

Table S1. Percentage of monoallelic, biallelic and nonscorable nuclei measured by RNA FISH

Gene	Stage	<i>n</i> *	Percent biallelicism (nuclei per embryo; mean \pm s.d.)	Percent monoallelicism (nuclei per embryo; mean \pm s.d.)	Percent nonscorable (nuclei per embryo; mean \pm s.d.)	<i>P</i> -value [†] (difference in observed nonscorable)	<i>P</i> -value [‡] (difference between early and mid-stage ICMs)
<i>Ube1x</i>	Early	14	23 \pm 13	65 \pm 19	12 \pm 20	0.97	8.735×10^{-6}
	Mid	7	47 \pm 10	39 \pm 11	11 \pm 14		
<i>Mecp2</i>	Early	15	18 \pm 15	60 \pm 14	22 \pm 18	0.94	1.563×10^{-10}
	Mid	20	44 \pm 13	37 \pm 18	18 \pm 20		
<i>Abcb7</i>	Early	9	14 \pm 12	75 \pm 8	10 \pm 7	0.66	9.587×10^{-10}
	Mid	7	54 \pm 12	37 \pm 11	9 \pm 11		
<i>Rnf12</i>	Early	8	7 \pm 8	75 \pm 23	16 \pm 22	0.44	1.825×10^{-7}
	Mid	20	36 \pm 23	55 \pm 27	9 \pm 15		
<i>Atp7a</i>	Early	7	8 \pm 5	76 \pm 13	16 \pm 16	0.78	2.235×10^{-7}
	Mid	10	36 \pm 13	44 \pm 15	20 \pm 16		

*The number of female ICMs.

[†]*P* values were calculated using a binomial exact test. The null hypothesis is that for each X-linked gene analyzed, the number of nonscorable nuclei is the same between early and mid-stage ICMs. We reject the null hypothesis when *P*<0.01. In all cases examined, failure to reject the null hypothesis indicates that the number of nonscorable nuclei is not statistically different between early and mid-stage ICMs.

[‡]Fisher's exact test was used to calculate *P* values. The null hypothesis is that the average percentage of biallelic and monoallelic nuclei is the same between early and mid-stage ICMs. We reject the null hypothesis if *P*<0.01 indicating in all cases there is a statistically significant difference between average percentage of biallelic and monoallelic nuclei between early and mid-stage ICMs.