

## TABLES

**TABLE 1**

Cell Line	X:A	Y:A	Gene Expression Levels (FPKM)				Splicing events (PSI)	
			roX1	roX2	msl-2	traF	tra <i>female</i>	Sxl <i>female</i>
Kc167	0.94	0.00	0.41	1.17	1.94	9.04	0.22	1.00
1182-4H	0.95	0.00	5.19	0.11	3.75	16.67	0.52	0.96
D8	1.01	0.00	0.77	0.22	3.64	7.99	0.35	0.87
D16-c3	0.87	0.00	2.88	0.00	5.94	16.75	0.38	0.71
D17-c3	0.84	0.00	0.23	0.13	6.79	6.93	0.74	0.56
D9	0.86	0.00	66.98	8.82	14.34	6.35	0.87	0.14
D4-c1	0.56	0.00	70.44	1.48	10.18	0.32	0.99	0.25
BG3-c2	0.56	0.63	0.16	29.65	19.79	0.54	1.00	0.00
Cl.8	0.50	0.34	212.07	38.37	20.95	0.54	1.00	0.00
D20-c5	0.53	0.00	19.06	4.94	11.13	0.00	1.00	0.00
L1	0.54	0.00	96.50	7.73	24.10	0.00	1.00	0.00
mbn2	0.61	0.00	156.02	11.54	22.64	0.00	1.00	0.00
S2-DRSC	0.55	0.01	8.17	51.43	16.08	0.00	1.00	0.00
S2R	0.68	0.00	0.00	29.60	13.27	0.48	1.00	0.00
S3	0.53	0.00	6.13	11.42	18.75	0.00	1.00	0.00
Sg4	0.54	0.00	106.46	18.82	29.44	0.00	1.00	0.00
W2	0.55	0.04	60.20	2.99	12.93	1.65	1.00	0.00
S1	0.52	0.24	198.00	1.05	18.26	0.00	1.00	NA

**Table 1. Sex-determination of Drosophila cell lines based on DNA and RNA sequencing.** X chromosome, or Y chromosome to Autosome ratio (DNA amount), expression levels of sex-specific genes, and quantified levels splicing events are summarized. Red and Blue shades indicate male or female characteristics, respectively, that are determined based on RNA-Seq analyses of 100 different fly lines (whole animals,  $p < 0.05$ , one sampled t-test). Expression levels are FPKM values. Please note that we used not the whole Y chromosome, but a 5 kb region with no obvious repeats (chrYHet:140,000-145,000) to avoid the mappability issue. PSI : Proportion Spliced In. *D20-c5* cell line : 0.53 for X:A, 0 for Y:A ratios (no RNA-Seq result). The table is sorted based on the splicing event.