

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_fragment_correction_steps/s/"genome": "C.elegans", "assembler": "wtdbg2": "cli_arguments": "-x": "rs" /report.tex
- data/reports/A.thaliana_fragment_correction_steps/s/"genome": "A.thaliana", "assembler": "wtdbg2": "cli_arguments": "-x": "sq" /report.tex
- data/reports/D.melanogaster_A4_fragment_correction_steps/s/"genome": "D.melanogaster_A4", "assembler": "wtdbg2": "cli_arguments": "-x": "rs" /report.tex
- data/reports/D.melanogaster_ISO1_fragment_correction_steps/s/"genome": "D.melanogaster_ISO1", "assembler": "wtdbg2": "cli_arguments": "-x": "ont" /report.tex

Table 1: EA50max

EA50max/Strict EA50max	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	971911/650482	1009589/624411	1016174/604113	1039067/607788	1016095/606908	1016095/606913	970869/624411	948612/624411	948612/624411	1017769/624411	1011711/624411
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	6062701/2398686	6062825/2804941	5669385/2530232	6233906/2530232	6233929/2812297	6233923/2812297	6062531/2804944	6062720/2804940	6062686/2804938	6062697/2804938	6062667/2804945
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	8262222/2417890	8259734/2255136	7981461/3009244	7675726/3009244	9635945/2511290	9635945/2511292	8259533/2267454	8259528/2267455	8259486/2252381	8259515/2267456	8259515/2255138
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	2291499/227130	2726439/223482	3738521/231903	3738355/231335	3738342/231336	3738504/230762	3737854/231396	2938829/230572	2725615/221212	2725157/222720	2723511/221982

Table 2: EA75max

EA75max/Strict EA75max	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	536597/312849	557590/310064	595108/312233	595108/313527	594335/310064	595108/312233	577422/312742	557590/310064	557590/310064	557590/312233	557590/310064
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	2161036/673960	2161072/678387	2739973/678421	2746240/678367	2746202/678367	2740008/678370	2161046/673960	2161065/678387	2161100/678387	2161107/678387	2161032/678387
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	2255114/926524	2109319/953072	4199774/953023	4199772/989418	4200744/989415	4200744/989414	2109321/989417	2109319/989413	2109317/989413	2109314/989414	2109320/953072
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	613729/54773	613735/54115	667578/57539	693083/57844	693082/57666	693086/57542	693179/55802	613735/55119	613735/54669	613735/52841	613735/54660

Table 3: EAmeanmax

EAmeanmax/Strict EAmeanmax	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	1237230/724335	1280753/688368	1290563/683290	1295720/688045	1270344/679663	1270555/680533	1241533/692545	1234130/690506	1234048/690420	1280812/689024	1280768/688357
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	6014893/2813653	6015760/3015649	6000017/2891511	6331344/2892230	6366028/3017156	6365405/3017170	5915296/3008751	6015863/2950717	6015708/2950643	6016135/3014739	6016134/3014739
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	11373739/3625907	11316007/3507122	7460979/2953111	7710543/2963000	9735993/2966579	9733738/3007361	11321137/3589508	11321863/3552811	11390843/3540060	11316861/3889673	11389536/3507233
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	3678925/320688	3703616/312117	3914836/348842	3997918/348776	3957815/336522	3957345/335801	3974820/345151	3699980/331384	3695452/327203	3703510/332223	3704477/326309

Table 4: P5k

P5k/Strict P5k	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	0.962/0.961	0.965/0.964	0.967/0.966	0.967/0.966	0.966/0.965	0.966/0.965	0.966/0.965	0.965/0.964	0.965/0.964	0.965/0.964	0.965/0.964
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	0.946/0.945	0.946/0.945	0.948/0.947	0.948/0.946	0.948/0.946	0.947/0.945	0.946/0.945	0.946/0.945	0.946/0.945	0.946/0.945	0.946/0.945
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	0.901/0.899	0.903/0.901	0.904/0.902	0.904/0.902	0.904/0.902	0.903/0.901	0.903/0.901	0.903/0.901	0.903/0.901	0.903/0.901	0.903/0.901
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	0.847/0.841	0.846/0.840	0.850/0.843	0.850/0.843	0.849/0.843	0.849/0.842	0.849/0.843	0.847/0.841	0.846/0.840	0.846/0.840	0.846/0.840

Table 5: P10k

P10k/Strict P10k	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	0.960/0.959	0.963/0.962	0.965/0.963	0.965/0.963	0.964/0.963	0.964/0.963	0.964/0.962	0.963/0.962	0.963/0.962	0.963/0.962	0.963/0.962
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	0.945/0.943	0.945/0.943	0.946/0.943	0.946/0.943	0.945/0.943	0.945/0.943	0.945/0.943	0.945/0.943	0.945/0.943	0.945/0.943	0.945/0.943
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	0.899/0.896	0.901/0.898	0.903/0.900	0.903/0.900	0.902/0.899	0.902/0.899	0.902/0.899	0.902/0.899	0.901/0.899	0.901/0.899	0.901/0.898
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	0.843/0.831	0.842/0.830	0.848/0.835	0.848/0.835	0.847/0.834	0.846/0.833	0.846/0.833	0.844/0.832	0.843/0.831	0.843/0.830	0.843/0.831

Table 6: P15k

P15k/Strict P15k	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	0.957/0.955	0.960/0.958	0.962/0.960	0.962/0.960	0.961/0.959	0.962/0.960	0.961/0.959	0.961/0.959	0.960/0.958	0.960/0.958	0.960/0.958
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	0.943/0.941	0.944/0.941	0.944/0.942	0.944/0.942	0.944/0.941	0.944/0.941	0.944/0.941	0.944/0.941	0.944/0.941	0.944/0.941	0.944/0.941
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	0.897/0.893	0.900/0.896	0.901/0.897	0.901/0.897	0.901/0.896	0.900/0.896	0.900/0.896	0.900/0.896	0.900/0.896	0.900/0.896	0.900/0.896
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	0.842/0.823	0.841/0.821	0.846/0.826	0.846/0.826	0.845/0.825	0.845/0.824	0.845/0.825	0.843/0.823	0.842/0.822	0.841/0.821	0.841/0.821

Table 7: P20k

P20k/Strict P20k	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	0.954/0.952	0.958/0.956	0.960/0.957	0.960/0.957	0.959/0.956	0.959/0.957	0.959/0.956	0.958/0.956	0.958/0.956	0.958/0.956	0.958/0.956
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	0.943/0.939	0.943/0.939	0.944/0.940	0.944/0.940	0.943/0.939	0.943/0.939	0.943/0.940	0.943/0.939	0.943/0.939	0.943/0.939	0.943/0.939
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	0.896/0.890	0.898/0.892	0.901/0.894	0.901/0.894	0.900/0.894	0.900/0.893	0.898/0.893	0.898/0.893	0.898/0.893	0.898/0.892	0.898/0.892
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	0.840/0.813	0.839/0.811	0.845/0.816	0.845/0.817	0.844/0.815	0.843/0.816	0.843/0.815	0.841/0.813	0.840/0.812	0.839/0.811	0.839/0.812

Table 8: EAmearmax and unique misassemblies

EAmearmax/unique mis	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	1237230/79	1280753/85	1290563/117	1295720/116	1270344/110	1270555/111	1241533/94	1234130/92	1234048/91	1280812/87	1280768/85
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	6014893/52	6015760/61	6000017/92	6331344/99	6366028/89	6365405/86	5915296/67	6015863/61	6015708/61	6016135/61	6016134/61
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	11373739/164	11316007/167	7460979/238	7710543/237	9735993/235	9733738/227	11321137/180	11321863/168	11390843/168	11316861/170	11389536/167
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	3678925/120	3703616/123	3914836/241	3997918/247	3957815/231	3957345/223	3974820/172	3699980/159	3695452/131	3703510/125	3704477/123

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

unique/total ext. mis.	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	79/80	85/97	117/203	116/207	110/153	111/153	94/116	92/107	91/105	87/101	85/97
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	52/53	61/63	92/141	99/144	89/114	86/116	67/71	61/63	61/63	61/63	61/63
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	164/166	167/174	238/448	237/448	235/404	227/375	180/221	168/178	168/177	170/180	167/174
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	120/120	123/128	241/421	247/448	231/355	223/343	172/210	159/187	131/134	125/130	123/128

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

unique/total loc. mis.	wtdbg2	w2 frg1 YV	w2 frg2 YV	w2 frg3 YV	w2 frg4 YV	w2 frg5 YV	w2 frg6 YV	w2 frg7 YV	w2 frg8 YV	w2 frg9 YV	w2 frg10 YV
C.elegans_fragment_correction_steps/a:(w:(x:rs))	153/153	168/180	214/406	215/403	198/281	200/281	181/214	174/195	174/195	168/182	168/180
A.thaliana_fragment_correction_steps/a:(w:(x:sq))	246/251	252/257	388/564	372/536	320/389	303/375	265/277	253/258	253/258	253/258	253/258
D.melanogaster_A4_fragment_correction_steps/a:(w:(x:rs))	324/330	345/361	578/979	565/956	473/771	445/704	372/460	354/393	353/386	351/375	345/363
D.melanogaster_ISO1_fragment_correction_steps/a:(w:(x:on))	1228/1229	1278/1309	1917/4057	1907/4126	1690/3181	1674/3126	1430/2044	1411/1767	1283/1320	1285/1318	1265/1296