

Attention: this file was produced automatically, and some statistics might not make sense for certain pipelines.

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This file contains statistics about the following genome(s):

- data/reports/C.elegans_contigbreaker/s/"genome": "C.elegans", "assembler": "wtdbg2": "cli_arguments": "-x": "rs" /report.tex
- data/reports/A.thaliana_contigbreaker/s/"genome": "A.thaliana", "assembler": "wtdbg2": "cli_arguments": "-x": "sq" /report.tex
- data/reports/D.melanogaster_A4_contigbreaker/s/"genome": "D.melanogaster_A4", "assembler": "wtdbg2": "cli_arguments": "-x": "rs" /report.tex
- data/reports/D.melanogaster_ISO1_contigbreaker/s/"genome": "D.melanogaster_ISO1", "assembler": "wtdbg2": "cli_arguments": "-x": "ont" /report.tex
- data/reports/Minghui63_contigbreaker/s/"genome": "Minghui63", "assembler": "wtdbg2": "cli_arguments": "-x": "ccs" /report.tex

Table 1: EA50max

EA50max/Strict EA50max	YV sfa		w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	978031/604113	846349/590484	986630/621916	1009589/624411	971911/650482	891451/566232	780035/518363	891226/601679	891069/566232	891226/601679	
A.thaliana_contigbreaker/a:(w:(x:sq))	5066278/2397721	4192426/2159187	5690800/2530237	6062526/2804952	6062701/2398686	5066278/2397721	4192426/2159187	6062694/2077488	6062526/2804952	6062701/2077492	
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	5365061/2256857	3826170/1741840	5610880/2511301	8259445/2267451	8262222/2417890	3523151/1599120	1877802/1089505	188864/88578	627290/395357	180440/89719	
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	2648288/231882	2286441/231304	2285784/219411	2725710/223209	2291499/227130	2258960/184556	613726/75976	683828/89467	1207726/106666	678740/94022	
Minghui63_contigbreaker/a:(w:(x:cc))	565115/541129	255636/242084	585161/558951	1083985/969103	406172/376146	558951/535154	254019/241007	393414/365954	1003622/899831	388602/365954	

Table 2: EA75max

EA75max/Strict EA75max	YV sfa		w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	536678/308970	418864/245444	536678/309257	557590/310064	536597/312849	498159/271665	354708/222806	405300/235007	464265/242041	405300/235007	
A.thaliana_contigbreaker/a:(w:(x:sq))	2159111/673960	1474012/472408	2460959/673960	2161051/678385	2161036/673960	1712342/673960	1474012/472408	806452/236340	2097897/678385	806454/236339	
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	1412288/926524	953431/523044	2355902/953025	2109306/952980	2255114/926524	558801/389325	0/0	0/0	0/0	0/0	
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	410385/56971	394458/52440	286082/47854	613735/53397	613729/54773	38006/9673	0/0	0/0	0/0	0/0	
Minghui63_contigbreaker/a:(w:(x:cc))	297054/277366	106868/102135	318929/293899	544689/473905	143046/136119	293204/271944	105010/99847	135504/125326	462314/406239	130888/120385	

Table 3: EAmeanmax

EAmeanmax/Strict EAmeanmax	YV sfa		w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	1252493/672781	1071991/672031	1275999/702848	1280753/688368	1237230/724335	1181874/659695	997743/651322	1107528/690835	1143788/660320	1107758/691121	
A.thaliana_contigbreaker/a:(w:(x:sq))	5009075/2861911	3874474/2432639	5472419/2915163	6016193/3015332	6014893/2813653	4978245/2859989	3866792/2431004	5614083/2595674	5989112/3012447	5614172/2597836	
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	6284403/2612610	3772457/2083601	7821887/2928302	11316405/3856188	11373739/3625907	3448716/1998969	2486850/1521233	3113314/2019625	3361532/1460166	3112979/1847686	
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	3648311/349632	3032196/321113	3621903/345472	3704953/334838	3678925/320688	3190645/323741	2029177/198930	2784698/245736	2718226/260673	2788302/243590	
Minghui63_contigbreaker/a:(w:(x:cc))	696734/670066	353978/345111	737036/696038	1318891/1200888	582357/562628	686771/665076	352234/343543	561008/543246	1249864/1138268	570534/551680	

Table 4: P5k

P5k/Strict P5k	YV sfa	w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	0.967/0.966	0.962/0.961	0.967/0.966	0.965/0.964	0.962/0.961	0.944/0.944	0.928/0.927	0.895/0.894	0.911/0.910	0.895/0.894
A.thaliana_contigbreaker/a:(w:(x:sq))	0.947/0.946	0.944/0.943	0.947/0.946	0.946/0.945	0.946/0.945	0.933/0.932	0.928/0.927	0.834/0.833	0.930/0.929	0.834/0.833
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	0.907/0.905	0.900/0.899	0.907/0.905	0.903/0.901	0.901/0.899	0.867/0.865	0.741/0.739	0.541/0.540	0.607/0.605	0.541/0.540
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	0.855/0.848	0.845/0.840	0.833/0.827	0.846/0.840	0.847/0.841	0.765/0.759	0.612/0.607	0.589/0.585	0.635/0.631	0.591/0.587
Minghui63_contigbreaker/a:(w:(x:cc))	0.981/0.980	0.936/0.936	0.981/0.980	0.972/0.971	0.888/0.888	0.974/0.973	0.932/0.931	0.875/0.875	0.946/0.945	0.873/0.873

Table 5: P10k

P10k/Strict P10k	YV sfa	w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	0.964/0.963	0.959/0.958	0.965/0.963	0.963/0.962	0.960/0.959	0.942/0.941	0.925/0.924	0.893/0.891	0.910/0.908	0.893/0.892
A.thaliana_contigbreaker/a:(w:(x:sq))	0.946/0.944	0.943/0.941	0.946/0.944	0.945/0.943	0.945/0.943	0.932/0.930	0.926/0.925	0.833/0.831	0.929/0.927	0.833/0.831
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	0.905/0.902	0.898/0.895	0.905/0.902	0.901/0.898	0.899/0.896	0.866/0.863	0.738/0.735	0.540/0.537	0.605/0.602	0.540/0.537
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	0.852/0.838	0.841/0.830	0.830/0.817	0.843/0.830	0.843/0.830	0.762/0.749	0.609/0.598	0.587/0.578	0.633/0.624	0.589/0.581
Minghui63_contigbreaker/a:(w:(x:cc))	0.980/0.979	0.931/0.930	0.980/0.979	0.971/0.970	0.886/0.885	0.973/0.971	0.927/0.925	0.873/0.871	0.944/0.943	0.870/0.869

Table 6: P15k

P15k/Strict P15k	YV sfa	w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	0.962/0.960	0.956/0.954	0.962/0.960	0.960/0.958	0.957/0.955	0.940/0.938	0.922/0.920	0.890/0.888	0.907/0.905	0.890/0.888
A.thaliana_contigbreaker/a:(w:(x:sq))	0.945/0.942	0.942/0.939	0.945/0.942	0.944/0.941	0.943/0.941	0.931/0.929	0.925/0.923	0.832/0.829	0.928/0.926	0.832/0.829
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	0.903/0.899	0.895/0.891	0.903/0.899	0.900/0.896	0.897/0.893	0.864/0.859	0.735/0.731	0.538/0.534	0.603/0.600	0.537/0.534
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	0.850/0.829	0.836/0.821	0.829/0.808	0.841/0.821	0.842/0.823	0.760/0.741	0.606/0.590	0.585/0.572	0.632/0.617	0.588/0.574
Minghui63_contigbreaker/a:(w:(x:cc))	0.979/0.976	0.925/0.923	0.979/0.977	0.970/0.968	0.883/0.881	0.971/0.969	0.921/0.919	0.870/0.868	0.943/0.941	0.867/0.866

Table 7: P20k

P20k/Strict P20k	YV sfa	w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	0.959/0.956	0.953/0.950	0.960/0.957	0.958/0.956	0.954/0.952	0.937/0.934	0.918/0.916	0.887/0.885	0.904/0.902	0.887/0.885
A.thaliana_contigbreaker/a:(w:(x:sq))	0.944/0.941	0.941/0.937	0.945/0.941	0.943/0.939	0.943/0.939	0.930/0.927	0.924/0.921	0.831/0.828	0.927/0.924	0.831/0.828
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	0.902/0.896	0.894/0.888	0.902/0.896	0.898/0.892	0.896/0.890	0.863/0.856	0.734/0.729	0.536/0.531	0.602/0.596	0.536/0.531
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	0.848/0.818	0.836/0.811	0.827/0.798	0.839/0.812	0.840/0.813	0.758/0.731	0.603/0.582	0.584/0.567	0.630/0.610	0.586/0.569
Minghui63_contigbreaker/a:(w:(x:cc))	0.976/0.974	0.919/0.916	0.978/0.975	0.968/0.966	0.879/0.877	0.969/0.966	0.914/0.912	0.866/0.864	0.941/0.939	0.864/0.862

Table 8: EAmeanmax and unique misassemblies

EAmeanmax/unique mis	YV sfa	w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	1252493/111	1071991/64	1275999/119	1280753/85	1237230/79	1181874/105	997743/64	1107528/76	1143788/82	1107758/74
A.thaliana_contigbreaker/a:(w:(x:sq))	5009075/65	3874474/45	5472419/75	6016193/61	6014893/52	4978245/56	3866792/36	5614083/45	5989112/55	5614172/45
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	6284403/192	3772457/141	7821887/218	11316405/168	11373739/164	3448716/151	2486850/135	3113314/124	3361532/160	3112979/125
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	3648311/179	3032196/87	3621903/198	3704953/123	3678925/120	3190645/158	2029177/74	2784698/88	2718226/82	2788302/91
Minghui63_contigbreaker/a:(w:(x:cc))	696734/2389	353978/636	737036/2431	1318891/1531	582357/738	686771/2292	352234/613	561008/698	1249864/1428	570534/694

Table 9: Number of unique/total extensive misassemblies. These do not include local misassemblies. The ‘uniqueness’ is determined heuristically.

unique/total ext. mis.	YV sfa	w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	111/136	64/65	119/145	85/97	79/80	105/127	64/65	76/77	82/93	74/75
A.thaliana_contigbreaker/a:(w:(x:sq))	65/79	45/46	75/87	61/63	52/53	56/66	36/37	45/46	55/57	45/46
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	192/273	141/143	218/295	168/176	164/166	151/225	135/137	124/125	160/166	125/126
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	179/255	87/87	198/267	123/128	120/120	158/217	74/74	88/88	82/85	91/91
Minghui63_contigbreaker/a:(w:(x:cc))	2389/3398	636/662	2431/3470	1531/2559	738/767	2292/3243	613/637	698/724	1428/2356	694/718

Table 10: Number of unique/total local misassemblies. The ‘uniqueness’ is determined heuristically.

unique/total loc. mis.	YV sfa	w2 sfa	YV	frg YV	wtdbg2	YV sfa brk	w2 sfa brk	YV brk	frg YV brk	w2 brk
C.elegans_contigbreaker/a:(w:(x:rs))	215/305	158/158	216/300	168/180	153/153	200/279	149/149	144/148	155/166	137/137
A.thaliana_contigbreaker/a:(w:(x:sq))	302/386	222/226	312/397	252/257	246/251	259/327	192/195	220/222	220/225	212/217
D.melanogaster_A4_contigbreaker/a:(w:(x:rs))	474/679	315/321	469/673	343/359	324/330	425/592	301/307	263/267	300/310	264/268
D.melanogaster_ISO1_contigbreaker/a:(w:(x:on))	1542/2284	1167/1168	1522/2261	1274/1305	1228/1229	1313/1845	935/936	747/748	947/972	742/743
Minghui63_contigbreaker/a:(w:(x:cc))	682/1369	350/416	670/1342	485/1100	336/400	643/1302	341/397	316/369	471/1054	312/364