



Type		Read Coverage		Assembly	Pipeline Full Information
		Short	Long		
Genome Assembly	Long Read Only		40	CanuH	Canu full pipeline - 40X coverage long reads
			20	CanuL	Canu full pipeline - 20X coverage long reads
			40	MiniCH	Mini pipeline with read correction - Minimap+Racon+Minimap+Miniasm+Minimap+Racon - 40X coverage long reads
			20	MiniCL	Mini pipeline with read correction - Minimap+Racon+Minimap+Miniasm+Minimap+Racon - 20X coverage long reads
			40	MiniH	Mini pipeline without read correction - Minimap+Miniasm+Minimap+Racon - 40X coverage long reads
			20	MiniL	Mini pipeline without read correction - Minimap+Miniasm+Minimap+Racon - 20X coverage long reads
	Short Read Only	40		SGAH	SGA pipeline - 40X coverage short reads
		20		SGAL	SGA pipeline - 20X coverage short reads
		40		SoDe2H	SOAPdenovo2 pipeline - 40X coverage short reads
		20		SoDe2L	SOAPdenovo2 pipeline - 20X coverage short reads
		40		SpadesH	Spades pipeline for short read only assembly - 40X coverage short reads
		20		SpadesL	Spades pipeline for short read only assembly - 20X coverage short reads
	Hybrid Method	40	20	SpadesLRL	Spades Hybrid pipeline using long reads to improve contiguity - 40X short read and 20X long read coverage
		40	20	Colormap	20X long read are corrected by 40X shortread using colormap and the corrected reads are given to Canu as corrected reads
		40	40	CanuH.p1	Canu pipeline with 40X long reads + polishing once with 40X short reads using BWA+Pilon
		40	40	MiniH.p1	Mini pipeline with 40X long reads + polishing once with 40X short reads using BWA+Pilon
		40	40	MiniH.p2	Mini pipeline with 40X long reads + polishing twice with 40X short reads using BWA+Pilon
		40	40	MiniH.p3	Mini pipeline with 40X long reads + polishing thrice with 40X short reads using BWA+Pilon
Long Read Error Correction	Long Read Only		40	CanuH.cr	40X long reads corrected by Canu correction module
			20	CanuL.cr	20X long reads corrected by Canu correction module
			40	MiniCH.cr	40X long reads corrected by Minimap+Racon
			20	MiniCL.cr	20X long reads corrected by Minimap+Racon
	Hybrid	40	20	Colormap.cr	20X long reads corrected by colormap using 40X short reads

AJ055 (~5.5Mbp genome - real dataset)

		Long read only assembly						Short read only assembly						Hybrid assembly						
	Pipeline info	Canu		MiniC		MiniH		SGA		SOAPdenovo2		Spades		Spades	Colormap	Canu+pilon	Mini+pilon			Metasm
	Coverage	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X long	20X short	40X long reads 40X short reads				
	Assembly	CanuH	CanuL	MiniCH	MiniCL	MiniH	MiniL	SGAH	SGAL	SoDe2H	SoDe2L	SpadesH	SpadesL	SpadesLRL	Colormap	CanuH.p1	MiniH.p1	MiniH.p2	MiniH.p3	Metasm
Statistics with reference	Genome fraction (%)	99.877	99.785	99.999	98.626	99.934	97.962	97.757	97.119	27.577	55.537	99.131	98.932	99.882	97.625	99.877	99.939	99.939	99.939	99.877
	Duplication ratio	1	1.003	1.005	1.007	1.005	1.009	1.024	1.015	1.011	1.005	1	1.001	1	1.094	1	1	1	1	1
	Largest alignment	5496967	3169756	5529367	1138217	5529303	833675	37194	33813	3463	4124	585792	342668	1587076	504450	5497400	5500863	5501187	5501107	5496967
	Total aligned length	5498061	5506645	5530466	5467427	5530402	5435975	5508142	5427729	1521547	3069319	5458002	5447750	5498433	5871337	5498494	5501955	5502281	5502201	5498061
	NG50	5496970	3169885	5529667	470381	5534010	455694	6594	7167		589	226024	164005	1571477	305685	5497403	5505273	5505584	5505476	5496970
	NG75	5496970	1809348	5529667	298434	5534010	353027	3728	4097			163120	89646	552169	132047	5497403	5505273	5505584	5505476	5496970
	NA50	5496967	3169756	5529367	470380	5529303	455694	6096	6988	714	875	226024	164005	1571477	218907	5497400	5500863	5501187	5501107	5496967
	NA75	5496967	688559	5529367	298434	5529303	243400	3240	3760	575	645	163120	86634	552169	81683	5497400	5500863	5501187	5501107	5496967
	NGA50	5496967	3169756	5529367	470380	5529303	455694	6296	7092		568	226024	164005	1571477	305685	5497400	5500863	5501187	5501107	5496967
	NGA75	5496967	1120789	5529367	298434	5529303	351127	3474	3879			163120	89646	552169	130178	5497400	5500863	5501187	5501107	5496967
	LG50	1	1	1	4	1	5	249	237		2801	9	12	2	7	1	1	1	1	1
	LG75	1	2	1	7	1	8	524	490			16	23	4	15	1	1	1	1	1
	LA50	1	1	1	4	1	5	272	247	813	1240	9	12	2	8	1	1	1	1	1
	LA75	1	3	1	7	1	9	587	519	1447	2305	16	24	4	19	1	1	1	1	1
	LGA50	1	1	1	4	1	5	258	241		2900	9	12	2	7	1	1	1	1	1
	LGA75	1	2	1	7	1	8	550	503			16	23	4	15	1	1	1	1	1
Misassemblies	No of local misassemblies	0	1	1	2	5	4	0	0	548	197	11	17	1	12	0	2	2	1	0
	No of unaligned mis. contigs	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Mismatches	No of mismatches per 100 kbp	0.27	6.28	15.03	34.91	29.62	49.96	0.06	0.24	1.71	2.78	5.22	7.09	5.57	24.7	0	1.04	0.69	0.8	0.27
	No of indels per 100 kbp	34.76	165.41	330.97	639.88	466.43	726.07	0.59	0.47	1.91	1.01	1.45	1.4	1.75	8.04	2.58	55.57	8.05	7.82	34.76
	No of N's per 100 kbp	0	0	0	0	0	0	0	0	578.49	95.3	17.33	25.66	1.77	0	0	0	0	0	0
Statistics without referen	No of contigs	4	9	2	16	2	18	1370	1228	2124	3607	64	103	16	73	4	2	2	2	4
	Largest contig	5496970	3169885	5529667	1138302	5534010	833810	37194	33813	3463	4124	585792	342678	1845647	509223	5497403	5505273	5505584	5505476	5496970
	Total length	5727073	5728738	5696122	5634250	5700578	5602098	5670252	5585990	1618182	3190953	5621063	5611391	5663299	6030828	5727525	5670982	5671342	5671230	5727073
	N50	5496970	3169885	5529667	470381	5534010	455694	6394	7111	751	907	226024	164005	1571477	218907	5497403	5505273	5505584	5505476	5496970
	N75	5496970	1809348	5529667	298434	5534010	243471	3500	3969	603	672	163120	86650	552169	104347	5497403	5505273	5505584	5505476	5496970
	L50	1	1	1	4	1	5	262	243	779	1204	9	12	2	8	1	1	1	1	1
	L75	1	2	1	7	1	9	559	505	1384	2230	16	24	4	18	1	1	1	1	1
	GC (%)	57.18	57.14	57.21	57.13	57.19	57.17	57.39	57.5	54.53	56.21	57.28	57.32	57.25	57.27	57.19	57.24	57.23	57.23	57.18

AJ218 (~5.5Mbp genome - real dataset)

		Long read only assembly						Short read only assembly						Hybrid assembly					
	Pipeline info	Canu		MiniC		MiniH		SGA		SOAPdenovo2		Spades		Spades	Canu+pilon	Mini+pilon			Metasm
	Coverage	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X L 20X S	40X long reads 40X short reads				
	Assembly	CanuH	CanuL	MiniCH	MiniCL	MiniH	MiniL	SGAH	SGAL	SoDe2H	SoDe2L	SpadesH	SpadesL	SpadesLRL	CanuH.p1	MiniH.p1	MiniH.p2	MiniH.p3	Metasm
Statistics with reference	Genome fraction (%)	99.905	99.759	99.977	99.273	99.978	98.857	97.384	96.726	33.369	58.833	98.766	98.683	99.887	99.905	99.994	100	100	99.905
	Duplication ratio	1.002	1.002	1.006	1.009	1.007	1.008	1.021	1.013	1.013	1.005	1.001	1.001	1.003	1.002	1.002	1.002	1.002	1.69
	Largest alignment	5460340	1804543	5049176	1163455	5488283	1150331	33112	48400	3250	4511	524880	369879	1511928	5460804	5464934	5466181	5466142	5244427
	Total aligned length	5473703	5464844	5496411	5472727	5500551	5447535	5437178	5355772	1828053	3229100	5402362	5398386	5474706	5474167	5477150	5478396	5478358	9228948
	NG50	5460449	1353042	5485519	615749	5488527	610819	7143	7778		631	158473	109857	946530	5460804	5464938	5466185	5466146	9215694
	NG75	5460449	533216	5485519	459808	5488527	496782	3981	4365			71228	55877	454623	5460804	5464938	5466185	5466146	9215694
	NA50	5460340	1353042	5049176	610591	5488283	606793	6581	7326	738	908	158473	102472	946530	5460804	5464934	5466181	5466142	5244427
	NA75	5460340	533216	5049176	459808	5488283	496779	3400	3885	590	666	68894	46985	329188	5460804	5464934	5466181	5466142	3299401
	NGA50	5460340	1353042	5049176	610591	5488283	606793	6968	7452		604	158473	109857	946530	5460804	5464934	5466181	5466142	5244427
	NGA75	5460340	533216	5049176	459808	5488283	496779	3707	4011			71228	48179	454623	5460804	5464934	5466181	5466142	5244427
	LG50	1	2	1	3	1	3	243	219		2637	11	16	3	1	1	1	1	1
	LG75	1	4	1	6	1	6	501	452			23	35	4	1	1	1	1	1
	LA50	1	2	1	3	1	3	258	228	935	1263	11	17	3	1	1	1	1	1
	LA75	1	4	1	6	1	6	551	483	1661	2348	24	37	5	1	1	1	1	2
	LGA50	1	2	1	3	1	3	246	224		2703	11	16	3	1	1	1	1	1
	LGA75	1	4	1	6	1	6	518	470			23	35	4	1	1	1	1	1
Misassemblies	No of local misassemblies	1	0	4	10	7	10	0	0	733	137	10	9	0	0	1	0	0	1
	No of unaligned mis. contigs	1	1	1	1	1	1	0	0	3	0	0	0	1	1	1	1	1	1
Mismatches	No of mismatches per 100 kbp	0.18	4.62	9.44	20.6	15.72	31.48	0.41	0.76	1.64	1.55	7.87	9.4	9.1	0	0.48	0.13	0.13	0.18
	No of indels per 100 kbp	12.53	86.34	248.34	455.2	343.89	566.22	0.28	0.21	2.14	0.44	1.15	1.43	2.18	0.6	30.55	4.68	3.84	12.32
	No of N's per 100 kbp	0	0	0	0	0	0	0	0	686.69	63.89	13.02	3.37	3.53	0	0	0	0	0
Statistics without referen	No of contigs	4	9	2	14	2	11	1307	1172	2476	3727	102	161	20	4	2	2	2	4
	Largest contig	5460449	1804543	5485519	1168567	5488527	1150335	33112	48400	3250	4511	525273	369879	1512445	5460804	5464938	5466185	5466146	9215694
	Total length	5717255	5696719	5688657	5675913	5691650	5642861	5619230	5534836	1913384	3343474	5591801	5586184	5669505	5717621	5667286	5668555	5668517	9472500
	N50	5460449	1353042	5485519	615749	5488527	610819	6970	7641	761	926	158473	102472	946530	5460804	5464938	5466185	5466146	9215694
	N75	5460449	533216	5485519	459808	5488527	496782	3735	4227	611	689	68938	48179	329188	5460804	5464938	5466185	5466146	9215694
	L50	1	2	1	3	1	3	254	224	910	1241	11	17	3	1	1	1	1	1
	L75	1	4	1	6	1	6	531	464	1612	2296	24	37	5	1	1	1	1	1
	GC (%)	57.09	57.08	57.12	57.08	57.11	57.06	57.28	57.41	55.04	56.37	57.18	57.21	57.14	57.1	57.15	57.14	57.14	57.22

AJ292 (~5.5Mbp genome - real dataset)

		Long read only assembly						Short read only assembly						Hybrid assembly					
	Pipeline info	Canu		MiniC		MiniH		SGA		SOAPdenovo2		Spades		Spades	Canu+pilon	Mini+pilon			Metasm
	Coverage	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X L 20X S	40X long reads 40X short reads				
	Assembly	CanuH	CanuL	MiniCH	MiniCL	MiniH	MiniL	SGAH	SGAL	SoDe2H	SoDe2L	SpadesH	SpadesL	SpadesLRL	CanuH.p1	MiniH.p1	MiniH.p2	MiniH.p3	Metasm
Statistics with reference	Genome fraction (%)	100	99.692	99.999	98.916	99.999	99.969	97.769	97.563	31.15	56.646	99.156	98.987	99.884	100	99.999	99.999	99.999	100
	Duplication ratio	1.013	1.011	1.004	1.005	1.004	1.004	1.024	1.008	1.017	1.006	1.001	1.001	1.001	1.013	1	1	1	1.009
	Largest alignment	5442094	5055382	5463805	1660035	5465515	3797549	27490	53154	4141	4233	578656	569275	1152521	5442825	5444836	5445266	5445232	4453337
	Total aligned length	5516556	5488607	5463805	5410760	5465515	5465701	5453165	5353895	1700272	3098285	5404580	5394955	5443429	5517289	5444836	5445266	5445232	5496807
	NG50	5442094	5055382	5464361	1327492	5465679	3797896	6126	11318		579	206004	122970	610748	5442825	5444912	5445266	5445232	5458553
	NG75	5442094	5055382	5464361	720527	5465679	1668194	3480	5846			165361	60489	480226	5442825	5444912	5445266	5445232	5458553
	NA50	5442094	5055382	5463805	1327480	5465515	3797549	6126	11507	735	891	202814	127859	578636	5442825	5444836	5445266	5445232	4453337
	NA75	5442094	5055382	5463805	638853	5465515	1668152	3477	6029	595	670	134093	60489	480226	5442825	5444836	5445266	5445232	4453337
	NGA50	5442094	5055382	5463805	1327480	5465515	3797549	6126	11318		577	202814	122970	578636	5442825	5444836	5445266	5445232	4453337
	NGA75	5442094	5055382	5463805	638853	5465515	1668152	3480	5846			134093	60489	480226	5442825	5444836	5445266	5445232	4453337
	LG50	1	1	1	2	1	1	262	150		2806	9	13	3	1	1	1	1	1
	LG75	1	1	1	4	1	2	560	320			16	29	5	1	1	1	1	1
	LA50	1	1	1	2	1	1	262	146	848	1175	9	12	4	1	1	1	1	1
	LA75	1	1	1	4	1	2	562	309	1511	2180	17	29	6	1	1	1	1	1
LGA50	1	1	1	2	1	1	262	150		2813	9	13	4	1	1	1	1	1	
LGA75	1	1	1	4	1	2	560	320			17	29	6	1	1	1	1	1	
Misassemblies	No of local misassemblies	0	0	2	1	2	5	0	0	859	205	16	11	0	0	1	0	0	0
	No of unaligned mis. contigs	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
Mismatches	No of mismatches per 100 kbp	0.18	1.84	9.64	17.79	20.05	26.97	0.06	0.19	3.48	1.78	4.13	6.22	4.71	0.13	0.64	0.24	0.24	0.15
	No of indels per 100 kbp	15.1	80.39	247.97	409.22	342.92	481.63	0.19	0.17	2.77	0.65	0.74	1.02	1.64	1.38	29	5.2	4.13	13.31
	No of N's per 100 kbp	0	0	0	0	0	0	0	0	890.28	116.62	36.14	1.04	1.84	0	0	0	0	0
Statistics without referen	No of contigs	4	7	1	6	1	2	1357	798	2267	3521	54	104	15	4	1	1	1	3
	Largest contig	5442094	5055382	5464361	1660035	5465679	3797896	27490	53154	4141	4259	578656	569275	1731157	5442825	5444912	5445266	5445232	5458553
	Total length	5516556	5490581	5464361	5414604	5465679	5466090	5453167	5353915	1744167	3106641	5406608	5395329	5446618	5517289	5444912	5445266	5445232	5496807
	N50	5442094	5055382	5464361	1327492	5465679	3797896	6126	11507	757	894	206004	127859	610748	5442825	5444912	5445266	5445232	5458553
	N75	5442094	5055382	5464361	720527	5465679	1668194	3477	6029	606	673	165361	60489	480226	5442825	5444912	5445266	5445232	5458553
	L50	1	1	1	2	1	1	262	146	830	1173	9	12	3	1	1	1	1	1
	L75	1	1	1	4	1	2	562	309	1475	2175	16	29	5	1	1	1	1	1
	GC (%)	57.63	57.57	57.6	57.57	57.59	57.55	57.79	57.84	55.5	56.68	57.68	57.7	57.62	57.64	57.62	57.62	57.62	57.63

SIM5M (5Mbp genome - synthetic dataset)

		Long read only assembly						Short read only assembly						Hybrid assembly						
	Pipeline info	Canu		MiniC		MiniH		SGA		SOAPdenovo2		Spades		Spades	Colormap	Canu+pilon	Mini+pilon			Metasm
	Coverage	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X long 20X short		40X long reads 40X short reads				
	Assembly	CanuH	CanuL	MiniCH	MiniCL	MiniH	MiniL	SGAH	SGAL	SoDe2H	SoDe2L	SpadesH	SpadesL	SpadesLRL	Colormap	CanuH.p1	MiniH.p1	MiniH.p2	MiniH.p3	Metasm
Statistics with reference	Genome fraction (%)	99.91	96.454	99.896	99.556	99.632	98.649	95.891	96.53	82.934	84.355	98.729	98.616	99.714	99.453	99.91	99.632	99.632	99.632	28.685
	Duplication ratio	1.028	1.02	1.007	1.021	1.003	1.008	1.009	1.009	1.017	1.011	1.001	1.002	1.006	1.011	1.028	1	1	1	4.04
	Largest alignment	1474850	663575	3537045	1341548	2869030	2070177	43317	46979	35307	20287	281680	201112	866471	1779657	1474852	2861494	2861746	2861745	1429727
	Total aligned length	5135271	4920160	5029349	5077176	4996352	4969798	4839182	4868971	4141792	4221589	4943002	4940625	5010201	5025780	5135272	4982836	4983302	4983301	5794912
	NG50	1313778	297761	3537045	704173	2869036	874118	9782	10435	7761	3373	116695	81519	503768	1259797	1313777	2861500	2861752	2861751	5794912
	NG75	623531	182381	1235134	413350	1157358	427859	4947	5659	3868	1470	63668	36839	334297	368449	623531	1154331	1154416	1154416	5794912
	NA50	1313776	297761	3537045	704169	2869030	874118	10025	10870	7711	3751	114800	81519	494811	1259795	1313775	2861494	2861746	2861745	1137402
	NA75	623528	186935	1235133	413350	1157357	427859	5308	5920	3519	2014	60805	36839	294247	368449	623528	1154330	1154415	1154415	1045178
	NGA50	1313776	297761	3537045	704169	2869030	874118	9782	10435	7115	3269	114800	81519	494811	1259795	1313775	2861494	2861746	2861745	1137942
	NGA75	623528	182381	1235133	413350	1157357	427859	4947	5659	2643	1325	59890	36169	294247	368449	623528	1154330	1154415	1154415	1045178
	LG50	2	6	1	3	1	2	163	144	192	417	14	21	4	2	2	1	1	1	1
	LG75	4	12	2	5	2	4	346	307	420	965	29	43	7	4	4	2	2	2	1
	LA50	2	6	1	3	1	2	155	138	180	339	14	21	4	2	2	1	1	1	3
	LA75	4	11	2	5	2	4	322	290	402	733	29	44	8	4	4	2	2	2	4
	LGA50	2	6	1	3	1	2	163	144	201	423	14	21	4	2	2	1	1	1	2
LGA75	4	12	2	5	2	4	346	307	480	998	30	45	8	4	4	2	2	2	4	
Misassemblies	No of local misassemblies	0	0	0	0	0	1	0	0	66	12	1	2	3	0	0	0	0	0	0
	No of unaligned mis. contigs	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0
Mismatches	No of mismatches per 100 kbp	0.48	4.96	1.28	5.75	1.51	4.64	0	0	147.08	34.4	27.85	27.7	47.86	30.06	0.4	0.76	0.72	0.68	0
	No of indels per 100 kbp	0.42	9.54	165.99	207.88	195.42	207.08	0.04	0.1	120.67	46.49	0.49	0.53	1.91	1.31	0.28	9.17	2.69	2.67	0.21
	No of N's per 100 kbp	0	0	0	0	0	0	0	0	3896.67	1539.38	19.6	20.21	0	0	0	0	0	0	0
Statistics without referen	No of contigs	17	35	3	13	3	8	871	800	934	1681	124	161	38	13	17	3	3	3	1
	Largest contig	1474850	663575	3537045	1348395	2869036	2070178	43317	46979	35592	20287	281683	201112	866471	1779657	1474852	2861500	2861752	2861751	5794912
	Total length	5135279	4920161	5029350	5087756	4996359	4969802	4839182	4868971	4679359	4413323	4944427	4942195	5015744	5025782	5135280	4982843	4983309	4983308	5794912
	N50	1313778	297761	3537045	704173	2869036	874118	10025	10870	8376	3847	116695	85214	503768	1259797	1313777	2861500	2861752	2861751	5794912
	N75	623531	186935	1235134	413350	1157358	427859	5308	5920	4520	2118	65903	38606	334297	368449	623531	1154331	1154416	1154416	5794912
	L50	2	6	1	3	1	2	155	138	172	336	14	20	4	2	2	1	1	1	1
	L75	4	11	2	5	2	4	322	290	363	718	28	42	7	4	4	2	2	2	1
	GC (%)	35.86	35.8	35.86	35.84	35.83	35.83	35.67	35.74	35.09	34.85	35.81	35.8	35.85	35.84	35.86	35.83	35.83	35.83	35.03

SIM5M (25Mbp genome - synthetic dataset)

		Long read only assembly						Short read only assembly						Hybrid assembly					
	Pipeline info	Canu		MiniC		MiniH		SGA		SOAPdenovo2		Spades		Spades	Canu+pilon	Mini+pilon			Metasm
	Coverage	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X	20X	40X L 20X S					
	Assembly	CanuH	CanuL	MiniCH	MiniCL	MiniH	MiniL	SGAH	SGAL	SoDe2H	SoDe2L	SpadesH	SpadesL	SpadesLRL	CanuH.p1	MiniH.p1	MiniH.p2	MiniH.p3	Metasm
Statistics with reference	Genome fraction (%)	99.266	85.629	99.937	99.536	99.79	98.411	89.996	92.125	69.499	71.308	98.686	98.437	99.468	99.266	99.79	99.79	99.79	5.844
	Duplication ratio	1.049	1.066	1.011	1.012	1.006	1.004	1.01	1.012	1.026	1.013	1.002	1.003	1.008	1.049	1.003	1.003	1.003	12.922
	Largest alignment	1544089	738962	4236176	2343337	7665207	2561227	42930	38190	33767	22442	494497	413564	2267284	1544088	7644533	7645271	7645271	1459426
	Total aligned length	26035008	22820813	25259712	25170834	25089836	24705328	22720373	23298298	17359847	17838734	24711599	24673647	25043025	26034810	25020001	25022691	25022685	18879454
	NG50	644130	90296	2347005	1073552	7138142	1264603	3755	4134	2953	1779	152292	87387	653521	644129	7116888	7117842	7117838	18879454
	NG75	326121	30178	1588793	761653	1757646	938279	1511	1755	985	530	65000	36639	429370	326121	1752769	1752972	1752972	18879454
	NA50	556355	109830	2347005	1073551	7138139	1264603	4302	4598	3467	2595	140014	84415	524800	556354	7116885	7117839	7117835	1429087
	NA75	303817	42805	1189240	758216	1757645	938277	2033	2163	1175	1284	66116	36548	276994	303814	1752768	1752971	1752971	646263
	NGA50	644130	90296	2347005	1073551	7138139	1264603	3755	4134	2369	1710	139195	83370	524800	644129	7116885	7117839	7117835	779223
	NGA75	326121	30178	1189240	758216	1757645	938277	1511	1755			64502	34884	276994	326121	1752768	1752971	1752971	402579
	LG50	14	51	4	8	2	8	1664	1567	2060	3426	50	85	13	14	2	2	2	1
	LG75	27	170	7	15	4	14	4296	3893	5704	9692	111	196	25	27	4	4	4	1
	LA50	15	40	4	8	2	8	1381	1372	1515	2044	52	89	15	15	2	2	2	7
	LA75	30	124	8	15	4	14	3317	3239	4022	4626	113	202	30	30	4	4	4	12
	LGA50	14	51	4	8	2	8	1664	1567	2283	3489	53	91	15	14	2	2	2	10
LGA75	27	170	8	15	4	14	4296	3893			116	209	30	27	4	4	4	21	
Misassemblies	No of local misassemblies	0	0	0	6	1	4	0	0	241	43	11	13	53	0	1	1	1	0
	No of unaligned mis. contigs	0	0	0	0	0	0	0	0	68	7	0	0	0	0	0	0	0	0
Mismatches	No of mismatches per 100 kbp	1.05	22.86	2.77	8.92	3	9.53	0.1	0.18	153.15	43.83	24.39	28.89	52.15	0.94	1.77	1.72	1.72	0.48
	No of indels per 100 kbp	3.92	76.13	166.48	198.9	201.47	211.38	0.03	0.05	111.48	42.8	0.92	0.99	3.17	1.78	11.1	7.22	7.2	1.98
	No of N's per 100 kbp	0	0	0	0	0	0	0	0	4333.43	1714.44	2.02	1.22	0.08	0	0	0	0	0
Statistics without referen	No of contigs	182	447	23	43	13	35	8661	8469	8262	10029	669	891	292	182	13	13	13	1
	Largest contig	1544089	738962	4487765	2343337	7666928	2770879	42930	38190	34118	22442	494497	413672	2267284	1544088	7646254	7646992	7646992	18879454
	Total length	26035048	22820914	25259994	25176816	25094927	24726068	22720373	23298318	20585734	18923372	24713527	24677390	25060402	26034850	25025092	25027782	25027776	18879454
	N50	556356	109830	2347005	1073552	7138142	1264603	4302	4598	3928	2663	159119	90427	653521	556355	7116888	7117842	7117838	18879454
	N75	303817	42805	1189240	761653	1757646	988893	2033	2163	1899	1388	67532	37984	429370	303814	1752769	1752972	1752972	18879454
	L50	15	40	4	8	2	8	1381	1372	1412	2021	49	83	13	15	2	2	2	1
	L75	30	124	8	15	4	13	3317	3239	3306	4501	107	189	25	30	4	4	4	1
	GC (%)	43.68	43.69	43.69	43.69	43.71	43.74	43.39	43.52	42.87	43.03	43.72	43.72	43.72	43.68	43.71	43.71	43.71	43.35

Canu

	40X coverage long reads						40X long reads + polishing once with 40X short reads						20X coverage long reads						20X long read corrected by 40X shortread	
Assembly	CanuH						CanuH.p1						CanuL						Colormap	
Dataset	AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	sim5M
Genome fraction (%)	99.877	99.905	100	99.91	99.266		99.877	99.905	100	99.91	99.266		99.785	99.759	99.692	96.454	85.629		97.625	99.453
Duplication ratio	1	1.002	1.013	1.028	1.049		1	1.002	1.013	1.028	1.049		1.003	1.002	1.011	1.02	1.066		1.094	1.011
Largest alignment	5496967	5460340	5442094	1474850	1544089		5497400	5460804	5442825	1474852	1544088		3169756	1804543	5055382	663575	738962		504450	1779657
Total aligned length	5498061	5473703	5516556	5135271	26035008		5498494	5474167	5517289	5135272	26034810		5506645	5464844	5488607	4920160	22820813		5871337	5025780
NG50	5496970	5460449	5442094	1313778	644130		5497403	5460804	5442825	1313777	644129		3169885	1353042	5055382	297761	90296		305685	1259797
NG75	5496970	5460449	5442094	623531	326121		5497403	5460804	5442825	623531	326121		1809348	533216	5055382	182381	30178		132047	368449
NA50	5496967	5460340	5442094	1313776	556355		5497400	5460804	5442825	1313775	556354		3169756	1353042	5055382	297761	109830		218907	1259795
NA75	5496967	5460340	5442094	623528	303817		5497400	5460804	5442825	623528	303814		688559	533216	5055382	186935	42805		81683	368449
NGA50	5496967	5460340	5442094	1313776	644130		5497400	5460804	5442825	1313775	644129		3169756	1353042	5055382	297761	90296		305685	1259795
NGA75	5496967	5460340	5442094	623528	326121		5497400	5460804	5442825	623528	326121		1120789	533216	5055382	182381	30178		130178	368449
LG50	1	1	1	2	14		1	1	1	2	14		1	2	1	6	51		7	2
LG75	1	1	1	4	27		1	1	1	4	27		2	4	1	12	170		15	4
LA50	1	1	1	2	15		1	1	1	2	15		1	2	1	6	40		8	2
LA75	1	1	1	4	30		1	1	1	4	30		3	4	1	11	124		19	4
LGA50	1	1	1	2	14		1	1	1	2	14		1	2	1	6	51		7	2
LGA75	1	1	1	4	27		1	1	1	4	27		2	4	1	12	170		15	4
No of local misassemblies	0	1	0	0	0		0	0	0	0	0		1	0	0	0	0		12	0
No of unaligned mis. contigs	0	1	0	0	0		0	1	0	0	0		0	1	0	0	0		0	0
No of mismatches per 100 kbp	0.27	0.18	0.18	0.48	1.05		0	0	0.13	0.4	0.94		6.28	4.62	1.84	4.96	22.86		24.7	30.06
No of indels per 100 kbp	34.76	12.53	15.1	0.42	3.92		2.58	0.6	1.38	0.28	1.78		165.41	86.34	80.39	9.54	76.13		8.04	1.31
No of N's per 100 kbp	0	0	0	0	0		0	0	0	0	0		0	0	0	0	0		0	0
No of contigs	4	4	4	17	182		4	4	4	17	182		9	9	7	35	447		73	13
Largest contig	5496970	5460449	5442094	1474850	1544089		5497403	5460804	5442825	1474852	1544088		3169885	1804543	5055382	663575	738962		509223	1779657
Total length	5727073	5717255	5516556	5135279	26035048		5727525	5717621	5517289	5135280	26034850		5728738	5696719	5490581	4920161	22820914		6030828	5025782
N50	5496970	5460449	5442094	1313778	556356		5497403	5460804	5442825	1313777	556355		3169885	1353042	5055382	297761	109830		218907	1259797
N75	5496970	5460449	5442094	623531	303817		5497403	5460804	5442825	623531	303814		1809348	533216	5055382	186935	42805		104347	368449
L50	1	1	1	2	15		1	1	1	2	15		1	2	1	6	40		8	2
L75	1	1	1	4	30		1	1	1	4	30		2	4	1	11	124		18	4
GC (%)	57.18	57.09	57.63	35.86	43.68		57.19	57.1	57.64	35.86	43.68		57.14	57.08	57.57	35.8	43.69		57.27	35.84

MiniC

	40X coverage long reads						20X coverage long reads				
Assembly	MiniCH						MiniCL				
Dataset	AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M
Genome fraction (%)	99.999	99.977	99.999	99.896	99.937		98.626	99.273	98.916	99.556	99.536
Duplication ratio	1.005	1.006	1.004	1.007	1.011		1.007	1.009	1.005	1.021	1.012
Largest alignment	5529367	5049176	5463805	3537045	4236176		1138217	1163455	1660035	1341548	2343337
Total aligned length	5530466	5496411	5463805	5029349	25259712		5467427	5472727	5410760	5077176	25170834
NG50	5529667	5485519	5464361	3537045	2347005		470381	615749	1327492	704173	1073552
NG75	5529667	5485519	5464361	1235134	1588793		298434	459808	720527	413350	761653
NA50	5529367	5049176	5463805	3537045	2347005		470380	610591	1327480	704169	1073551
NA75	5529367	5049176	5463805	1235133	1189240		298434	459808	638853	413350	758216
NGA50	5529367	5049176	5463805	3537045	2347005		470380	610591	1327480	704169	1073551
NGA75	5529367	5049176	5463805	1235133	1189240		298434	459808	638853	413350	758216
LG50	1	1	1	1	4		4	3	2	3	8
LG75	1	1	1	2	7		7	6	4	5	15
LA50	1	1	1	1	4		4	3	2	3	8
LA75	1	1	1	2	8		7	6	4	5	15
LGA50	1	1	1	1	4		4	3	2	3	8
LGA75	1	1	1	2	8		7	6	4	5	15
No of local misassemblies	1	4	2	0	0		2	10	1	0	6
No of unaligned mis. contigs	0	1	0	0	0		0	1	0	0	0
No of mismatches per 100 kbp	15.03	9.44	9.64	1.28	2.77		34.91	20.6	17.79	5.75	8.92
No of indels per 100 kbp	330.97	248.34	247.97	165.99	166.48		639.88	455.2	409.22	207.88	198.9
No of N's per 100 kbp	0	0	0	0	0		0	0	0	0	0
No of contigs	2	2	1	3	23		16	14	6	13	43
Largest contig	5529667	5485519	5464361	3537045	4487765		1138302	1168567	1660035	1348395	2343337
Total length	5696122	5688657	5464361	5029350	25259994		5634250	5675913	5414604	5087756	25176816
N50	5529667	5485519	5464361	3537045	2347005		470381	615749	1327492	704173	1073552
N75	5529667	5485519	5464361	1235134	1189240		298434	459808	720527	413350	761653
L50	1	1	1	1	4		4	3	2	3	8
L75	1	1	1	2	8		7	6	4	5	15
GC (%)	57.21	57.12	57.6	35.86	43.69		57.13	57.08	57.57	35.84	43.69

Mini

	40X coverage long reads						40X long reads + polishing once with 40X short reads						40X long reads + polishing twice with 40X short reads						40X long reads + polishing thrice with 40X short reads						20X coverage long reads				
Assembly	MiniH						MiniH.p1						MiniH.p2						MiniH.p3						MiniL				
Dataset	AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M
Genome fraction (%)	99.934	99.978	99.999	99.632	99.79		99.939	99.994	99.999	99.632	99.79		99.939	100	99.999	99.632	99.79		99.939	100	99.999	99.632	99.79		97.962	98.857	99.969	98.649	98.411
Duplication ratio	1.005	1.007	1.004	1.003	1.006		1	1.002	1	1	1.003		1	1.002	1	1	1.003		1	1.002	1	1	1.003		1.009	1.008	1.004	1.008	1.004
Largest alignment	5529303	5488283	5465515	2869030	7665207		5500863	5464934	5444836	2861494	7644533		5501187	5466181	5445266	2861746	7645271		5501107	5466142	5445232	2861745	7645271		833675	1150331	3797549	2070177	2561227
Total aligned length	5530402	5500551	5465515	4996352	25089836		5501955	5477150	5444836	4982836	25020001		5502281	5478396	5445266	4983302	25022691		5502201	5478358	5445232	4983301	25022685		5435975	5447535	5465701	4969798	24705328
NG50	5534010	5488527	5465679	2869036	7138142		5505273	5464938	5444912	2861500	7116888		5505584	5466185	5445266	2861752	7117842		5505476	5466146	5445232	2861751	7117838		455694	610819	3797896	874118	1264603
NG75	5534010	5488527	5465679	1157358	1757646		5505273	5464938	5444912	1154331	1752769		5505584	5466185	5445266	1154416	1752972		5505476	5466146	5445232	1154416	1752972		353027	496782	1668194	427859	938279
NA50	5529303	5488283	5465515	2869030	7138139		5500863	5464934	5444836	2861494	7116885		5501187	5466181	5445266	2861746	7117839		5501107	5466142	5445232	2861745	7117835		455694	606793	3797549	874118	1264603
NA75	5529303	5488283	5465515	1157357	1757645		5500863	5464934	5444836	1154330	1752768		5501187	5466181	5445266	1154415	1752971		5501107	5466142	5445232	1154415	1752971		243400	496779	1668152	427859	938277
NGA50	5529303	5488283	5465515	2869030	7138139		5500863	5464934	5444836	2861494	7116885		5501187	5466181	5445266	2861746	7117839		5501107	5466142	5445232	2861745	7117835		455694	606793	3797549	874118	1264603
NGA75	5529303	5488283	5465515	1157357	1757645		5500863	5464934	5444836	1154330	1752768		5501187	5466181	5445266	1154415	1752971		5501107	5466142	5445232	1154415	1752971		351127	496779	1668152	427859	938277
LG50	1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		5	3	1	2	8
LG75	1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		8	6	2	4	14
LA50	1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		5	3	1	2	8
LA75	1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		9	6	2	4	14
LGA50	1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		5	3	1	2	8
LGA75	1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		8	6	2	4	14
No of local misassemblies	5	7	2	0	1		2	1	1	0	1		2	0	0	0	1		1	0	0	0	1		4	10	5	1	4
No of unaligned mis. contigs	0	1	0	0	0		0	1	0	0	0		0	1	0	0	0		0	1	0	0	0		0	1	0	0	0
No of mismatches per 100 kbp	29.62	15.72	20.05	1.51	3		1.04	0.48	0.64	0.76	1.77		0.69	0.13	0.24	0.72	1.72		0.8	0.13	0.24	0.68	1.72		49.96	31.48	26.97	4.64	9.53
No of indels per 100 kbp	466.43	343.89	342.92	195.42	201.47		55.57	30.55	29	9.17	11.1		8.05	4.68	5.2	2.69	7.22		7.82	3.84	4.13	2.67	7.2		726.07	566.22	481.63	207.08	211.38
No of N's per 100 kbp	0	0	0	0	0		0	0	0	0	0		0	0	0	0	0		0	0	0	0	0		0	0	0	0	0
No of contigs	2	2	1	3	13		2	2	1	3	13		2	2	1	3	13		2	2	1	3	13		18	11	2	8	35
Largest contig	5534010	5488527	5465679	2869036	7666928		5505273	5464938	5444912	2861500	7646254		5505584	5466185	5445266	2861752	7646992		5505476	5466146	5445232	2861751	7646992		833810	1150335	3797896	2070178	2770879
Total length	5700578	5691650	5465679	4996359	25094927		5670982	5667286	5444912	4982843	25025092		5671342	5668555	5445266	4983309	25027782		5671230	5668517	5445232	4983308	25027776		5602098	5642861	5466090	4969802	24726068
N50	5534010	5488527	5465679	2869036	7138142		5505273	5464938	5444912	2861500	7116888		5505584	5466185	5445266	2861752	7117842		5505476	5466146	5445232	2861751	7117838		455694	610819	3797896	874118	1264603
N75	5534010	5488527	5465679	1157358	1757646		5505273	5464938	5444912	1154331	1752769		5505584	5466185	5445266	1154416	1752972		5505476	5466146	5445232	1154416	1752972		243471	496782	1668194	427859	988893
L50	1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		5	3	1	2	8
L75	1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		1	1	1	1	2		9	6	2	4	13
GC (%)	57.19	57.11	57.59	35.83	43.71		57.24	57.15	57.62	35.83	43.71		57.23	57.14	57.62	35.83	43.71		57.23	57.14	57.62	35.83	43.71		57.17	57.06	57.55	35.83	43.74

Metasm

Assembly	Metasm				
Dataset	AJ055	AJ218	AJ292	sim5M	sim25M
Genome fraction (%)	99.877	99.905	100	28.685	5.844
Duplication ratio	1	1.69	1.009	4.04	12.922
Largest alignment	5496967	5244427	4453337	1429727	1459426
Total aligned length	5498061	9228948	5496807	5794912	18879454
NG50	5496970	9215694	5458553	5794912	18879454
NG75	5496970	9215694	5458553	5794912	18879454
NA50	5496967	5244427	4453337	1137402	1429087
NA75	5496967	3299401	4453337	1045178	646263
NGA50	5496967	5244427	4453337	1137942	779223
NGA75	5496967	5244427	4453337	1045178	402579
LG50	1	1	1	1	1
LG75	1	1	1	1	1
LA50	1	1	1	3	7
LA75	1	2	1	4	12
LGA50	1	1	1	2	10
LGA75	1	1	1	4	21
No of local misassemblies	0	1	0	0	0
No of unaligned mis. contigs	0	1	0	0	0
No of mismatches per 100 kbp	0.27	0.18	0.15	0	0.48
No of indels per 100 kbp	34.76	12.32	13.31	0.21	1.98
No of N's per 100 kbp	0	0	0	0	0
No of contigs	4	4	3	1	1
Largest contig	5496970	9215694	5458553	5794912	18879454
Total length	5727073	9472500	5496807	5794912	18879454
N50	5496970	9215694	5458553	5794912	18879454
N75	5496970	9215694	5458553	5794912	18879454
L50	1	1	1	1	1
L75	1	1	1	1	1
GC (%)	57.18	57.22	57.63	35.03	43.35

Spades

	40X coverage short reads						20X coverage short reads						40X short read and 20X long read coverage				
Assembly	SpadesH						SpadesL						SpadesLRL				
Dataset	AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M
Genome_fraction_ (%)	99.131	98.766	99.156	98.729	98.686		98.932	98.683	98.987	98.616	98.437		99.882	99.887	99.884	99.714	99.468
Duplication_ratio	1	1.001	1.001	1.001	1.002		1.001	1.001	1.001	1.002	1.003		1	1.003	1.001	1.006	1.008
Largest_alignment	585792	524880	578656	281680	494497		342668	369879	569275	201112	413564		1587076	1511928	1152521	866471	2267284
Total_aligned_length	5458002	5402362	5404580	4943002	24711599		5447750	5398386	5394955	4940625	24673647		5498433	5474706	5443429	5010201	25043025
NG50	226024	158473	206004	116695	152292		164005	109857	122970	81519	87387		1571477	946530	610748	503768	653521
NG75	163120	71228	165361	63668	65000		89646	55877	60489	36839	36639		552169	454623	480226	334297	429370
NA50	226024	158473	202814	114800	140014		164005	102472	127859	81519	84415		1571477	946530	578636	494811	524800
NA75	163120	68894	134093	60805	66116		86634	46985	60489	36839	36548		552169	329188	480226	294247	276994
NGA50	226024	158473	202814	114800	139195		164005	109857	122970	81519	83370		1571477	946530	578636	494811	524800
NGA75	163120	71228	134093	59890	64502		89646	48179	60489	36169	34884		552169	454623	480226	294247	276994
LG50	9	11	9	14	50		12	16	13	21	85		2	3	3	4	13
LG75	16	23	16	29	111		23	35	29	43	196		4	4	5	7	25
LA50	9	11	9	14	52		12	17	12	21	89		2	3	4	4	15
LA75	16	24	17	29	113		24	37	29	44	202		4	5	6	8	30
LGA50	9	11	9	14	53		12	16	13	21	91		2	3	4	4	15
LGA75	16	23	17	30	116		23	35	29	45	209		4	4	6	8	30
No_of_local_misassemblies	11	10	16	1	11		17	9	11	2	13		1	0	0	3	53
No_of_unaligned_mis_contigs	0	0	0	0	0		0	0	0	0	0		0	1	0	0	0
No_of_mismatches_per_100_kbp	5.22	7.87	4.13	27.85	24.39		7.09	9.4	6.22	27.7	28.89		5.57	9.1	4.71	47.86	52.15
No_of_indels_per_100_kbp	1.45	1.15	0.74	0.49	0.92		1.4	1.43	1.02	0.53	0.99		1.75	2.18	1.64	1.91	3.17
No_of_N's_per_100_kbp	17.33	13.02	36.14	19.6	2.02		25.66	3.37	1.04	20.21	1.22		1.77	3.53	1.84	0	0.08
No_of_contigs	64	102	54	124	669		103	161	104	161	891		16	20	15	38	292
Largest_contig	585792	525273	578656	281683	494497		342678	369879	569275	201112	413672		1845647	1512445	1731157	866471	2267284
Total_length	5621063	5591801	5406608	4944427	24713527		5611391	5586184	5395329	4942195	24677390		5663299	5669505	5446618	5015744	25060402
N50	226024	158473	206004	116695	159119		164005	102472	127859	85214	90427		1571477	946530	610748	503768	653521
N75	163120	68938	165361	65903	67532		86650	48179	60489	38606	37984		552169	329188	480226	334297	429370
L50	9	11	9	14	49		12	17	12	20	83		2	3	3	4	13
L75	16	24	16	28	107		24	37	29	42	189		4	5	5	7	25
GC_ (%)	57.28	57.18	57.68	35.81	43.72		57.32	57.21	57.7	35.8	43.72		57.25	57.14	57.62	35.85	43.72

SGA

	40X coverage short reads						20X coverage short reads				
Assembly	SGAH						SGAL				
Dataset	AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M
Genome fraction (%)	97.757	97.384	97.769	95.891	89.996		97.119	96.726	97.563	96.53	92.125
Duplication ratio	1.024	1.021	1.024	1.009	1.01		1.015	1.013	1.008	1.009	1.012
Largest alignment	37194	33112	27490	43317	42930		33813	48400	53154	46979	38190
Total aligned length	5508142	5437178	5453165	4839182	22720373		5427729	5355772	5353895	4868971	23298298
NG50	6594	7143	6126	9782	3755		7167	7778	11318	10435	4134
NG75	3728	3981	3480	4947	1511		4097	4365	5846	5659	1755
NA50	6096	6581	6126	10025	4302		6988	7326	11507	10870	4598
NA75	3240	3400	3477	5308	2033		3760	3885	6029	5920	2163
NGA50	6296	6968	6126	9782	3755		7092	7452	11318	10435	4134
NGA75	3474	3707	3480	4947	1511		3879	4011	5846	5659	1755
LG50	249	243	262	163	1664		237	219	150	144	1567
LG75	524	501	560	346	4296		490	452	320	307	3893
LA50	272	258	262	155	1381		247	228	146	138	1372
LA75	587	551	562	322	3317		519	483	309	290	3239
LGA50	258	246	262	163	1664		241	224	150	144	1567
LGA75	550	518	560	346	4296		503	470	320	307	3893
No of local misassemblies	0	0	0	0	0		0	0	0	0	0
No of unaligned mis. contigs	0	0	0	0	0		0	0	0	0	0
No of mismatches per 100 kbp	0.06	0.41	0.06	0	0.1		0.24	0.76	0.19	0	0.18
No of indels per 100 kbp	0.59	0.28	0.19	0.04	0.03		0.47	0.21	0.17	0.1	0.05
No of N's per 100 kbp	0	0	0	0	0		0	0	0	0	0
No of contigs	1370	1307	1357	871	8661		1228	1172	798	800	8469
Largest contig	37194	33112	27490	43317	42930		33813	48400	53154	46979	38190
Total length	5670252	5619230	5453167	4839182	22720373		5585990	5534836	5353915	4868971	23298318
N50	6394	6970	6126	10025	4302		7111	7641	11507	10870	4598
N75	3500	3735	3477	5308	2033		3969	4227	6029	5920	2163
L50	262	254	262	155	1381		243	224	146	138	1372
L75	559	531	562	322	3317		505	464	309	290	3239
GC (%)	57.39	57.28	57.79	35.67	43.39		57.5	57.41	57.84	35.74	43.52

SOAPdenovo2

	40X coverage short reads						20X coverage short reads				
Assembly	SoDe2H						SoDe2L				
Dataset	AJ055	AJ218	AJ292	sim5M	sim25M		AJ055	AJ218	AJ292	sim5M	sim25M
Genome fraction (%)	27.577	33.369	31.15	82.934	69.499		55.537	58.833	56.646	84.355	71.308
Duplication ratio	1.011	1.013	1.017	1.017	1.026		1.005	1.005	1.006	1.011	1.013
Largest alignment	3463	3250	4141	35307	33767		4124	4511	4233	20287	22442
Total aligned length	1521547	1828053	1700272	4141792	17359847		3069319	3229100	3098285	4221589	17838734
NG50				7761	2953		589	631	579	3373	1779
NG75				3868	985					1470	530
NA50	714	738	735	7711	3467		875	908	891	3751	2595
NA75	575	590	595	3519	1175		645	666	670	2014	1284
NGA50				7115	2369		568	604	577	3269	1710
NGA75				2643						1325	
LG50				192	2060		2801	2637	2806	417	3426
LG75				420	5704					965	9692
LA50	813	935	848	180	1515		1240	1263	1175	339	2044
LA75	1447	1661	1511	402	4022		2305	2348	2180	733	4626
LGA50				201	2283		2900	2703	2813	423	3489
LGA75				480						998	
No of local misassemblies	548	733	859	66	241		197	137	205	12	43
No of unaligned mis. contigs	1	3	3	13	68		0	0	0	0	7
No of mismatches per 100 kbp	1.71	1.64	3.48	147.08	153.15		2.78	1.55	1.78	34.4	43.83
No of indels per 100 kbp	1.91	2.14	2.77	120.67	111.48		1.01	0.44	0.65	46.49	42.8
No of N's per 100 kbp	578.49	686.69	890.28	3896.67	4333.43		95.3	63.89	116.62	1539.38	1714.44
No of contigs	2124	2476	2267	934	8262		3607	3727	3521	1681	10029
Largest contig	3463	3250	4141	35592	34118		4124	4511	4259	20287	22442
Total length	1618182	1913384	1744167	4679359	20585734		3190953	3343474	3106641	4413323	18923372
N50	751	761	757	8376	3928		907	926	894	3847	2663
N75	603	611	606	4520	1899		672	689	673	2118	1388
L50	779	910	830	172	1412		1204	1241	1173	336	2021
L75	1384	1612	1475	363	3306		2230	2296	2175	718	4501
GC (%)	54.53	55.04	55.5	35.09	42.87		56.21	56.37	56.68	34.85	43.03

Long read correction

Dataset	AJ055						AJ218				AJ292					SIM5M						SIM25M			
Assembly	CanuH.cr	CanuL.cr	MiniCH.cr	MiniCL.cr	Colormap.cr		CanuH.cr	CanuL.cr	MiniCH.cr		CanuH.cr	CanuL.cr	MiniCH.cr	MiniCL.cr		CanuH.cr	CanuL.cr	MiniCH.cr	MiniCL.cr	Colormap.cr		CanuH.cr	CanuL.cr	MiniCH.cr	MiniCL.cr
No_of_mismatches_per_100_kbp	49.78	95.67	109.27	134.01	90.27		36.12	71.06	108.22		29.73	58.33	82.89	86.8		4.5	42.74	62.46	167.02	234.14		15.68	89.88	86.65	192.4
No_of_indels_per_100_kbp	371.26	705.65	1032.45	1254.47	98.9		218.56	483.99	907.6		205.26	389.5	764.57	848.18		13.14	96.29	545.91	1308.09	146.06		45.18	314.12	552.14	1327.84
No_of_N's_per_100_kbp	0	0	0	0	0		0	0	0		0	0	0	0		0	0	0	0	0		0	0	0	0