Table S2. Six *Drosophila* species with sperm tails of extremely different length have comparable genome sizes

Species	Fluorescence intensity (mean ± s.e.m.)	DNA content (Mb) (mean ± s.e.m.)	Previous DNA content estimates (Mb)		
			Bosco et al., 2007		Others
			PI (mean ± s.e.m.)	DAPI (mean ± s.e.m.)	BC, CY, KI
D. bifurca (*n*=33)	126 ± 4	197 ± 6	-	-	-
D. hydei (*n*=24)	144 ± 5	226 ± 8	164 ± 16	177 ± 22	197 -246
D. nannoptera (*n*=39)	138 ± 3	217 ± 5	-	236 ±35	-
D. melanogaster (*n*=41)	124 ± 3	**195** ± 5	201 ± 16	**195** ± 10	176-180
D. pseudoobscura (*n*=14)	146 ± 6	230 ± 10	185 ± 12	135 ±6	168
D. persimilis (*n*=29)	143 ± 4	226 ± 6	183 ± 10	170 ± 34	197

G. Bosco et al. have previously estimated the genome size (Mb) of 26 *Drosophila* species, including *D. persimilis, D. pseudoobscura, D melanogaster, D. nannoptera* and *D. hydei* but not *D.bifurca*. To estimate the DNA content in the six *Drosophila* species studied here, we measured the fluorescence intensity of DAPI-stained brain cell nuclei using the Metamorph software. We selected the 30% of nuclei showing the highest fluorescence intensities, assuming that these nuclei were in the late S–G2 phase of the cell cycle; the numbers between brackets indicate the number of selected nuclei. We then calculated the mean nuclear fluorescence intensity and the standard error (s.e.m.) for each species. Using as a standard the DNA content value (Mb) obtained by Bosco et al. for *D. melanogaster* using DAPI staining (195 Mb), we estimated the DNA content of all species including *D. bifurca*. "Previous estimates" refer to those of Bosco et al., obtained by flow cytometry of nuclei stained either by propidium iodide (PI) or DAPI, and to estimates obtained before Bosco's study (others). The latter values were obtained through biochemical analysis (BC), cytometry (CY), or kinetics (KI); references for these estimates can be found in table 3 of Bosco et al. (2007).