



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
		40	40	Metaasm	Metaasm merging CanuH + SGAH + SpadesLRL
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		Mini		SGA		SOAPdenovo2		Spades		Spades	Colormap	Canu+pilon	Mini+pilon			Metasm
	Coverage	40X	20X	40X	20X	Mini	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 reference	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		Mini		SGA		SOAPdenovo2		Spades		Spades	Canu+pilon	Mini+pilon			Metasm
	Coverage	40X	20X	40X	20X	Mini	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 reference	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		Mini		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 reference	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		Mini		SGA		SOAPdenovo2		Spades		Spades	Colormap	Canu+pilon	Mini+pilon			Metasm
	Coverage	40X	20X	40X	20X	Mini	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 reference	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		Mini		SGA		SOAPdenovo2		Spades		Spades	Canu+pilon	Mini+pilon			Metasm
	Coverage	40X	20X	40X	20X	Mini	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 (%)	99.266	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 reference	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