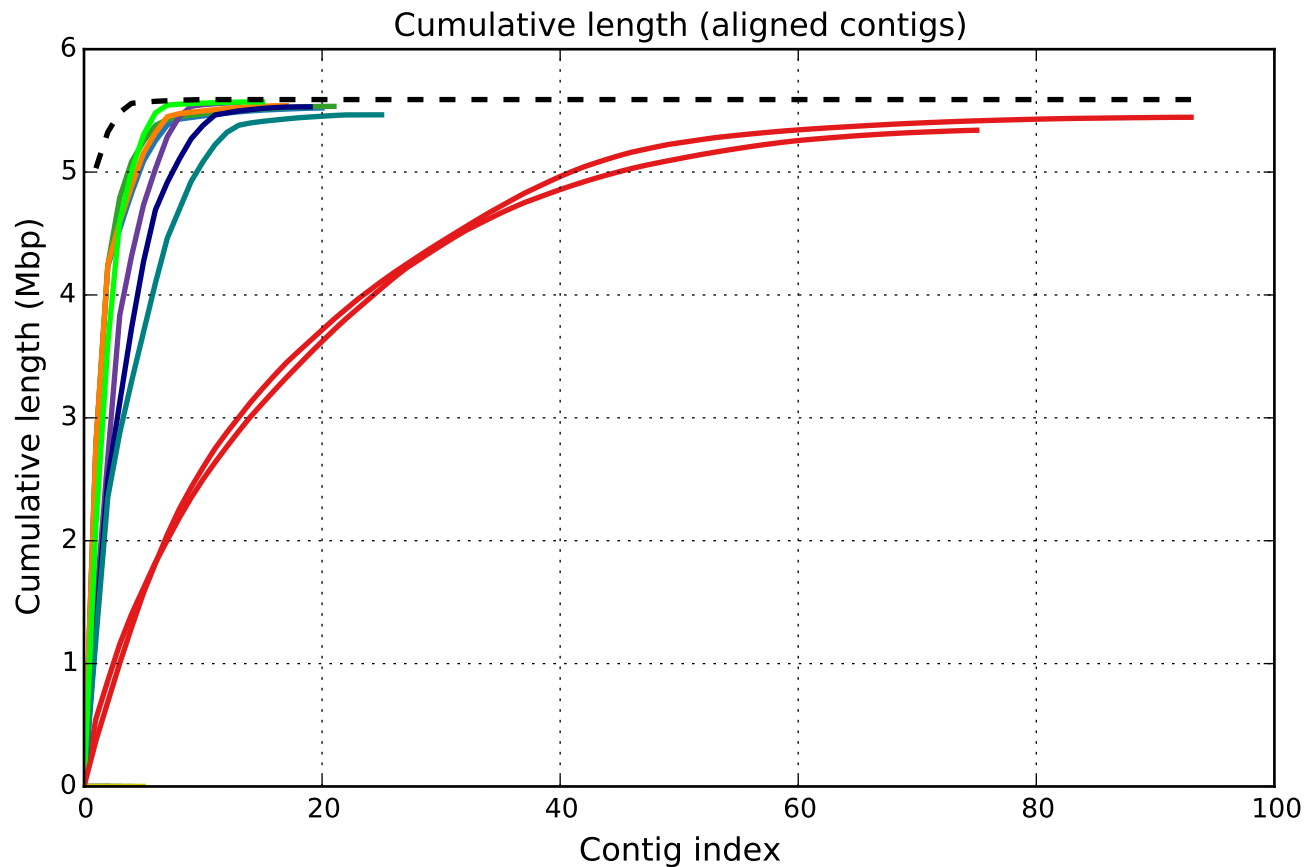


GC content

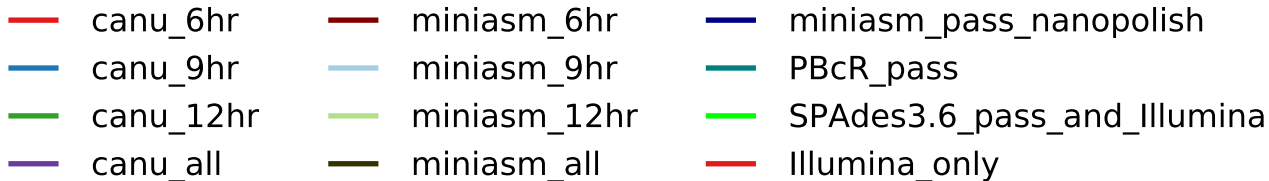
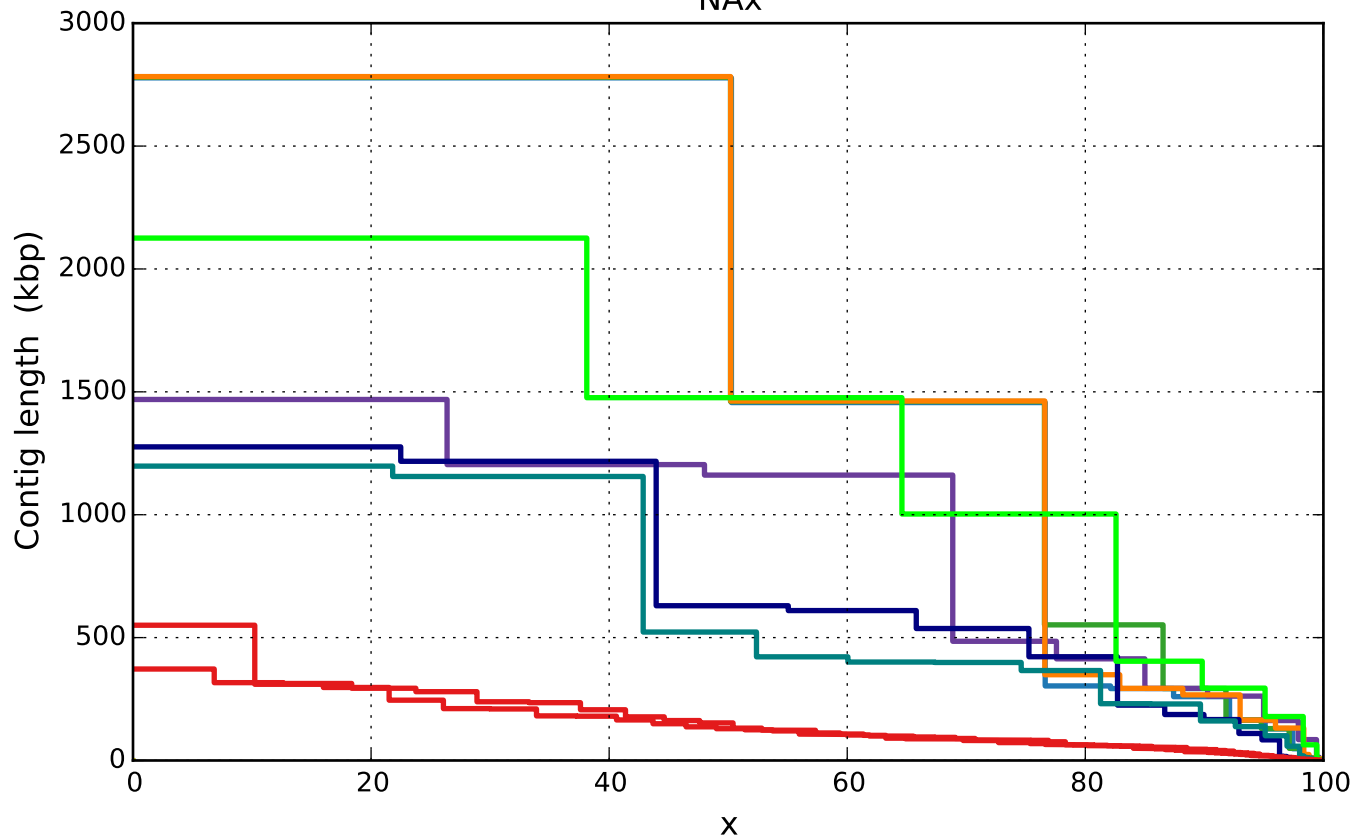


Misassemblies

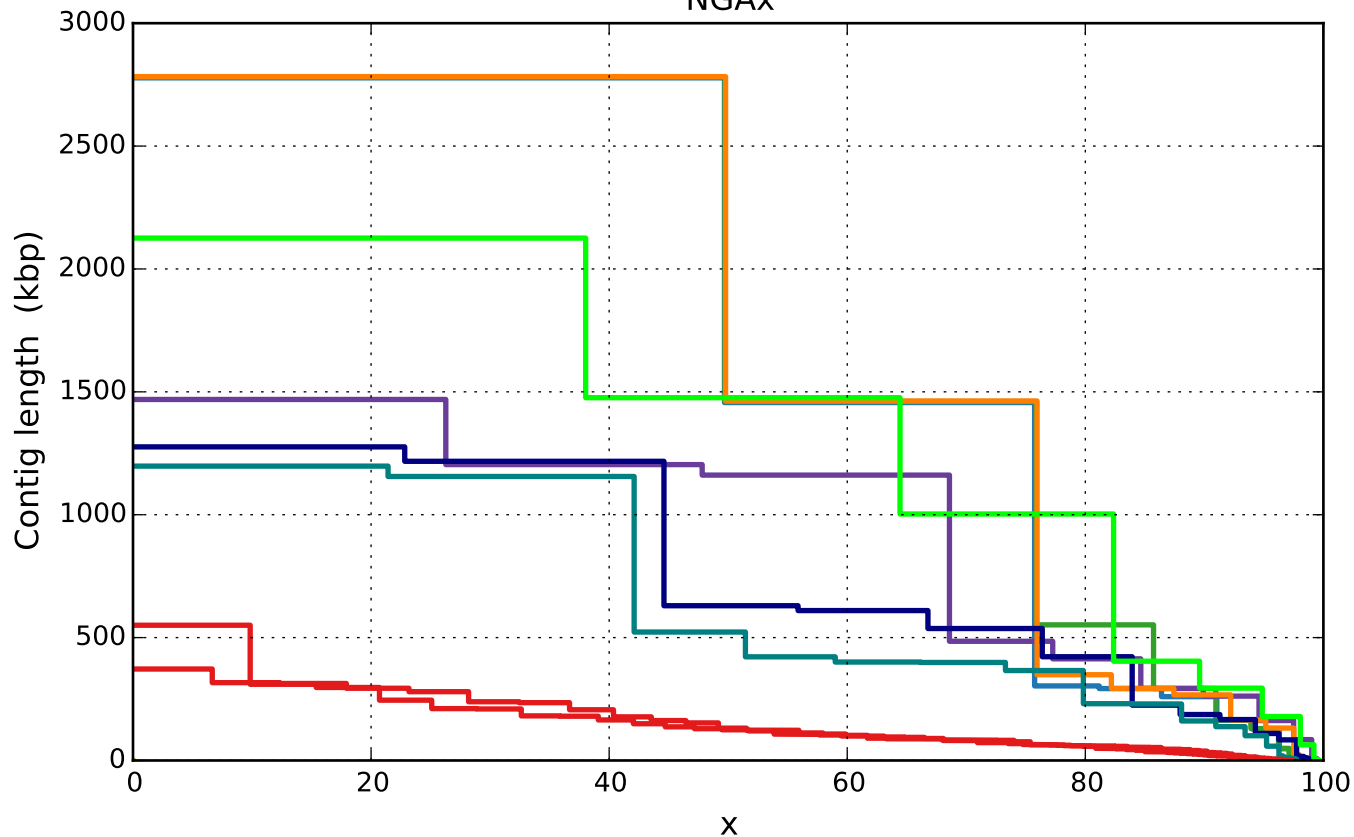




NAX



NGAx



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|------------------------------------------------|--------------------------------------------------------|------------------------------------------------------------------------|
| — 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 | — Illumina_only |

