color scheme

worst	
moderate	
best	
Non comparable	

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 piipeline - 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	Metasm	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

Canu

Assembly	40X coverage long reads						40X long reads + polishing once with 40X short reads						20X coverage long reads						20X long read corrected by 40X shortread	
	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

Assembly	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

Assembly	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				
	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	2	4		1	1	1	2	4		1	1	1	2	4		1	1	1	2	4		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	2	4		1	1	1	2	4		1	1	1	2	4		1	1	1	2	4		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	2	4		1	1	1	2	4		1	1	1	2	4		1	1	1	2	4		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	0	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	2	4		1	1	1	2	4		1	1	1	2	4		1	1	1	2	4		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

Assembly	40X coverage short reads						20X coverage short reads						40X short read and 20X long read coverage				
	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

Assembly	40X coverage short reads						20X coverage short reads				
	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