

**Table S2 Comparison with Kristensen et al gene lists**

	Number of probe sets in the Kristensen et al. list	Correspondences in our platform	Expressed in this experiment	<i>Inb</i> effects OBS	<i>Inb</i> effects EXP	<i>Inb</i> same dir. OBS	<i>Inb</i> same dir. EXP	<i>Dep</i> effects OBS	<i>Dep</i> effects EXP	<i>Dep</i> same dir. OBS	<i>Dep</i> same dir. EXP
Fast+	60	38	35	14	14.70	13	9.8	4	5.60	2	2.80
Fast-	13	15	11	4	4.62	3	1.2	4	1.76	2	1.20
Slow+	113	76	69	42	28.98	32	29.4	12	11.4	5	8.40
Slow-	41	20	19	7	7.98	4	2.1	4	3.04	3	1.20
Joint+	9	9	8	5	3.36	4	3.5	3	1.28	2	2.10
Joint-	12	12	12	9	5.04	8	2.7	2	1.92	1	0.60
25 <sup>a</sup> +	5	5	5	3	2.10	2	2.1	2	0.80	1	1.40
25 <sup>a</sup> -	7	7	7	5	2.94	1	1.5	1	1.12	0	0.3
Total	<b>260</b>	<b>182</b>	<b>166</b>	<b>89</b>	<b>69.72</b>	<b>67</b>	<b>52.3</b>	<b>32</b>	<b>26.92</b>	<b>16</b>	<b>18</b>
$\chi^2$ (7 d.f.)				5.09, P = 0.649		9.53, P = 0.217		5.73, P = 0.572		5.96, P = 0.544	

*Inb* and *Dep* effects for the probe sets listed as SAM-selected in the Fast and Slow inbreeding treatments and the Joint analysis in Kristensen et al. [2005] and in the 25°C treatment in Kristensen et al. [2006]. Plus and minus signs indicate over and down regulated probe sets in the inbred samples, respectively. Because their results correspond to the older Affymetrix Drosophila Genome Array Version 1, we show the number of equivalent probe sets in our Version 2 Array (note that the equivalences were not one to one); of these, the number expressed in the current experiment; the number of *Inb* or *Dep* significant, and the number showing these effects in the same direction. The expected numbers of probe sets showing *Inb* and *Dep* effects were calculated as: number of Kristensen et al.'s SAM-selected probe sets expressed in our experiment × our overall proportion of probe sets showing *Inb* or *Dep* effects (0.42 and 0.16). The expected counts in the same direction were calculated as: number of expressed probe sets showing *Inb* or *Dep* effects × overall proportion of up or down regulated genes in our experiment (0.7 and 0.3 for *Inb* and 0.41 and 0.59 for *Dep*).